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Mite Diet Sequences Obtained by High Throughput Sequencing of Gut Contents of Freshly Collected Water Mites

Adrian Amelio Vasquez
Wayne State University, adrian.amelio.vasquez@gmail.com

Obadeh Mohiddin
Wayne State University School Of Medicine

Zeyu Li
Wayne State University, zeyuli@wayne.edu

Brittany L. Bonnici
Wayne State University, eh5829@wayne.edu

Katherine Gurdziel
Wayne State University, gurdziel@wayne.edu

See next page for additional authors

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Authors

Adrian Amelio Vasquez, Obadeh Mohiddin, Zeyu Li, Brittany L. Bonnici, Katherine Gurdziel, and Jeffrey L. Ram

Mite Diet Sequences Obtained by High Throughput Sequencing of Gut Contents of Freshly Collected Water Mites

By Adrian A. Vasquez[1,2], Obadeh Mohiddin[3], Zeyu Li[3], Brittany L. Bonnici[3],Katherine Gurdziel[4], and Jeffrey L. Ram[3]
[1]Cooperative Institute for Great Lakes Research, School for Environment and Sustainability, University of Michigan, Ann Arbor, MI
[2]Healthy Urban Waters, Department of Civil and Environmental Engineering, Wayne State University, Detroit, MI
[3]Department of Physiology, Wayne State University School of Medicine, Detroit, MI
[4]Genome Sciences Core, Wayne State University, Detroit, MI

Cytochrome oxidase subunit I (COI) barcode sequences in this file were obtained from gut DNA extracted from 54 freshly collected water mites, comprising 21 *Lebertia quinquemaculosa* , 30 *Lebertia davidcooki* , 1 *Limnesia* , and 2 *Arrenurus* specimens. Methods and other details about these sequences are described in a paper by the same authors in a submitted publication (2021: URL to be given here when published). Data on collection locations, primers (mLep and LCOI), amino acid translations, etc. are included in corresponding sequences uploaded to GenBank. The right column below contains additional notes on naming the taxa of the sequences that were not included in the GenBank annotation. These notes include the highest percentage identity to a previous sequence in GenBank as determined by BLASTN in June 2018. The FASTA file name given here includes the Accession ID, followed by the best match taxon (at an appropriate taxonomic level, dependent on the percent identity, as described in the notes in the right-hand column), the phrase "water mite diet isolate", a specific RamLab sequence identifier of the sequence, and then the COI gene description. Accession IDs of sequences uploaded to GenBank begin with MW; other sequences begin with RL and a RamLab sequence identifier. The RamLab sequence identifier in the FASTA name includes information as follows: RamLab ID number-location and date of collection with three location letters (e.g., BHL stands for Blue Heron Lagoon) and the date usually in a 6-character format of MMDDYY-information on the location of sequence on the Illunina sequencing plate-and a 4- to 6-character identifier of the mite species (Lq=*L. quinquemaculosa* ; Ldc=*L. davidcooki* ; Lim=*Limnesia* ; Arr=*Arrenurus*) and the animal number in that series of experiments (2 digits).

Sequence in FASTA format	Percent identity to GenBank used to name the taxon
>MW605229 Ablabesmyia sp. water mite diet isolate 2342-BHL072216-GBD10364_7984-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTATACTTTATTTTCGGAGCTTGATCTGGAATAGTCGGAACTTCTTTAAGTATATTAATCCGTGCAGAATTAGGACACCCGGGAACTTTAATCGGAGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGTGGATTTGGTAATTGACTAGTACCCCTTATACTAGGAGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTACTACCCCCTTCTTTAACCTTACTATTATCTAGCTCTATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR624095, identified in GenBank as Ablabesmyia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605230 Amphichaeta raptisae water mite diet isolate 1896-BHL022317-GBD5321_8225-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTATTTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCTTTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTTTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605231 Amphichaeta raptisae water mite diet isolate 1966-BHL022317-GBD15392_15256-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAATAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTTGTTACTGCACATGCTTTTTTAATAATTTTTTTCATAGTAATACCAGTTTTAATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGAGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAACTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605232 Amphichaeta raptisae water mite diet isolate 1976-BHL022317-GBD28051_17165-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGAACAGGAACAAGACTATTAATTCGAATTGAATTAACACATCCAGGAGCATTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGACTAAATAATATAAGAT	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 -
>MW605233 Amphichaeta raptisae water mite diet isolate 3606-BHL032417-GBD23321_25173-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTATTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGTTTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGAGTTTGACTATTAGCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAGATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605234 Amphichaeta raptisae water mite diet isolate 4057-BHL032417-GBD21503_24710-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAATACTATTAATTCGCATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATAAAAGATATTGACTATTACCCCCATCACTAAATCGATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605235 Amphichaeta raptisae water mite diet isolate 4141-BHL032417-GBD23772_16607-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCATGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTACTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAGTTGAATTCTAGCTTTAATACTTGTGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW605236 Amphichaeta raptisae water mite diet isolate 4494-BHL032417-GBD16091_27897-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACTATTAAATAATAAAAGATTTTGACTATTATCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAA	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605237 Amphichaeta raptisae water mite diet isolate 4557-BHL032417-GBD8274_10892-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGATCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAAACCAACTATATAATACCTTAGTTACTGCACAAGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605238 Amphichaeta raptisae water mite diet isolate 4598-BHL032417-GBD6397_6142-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGATTATGAGCAGGAATAGTTGGTACAGGCACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCATAGTAATACCAGTTTTTATTGGAGGATTTGGAAGTTGAATTCTACCTTTAATACTTGGAGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605239 Amphichaeta raptisae water mite diet isolate 4860-BHL032417-GBD19485_21216-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTCTGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAACCTTTTTAGGAGGAGACCAACTATATAATACCTTAGTTACTGCTCATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATATTTGGGGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605240 Amphichaeta raptisae water mite diet isolate 4954-BHL032417-GBD13720_19923-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605241 Amphichaeta raptisae water mite diet isolate 6169-BHL032417-GBD22501_6326-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTGGAGCCTGATCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATCCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCTCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605242 Amphichaeta raptisae water mite diet isolate 6365-BHL032417-GBD13583_13475-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACTGCAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTTTATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCATAGTAATACCAATTTTTATTGGAGGATTTGGAAACTGAATTATACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAACTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605243 Amphichaeta raptisae water mite diet isolate 8858-BHL101416-GBD15966_10107-Lq60 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605244 Amphichaeta raptisae water mite diet isolate 9593-BHL032417-GBD14391_5569-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGGATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATGCCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCGCCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605245 Amphichaeta raptisae water mite diet isolate 9765-BHL040517-GBD25510_5628-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGGATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGAGTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW605246 Amphichaeta raptisae water mite diet isolate 9898-BHL040517-GBD20081_7808-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACAAACTGTATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTTGAGGGTTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGCTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605247 Amphichaeta raptisae water mite diet isolate 9949-BHL040517-GBD13887_3781-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAGTTAACCCATCCTGGAGCCTTTTTGTGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605248 Amphichaeta raptisae water mite diet isolate 9972-BHL040517-GBD12864_8941-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAACCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGAGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAACTCTACTAGTTGCAACGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605249 Amphichaeta raptisae water mite diet isolate 10035-BHL040517-GBD27572_12633-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGAATTGAATTAACCCACCCTGGAGCCTTTTTAGGTAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCGGATATAGCATTCCCACGAGTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605250 Amphichaeta raptisae water mite diet isolate 10061-BHL040517-GBD26250_15059-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATACTGGATCCTTTTTAGGAAGAGACCAACTATATAATCCCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATGTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605251 Amphichaeta raptisae water mite diet isolate 10116-BHL040517-GBD15671_5485-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAAGTCGGATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGTATCGGCTGCAGTAGAAACTGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605252 Amphichaeta raptisae water mite diet isolate 10217-BHL040517-GBD25730_20523-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTGTTGAATTAACACATCCTGGAGCCTTTTTAGGAAGAGACCAACTTTATAATACCTTTGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGAGCACCTGATATAGCATTCCCACGAGTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605253 Amphichaeta raptisae water mite diet isolate 10244-BHL040517-GBD15251_19684-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTGTTGAATTAACCCATCCTGGAGCCTTTTTAGGACGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGTGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTGGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605254 Amphichaeta raptisae water mite diet isolate 10254-BHL040517-GBD19730_2897-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCATTCTTAGGAAGAGATCAACTATATAATACCCTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGAGCACCAGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATCCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605255 Amphichaeta raptisae water mite diet isolate 10371-BHL040517-GBD19020_20822-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTAATTGGAGGATTTGGAAATTGAATTCTACCTTTAATAATTGGGGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAACTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW605256 Amphichaeta raptisae water mite diet isolate 10374-BHL040517-GBD25872_16697-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATATTTGTTACAGGAACAAGACTATTAATTCGTATTGAATTACCACATCCTGGAGCCTTTTTAGGAAGAGACCAACTATTTAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATGCTATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605257 Amphichaeta raptisae water mite diet isolate 10379-BHL040517-GBD18923_2734-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAATAAGACTATTAATTCGAATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTAATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATACAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCAGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605258 Amphichaeta raptisae water mite diet isolate 10400-BHL040517-GBD24919_5343-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTATAGGAAGAGACCAACTTTATAATACCATAGTTACTGCACATGCATTTTTAATAATTTTTTTCATAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTCAATACTTGGAGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAAATCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605259 Amphichaeta raptisae water mite diet isolate 10412-BHL040517-GBD26900_11832-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGAACAGCAACAAGACTATTAATTCGTATTGAATTAACACAACCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATGCCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605260 Amphichaeta raptisae water mite diet isolate 10455-BHL040517-GBD13291_26509-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCAACCTGGAGCATTTCTAGGAAGAGACCAACTATATAATATCTTAGTAACTGCACATGCATTTTTAATAATTTTTTTCCTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605261 Amphichaeta raptisae water mite diet isolate 10475-BHL040517-GBD15314_27077-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTGGAGCTTGATCTGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605262 Amphichaeta raptisae water mite diet isolate 10476-BHL040517-GBD23744_6301-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTTTGAGCAGGAATAGTTGGTACTGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGGACAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGAGTTTGACTATTACCCCCATCACTAATTCTATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605263 Amphichaeta raptisae water mite diet isolate 10500-BHL040517-GBD22917_21053-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACTAGACTACTAATTCGAATTGAATTATCCCATCCTGGAGCCTTCTTAGGAAGAGATCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTCTAATACTTGGAGCACCTGATATAGCATTCCCACGACTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605264 Amphichaeta raptisae water mite diet isolate 10502-BHL040517-GBD27013_20295-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGGGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTATTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAACAATATAAGAGTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCAACGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605265 Amphichaeta raptisae water mite diet isolate 10531-BHL040517-GBD10625_19126-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGATTATGAGCAGGAATAGTTGGTACTGGAACTAGACTATTAATTCGAATTGAGTTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW605266 Amphichaeta raptisae water mite diet isolate 10535-BHL040517-GBD27949_9908-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAATAAGACTATTAATTCGAATTGAATTAACCCAACCTGGAACCTTTTTAGGAGAAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605267 Amphichaeta raptisae water mite diet isolate 10546-BHL040517-GBD11544_24352-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGATACAGGGACAAGACTATTAATTCGTATTGAATTATCCCATCCAGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCCTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGTATCGGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605268 Amphichaeta raptisae water mite diet isolate 10561-BHL040517-GBD28062_9463-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACTGGAACAAGAATATTAATTCGTATTGAATTAAAACATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCATAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605269 Amphichaeta raptisae water mite diet isolate 10562-BHL040517-GBD25068_10558-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGAACAGGAACAAGACTATTAATTCGTATTGAATTAACACATCCAGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCATAGTTACTGCACATGCTTTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCAACACTAATTCTATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605270 Amphichaeta raptisae water mite diet isolate 10633-BHL040517-GBD3897_14494-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGATCAGGAATAGTTGGTACTTGAACAAGACTATTAATTCGTATTGAATTAGCCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCACCATCTCTAATTCTATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605271 Amphichaeta raptisae water mite diet isolate 10657-BHL040517-GBD18581_28826-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGGAGTATGAGCAGGAATAGTTGGTACAGGAACTAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCGTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGTGGCACCTGATATAGCATTCCCACGACTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605272 Amphichaeta raptisae water mite diet isolate 12581-BHL040517-GBD23466_12101-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACACATCATGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAGTTGAATTCTACCTTTAATACTTGGGGCATCTGATATAACATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605273 Amphichaeta sp. water mite diet isolate 4660-BHL032417-GBD24430_16652-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTTGTTACTGCACATGCATTTTTAATATTTTTTTTCATAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATATTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTGCCCCCATCACTAACTCTATTAGTAGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605274 Amphichaeta sp. water mite diet isolate 4837-BHL032417-GBD26144_24667-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTTTATAATACCTTTGTTACTGCACATGCATTTTTAATAATTTTTTTCATAGTAATACCAGTTTTAATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTAGGAGTTGCAACGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605275 Amphichaeta sp. water mite diet isolate 4851-BHL032417-GBD24175_20657-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTCGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCTTTTTTAATAATTTTTTTCATAGTAATACCAATTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAACCCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW605276 Amphichaeta sp. water mite diet isolate 4865-BHL032417-GBD10832_21719-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTTGTTACTGCACATGCATTTTTAATAATTTTTTTCATAGTAATACCAGTTTTAATTGGAGGATTTGGAAATTGAATACTACCTTTAATACTTGGTGCACCAGATATAGCATTCCCACGAATAAATAATATAAGATCTTGACTATTACCCCCATCACTAACTCTATTAGTTGCATCGGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605277 Amphichaeta sp. water mite diet isolate 4893-BHL032417-GBD26677_10906-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGTGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGAATTTGACTATTACCCCCAACACTAATTCGATTAGGAGCATCGGCTGCAGTAGAAAATGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605278 Amphichaeta sp. water mite diet isolate 4948-BHL032417-GBD24088_10205-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGATCAAGACTATTAATTCGTATTGAATTAAACCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGACACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCTCTAATTCTATTAGTTGCATCGGCAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605279 Amphichaeta sp. water mite diet isolate 4990-BHL032417-GBD17012_7189-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAACACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605280 Amphichaeta sp. water mite diet isolate 5280-BHL032417-GBD12512_10940-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGATCAGGAATAGTTGGTACATGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTTGTTACTGCACATGCATTTTTAATAATTTTTTTCATAGTAATACCAGTTTTAATTGGAGGATTTGGAAATTGAATACTACCTTTAATACTTGGTGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACAAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605281 Amphichaeta sp. water mite diet isolate 5355-BHL032417-GBD22594_18433-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACTGGATCAAGACTATTAATTCGTATTGAATTAAACCATCCTGGAACCTTTTTAGGAAGAGATCAAATATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCATAGTAATACCAGTTTTAATTGGAGGATTTGGAAATTGAATTCTACCTCTAATACTTGGGGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.7% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605282 Amphichaeta sp. water mite diet isolate 5363-BHL032417-GBD21749_17457-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGATCATTTTTAGGAAGAGATCAACTATATAATACCCTAGTTACTGCACATGCATTTTTAATAATTTTTTTCCTAGTAACACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGAGCACCAGATATAGCATTCCCACGACTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATCCTACTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605283 Amphichaeta sp. water mite diet isolate 5374-BHL032417-GBD15830_25939-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTTTGAGCTGGAATAGTTGGAACAGGAACTAGAATATTAATTCGTATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACCTTAGTTACTGCACATGCATTCTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGAGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTTCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605284 Amphichaeta sp. water mite diet isolate 5506-BHL032417-GBD27233_8465-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCATAGTAACACCAGTTTTAATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGAGCACCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTATTACCCCCATCATTAACACTATTAGTTGCATCAGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605285 Amphichaeta sp. water mite diet isolate 5625-BHL032417-GBD6016_16489-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGTATTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW605286 Amphichaeta sp. water mite diet isolate 5684-BHL032417-GBD22540_16155-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGAGCCTTTTTAGGAAGAGATCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGGAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACAATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605287 Amphichaeta sp. water mite diet isolate 8488-BHL101416-GBD16784_4033-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTCTGACTACTACCACCTTCACTAATCATATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605288 Amphichaeta sp. water mite diet isolate 8493-BHL101416-GBD9292_7979-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGAGCACCAGATATGGCCTTCCCACGACTTAACAATTTAAGATTTTGACTTCTACCACCTTCACTAATCCTACTAGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605289 Amphichaeta sp. water mite diet isolate 8673-BHL101416-GBD5587_14204-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTGGAGCTTGATCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGACTTTTTAGGAAGAGATCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTGCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGTGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCTCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605290 Amphichaeta sp. water mite diet isolate 8796-BHL101416-GBD26728_11856-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCTACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCATCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605291 Amphichaeta sp. water mite diet isolate 9918-BHL040517-GBD12089_5187-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGTGACCAACTATATAATACCATTGTTACTGCACATGCATTCTTAATAATTTTTTTCATAGTAATACCAGTTTTAATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605292 Amphichaeta sp. water mite diet isolate 10038-BHL040517-GBD13305_4984-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGACTAGTTGGTACAGGAACAAGACTATTAATTCGAATTGAATTAACCCATCCTGGAGCCTTTATAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCATAGTAATACCAGTTTTAATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTCCCCCCATCACTAATTCTATTAGTTTTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605293 Amphichaeta sp. water mite diet isolate 10048-BHL040517-GBD24542_12908-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGATCAGGAATAGTGGGAACTTCCCCAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.7% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605294 Amphichaeta sp. water mite diet isolate 10108-BHL040517-GBD19639_5543-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCTCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.4% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605295 Amphichaeta sp. water mite diet isolate 10126-BHL040517-GBD18423_9105-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGATCAGGAATAGTTGGTACAGTAACAAGACTATTAATTCGTATTGTATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGTGTCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGTATCGGCGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW605296 Amphichaeta sp. water mite diet isolate 10148-BHL040517-GBD22617_22847-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACTGGTACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGTAGAGACCAACTTTATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTAATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGGCTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605297 Amphichaeta sp. water mite diet isolate 10150-BHL040517-GBD18012_26782-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605298 Amphichaeta sp. water mite diet isolate 10167-BHL040517-GBD11365_4531-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGCACAAGACTATTAATTCGTATTGAATTCACCCAACCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCCTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCAGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTACTACCCCCATCACTAATCCTATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605299 Amphichaeta sp. water mite diet isolate 10229-BHL040517-GBD6998_23924-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTGGAGTATGAGCAGGAATAGTTGGTACTGGATTAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTATAGGAAGAGACCAACTATATAATACCTTTGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATATTTGGGGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605300 Amphichaeta sp. water mite diet isolate 10315-BHL040517-GBD9475_23599-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGCATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGAAGAAATAATATAAGATTATGACTATTACCCCCAGCACTAAAACTATTAGTGGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605301 Amphichaeta sp. water mite diet isolate 10319-BHL040517-GBD19943_19330-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACTGGATCAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAAATTTATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGTGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAACTCTATTAGTTGCAACGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.7% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605302 Amphichaeta sp. water mite diet isolate 10347-BHL040517-GBD4002_8176-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACTAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATGATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGAATAAAAAATATAAGATATTGACTAGTTCCCCCAGCACTAATACTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605303 Amphichaeta sp. water mite diet isolate 10388-BHL040517-GBD3958_11179-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAGACCATCCTGGATCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTAATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCTCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTAGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605304 Amphichaeta sp. water mite diet isolate 10398-BHL040517-GBD11202_24434-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACATGAACAAGACTATTAATTCGTATCGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAATTATATAATGCCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCATAGTAATACCAATTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAAATCTATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605305 Amphichaeta sp. water mite diet isolate 10406-BHL040517-GBD15579_24868-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAATAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATATCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGAGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGACAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW605306 Amphichaeta sp. water mite diet isolate 10424-BHL040517-GBD24549_15183-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAAGCCATCCTGGAACATTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAATTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATATTTGGTGCACCTGATATAGCAATCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605307 Amphichaeta sp. water mite diet isolate 10485-BHL040517-GBD24731_6514-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAAATATATAATACCTTAGTTACCGCACATGCATTTTTAATAATTTTTTTCTTAGGAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTAGGACACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605308 Amphichaeta sp. water mite diet isolate 10548-BHL040517-GBD17620_1965-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGCAACAAGACTATTAATTCGCATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTTTATAATACCCTAGTTACTGCTCATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTAATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTGAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605309 Amphichaeta sp. water mite diet isolate 10553-BHL040517-GBD8444_13663-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTAGGTACTGGATCAAGACTATTAATTCGTATTAAATTAACCCATCCTGGAGCCTTTTTAGGAGGAGACCAACTTTATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATATTTGGGGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTACTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605310 Amphichaeta sp. water mite diet isolate 10589-BHL040517-GBD29410_15863-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGAATATTAATTCGTATTGAATTAACCCATCCTGGAGCATTTTTAGGAAGAGACCAACTATATAATACATTTGTTACTGCACATGCATTTTTAATAATTTTTTTCTCAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCCCGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAACTCTATTAGTTGCATCGGCTACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605311 Amphichaeta sp. water mite diet isolate 10594-BHL040517-GBD2008_17107-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGAACAGGATCAAGACTATTAATTCGTATTGAATTAGCCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACATTAGTTACTGCACATGCATTTTTAATAATTTTTTTCATAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAACCCTATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605312 Amphichaeta sp. water mite diet isolate 10629-BHL040517-GBD11651_5792-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGAACAGGAACTAGACTATTAATTCGGATTGAGTTAACCCATCCTGGAGCCTTTCTAGGAAGAGACCAACTATATAATACCCTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGAGCACCAGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAGTTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605313 Amphichaeta sp. water mite diet isolate 10640-BHL040517-GBD24468_20122-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGATCAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAAAGACCAACTATATAATACCATTGTTACTGCACATGCATTTTTAATAATTTTTTTCATAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTAGGGGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAACCCTATTAGTAGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.7% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605314 Amphichaeta sp. water mite diet isolate 10648-BHL040517-GBD26339_17400-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGAACTGGATCAAGACTACTAATTCGTATTGAATTAACCCATCCTGGAGCATTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGAATGAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605315 Amphichaeta sp. water mite diet isolate 10682-BHL040517-GBD20140_10599-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGATCAAGACTATTAATTCGTATTGAATTAACCCATCCTGGATCCTTTTTAGGAAGAGACCAACTATATATTACATTTGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTAATTGGAGGATTTGGAAATTGAATACTACCTTTAATACTTGGAGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAACTCTATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW605316 Amphichaeta sp. water mite diet isolate 12127-BHL040517-GBD16784_4033-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTCTGACTACTACCACCTTCACTAATCATATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605317 Amphichaeta sp. water mite diet isolate 12132-BHL040517-GBD9292_7979-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGAGCACCAGATATGGCCTTCCCACGACTTAACAATTTAAGATTTTGACTTCTACCACCTTCACTAATCCTACTAGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605318 Amphichaeta sp. water mite diet isolate 12312-BHL040517-GBD5587_14204-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTGGAGCTTGATCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGACTTTTTAGGAAGAGATCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTGCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGTGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCTCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605319 Amphichaeta sp. water mite diet isolate 12435-BHL040517-GBD26728_11856-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCTACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCATCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605320 Annelida sp. water mite diet isolate 1262-BHL110116-GBD22269_17990-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTTTATACTTTATTTTAGGAGTATGAGCAGGAATAATGGGAACAGCGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACATCCTAGTTACTGCACATGCATTCATAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID MT425080, identified in GenBank as Cernosvitoviella minor sensu lato. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605321 Annelida sp. water mite diet isolate 5339-BHL032417-GBD12294_28694-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATAAAGATATTGGAACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTATCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.0% identical to accession ID KM000898, identified in GenBank as Eisenia fetida. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605322 Anopheles sp. water mite diet isolate 11141-BHL110116-GBD5420_7257-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGACTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID KM389466, identified in GenBank as Anopheles sacharovi. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605323 Archisepsis sp. water mite diet isolate 1857-BHL072216-GBD22260_6451-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTAAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACACTATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID KT272843, identified in GenBank as Archisepsis discolor. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605324 Archisepsis sp. water mite diet isolate 13036-BHL040517-GBD22619_20870-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATATCTGGAGCTTGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACACTATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID KT272843, identified in GenBank as Archisepsis discolor. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605325 Archisepsis sp. water mite diet isolate 14338-BHL040517-GBD9405_23602-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGATTTCTTCCTCCTTCACTTACACTATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KT272843, identified in GenBank as Archisepsis discolor. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605326 Benthalia sp. water mite diet isolate 8911-BHL032417-GBD5333_12512-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTTATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID DQ648198, identified in GenBank as Benthalia dissidens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605327 Ceratitis sp. water mite diet isolate 14760-BHL040517-GBD10764_13424-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATTTTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTTAGAATTTTAATTCGTGCTGAATTAGGACACCCGGGTGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGATTTTGACTACTTCCTCCTTCACTTACACTATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID AY788423, identified in GenBank as Ceratitis curvata. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605328 Ceratitis sp. water mite diet isolate 14963-BHL040517-GBD26138_19278-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGTATTTTTATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAAGATAAGTTTTTGACTACTACCTCCTTCACTTACACTATTATTAGGAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID AY788423, identified in GenBank as Ceratitis curvata. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605329 Ceratitis sp. water mite diet isolate 15030-BHL040517-GBD29148_16794-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATTTTTGGAGCATGAGCGGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGAGTTGAATTAGGACACCCAGGAGCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTACTACCTCCTTCACTGACACTATTATTAGCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID AY788423, identified in GenBank as Ceratitis curvata. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605330 Ceratitis sp. water mite diet isolate 15218-BHL040517-GBD14378_28784-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTTTATTTTATTTTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGAGCTGAATTAGGACATCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCTCCTTCACTAACACTATTACTAGCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID AY788423, identified in GenBank as Ceratitis curvata. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605331 Chaetogaster diastrophus water mite diet isolate 1167-BHL110116-GBD3090_14331-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATTCTACTAATTTCATCTGCAGCAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 98.9% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605332 Chaetogaster diastrophus water mite diet isolate 1357-BHL110116-GBD18715_8840-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTTCCACCTTCACGAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.9% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605333 Chaetogaster diastrophus water mite diet isolate 1420-BHL110116-GBD13056_8582-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATTCTACTAATTTCATCTGCAGCAGTAGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.3% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605334 Chaetogaster diastrophus water mite diet isolate 1423-BHL110116-GBD7878_5479-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGACATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGCTTTGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGAATAAACAATCTAAGATTTTGACTTCTTCCACCATCACTAAGTCTACTAATATCAGCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605335 Chaetogaster diastrophus water mite diet isolate 1425-BHL110116-GBD4556_7766-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGTGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTTTTTATAGTTATACCAATATTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGAATAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATCCTACTAATATCATCTACAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW605336 Chaetogaster diastrophus water mite diet isolate 1429-BHL110116-GBD15505_8676-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATGAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTAGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGACTAAACAATCTAAGAGTTTGACTTCTTCCACCTTCACTAATTCTACCAATTTCATATGCAGCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.1% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605337 Chaetogaster diastrophus water mite diet isolate 1430-BHL110116-GBD25231_15914-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAAATTTATAATACTCTAGTAACTGCCCACGCTTTTCTAATAATTTTTTTATAGTTATACCAGTATTAATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATAGCATTCCCACGAATAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605338 Chaetogaster diastrophus water mite diet isolate 1431-BHL110116-GBD16131_27489-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCTTTTCTAGGAAGGGACCAACTATATAATATTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTATAGTTATACCAGCTTTTATTGGTGGATTTGGAAATTGAATCTTACCTTTAATACTAGGGGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.6% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605339 Chaetogaster diastrophus water mite diet isolate 1433-BHL110116-GBD6201_13898-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATATTAATTCGACTTGAATTATCTCAACCAGGCTCATTACTAGGAAGAGAGCAACTATATAATACTCTAGTAACTGCCCATTCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTACTTCCACCTTCACTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605340 Chaetogaster diastrophus water mite diet isolate 1435-BHL110116-GBD23943_10455-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAAGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTACTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTACTTCCACCTTCACTAATTCTACTAATGTCATCTACAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.4% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605341 Chaetogaster diastrophus water mite diet isolate 1436-BHL110116-GBD15011_11196-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGATCAACTATATAATACTCTAGTAACTGCCCACGCATTATTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGAGGATTCGGAAATTGAATTCTACCATTAATACTAGGAGCCCCAGATATGGCATTCCCACGACTAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.1% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605342 Chaetogaster diastrophus water mite diet isolate 1437-BHL110116-GBD29603_13995-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTTTATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTATAGTTATACCAGTATTTATTGGTGGATTAGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCACTCCCACGAATAAACAATCTAAGATTTTGACTTCTACCACCTTCACTAATTCTACTAAAATCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605343 Chaetogaster diastrophus water mite diet isolate 1440-BHL110116-GBD14693_5974-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCACTGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTATAGTTATACCAGTATTTATTGGTGGATTAGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTTCCCCCTTCGCTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605344 Chaetogaster diastrophus water mite diet isolate 1442-BHL110116-GBD28266_12781-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGACATTCCTAGGAAGAGACCAAATATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTTTTCTTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGAATTCTTCCTTTAATATTAGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTTCCACCTTCTCTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605345 Chaetogaster diastrophus water mite diet isolate 1447-BHL110116-GBD25492_6280-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTTTATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTAATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCACCAGATATGGCATTCCCTCGAATAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAACTCTACTAATTTCAACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW605346 Chaetogaster diastrophus water mite diet isolate 1448-BHL110116-GBD26316_14883-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTTGGAAAGGACCAACTATATAATACTCTAGTTACTGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGAATAAACAATCTAAGATTTTGACTACTTCCACCTTCACTAACTCTACTAATATCATCAGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605347 Chaetogaster diastrophus water mite diet isolate 1451-BHL110116-GBD8494_22843-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTTATTCGAATTGAATTATCACAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAGTACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGACCCAGATATGGCATTCCCACGATTAAACAATCCAAGATTTCGACTTCTTCCACCTTCACTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.1% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605348 Chaetogaster diastrophus water mite diet isolate 1452-BHL110116-GBD4330_11149-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACGTCGTGCACCTGCACTAAAGGGACGAATATCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.6% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605349 Chaetogaster diastrophus water mite diet isolate 1463-BHL110116-GBD9668_3910-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATCTTAATTCGAATTGAATTATCTCATCCAGGGTCATTCCTAGGAAGTGACCAACTATATAATACTCTTGTAACTGCTCACGCATTTCTAATAATTTTCTTTATAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGAATTCTACTTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605350 Chaetogaster diastrophus water mite diet isolate 1470-BHL110116-GBD15415_20469-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAATCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTATAGTTATACCAGTATTAATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATAGCATTCCCACGAATAAACAATCTAAGATTTTGACTACTTCCACCTTCACTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605351 Chaetogaster diastrophus water mite diet isolate 1476-BHL110116-GBD12802_26700-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGGATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTCTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATAGCATTCCCATGACTAAACAATTTAAGATTCTGACTACTACCACCTTCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605352 Chaetogaster diastrophus water mite diet isolate 1481-BHL110116-GBD15595_25483-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTTTATAATACTCTTGTAACTGCCCATGCATTTCTAATAATTTTCTTTATAGTTATACCAGTATTAATTGGTGGATTTGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGAATAAACAATCTAAGATTTTGACTACTTCCACCTTCACTAACTCTACTAATATCATCTGCAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605353 Chaetogaster diastrophus water mite diet isolate 1488-BHL110116-GBD20675_16065-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGAATAAACAATCAAAGATATTGACTTCGTCCACCTTCACTAAAACGACAAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605354 Chaetogaster diastrophus water mite diet isolate 1500-BHL110116-GBD12310_4737-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGATCAACTATATAATCCTCTTGTAACCGCCCACGCATTTCTAATAATTTTCTTTTTAGTGATACCAGTATTAATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTACTTCCACCTTCACTAACTCTACTAATATCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605355 Chaetogaster diastrophus water mite diet isolate 1501-BHL110116-GBD10410_4853-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGGGATCAACTATATAATACTCTAGTAACTGCCCACGCATTCCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGAATTCTACCTCTAATACTAGGAGCCCCAGATATAGCATTCCCACGACTAAACAATCTAAGATTCTGACTACTACCACCTTCACTAATCCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW605356 Chaetogaster diastrophus water mite diet isolate 1524-BHL110116-GBD19556_19907-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCCGGATCATTCCTAGGAAATGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTCTTAGTTATACCAGTATTAATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.1% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605357 Chaetogaster diastrophus water mite diet isolate 1541-BHL110116-GBD27402_10478-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTTATTCGAATTGAATTATCACAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTTACTGCCCATGCATTTCTAATAATTTTTTTTTTAGTTATACCAGTACTAATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGAATAAACAATATAAGATTTTGACTACTTCCACCTTCACTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.6% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605358 Chaetogaster diastrophus water mite diet isolate 1546-BHL110116-GBD20850_20192-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAAGGACCAAATTTATAATACTATAGTAACTGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTTTTAATTGGTGGATTCGGAAATTGAATTCTACCCTTAATACTAGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAACTCTACTAATTTCAACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605359 Chaetogaster diastrophus water mite diet isolate 1550-BHL110116-GBD28179_9455-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAACGATCAACTATATAATATTCTAGTAACTGCCCACGCATTTCTAATAATCTTCTTTTTAGTTATACCAGTATTAATTGGTGGATTCGGAAATTGAATTCTACCTTTAATATTAGGAGCCCCAGATATAGCATTCCCACGAATAAACAATCTAAGATTTTGACTTCTTTCACCTTCACTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.6% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605360 Chaetogaster diastrophus water mite diet isolate 1551-BHL110116-GBD10646_12328-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTGTCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTTGTAACTGCCCACGCATTTCTAATAATTTTCTTTATAGTTATACCAGTATATATTGGAGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGAATAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAACCCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605361 Chaetogaster diastrophus water mite diet isolate 1583-BHL110116-GBD25907_19515-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCATGGTCATTCCTAGGAAGAGACCAACTATATAATACTCTAGTTACTGCCCACGCATTTCTAATAATTTTCTTTGTAGTTATACCAGTATTTATCGGAGGATTCGGAAATTGAATGCTACCTTTACTACTAGGAGCCCCAGATATGGCATTCCCACGAATAAACAATATAAGATTTTGACTTCTTCCACCATCACTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605362 Chaetogaster diastrophus water mite diet isolate 1588-BHL110116-GBD22349_3021-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGATCAACTATATAATACTCTAGTAACTGCCCATGCATTCCTAATAATTTTCTTTATGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGACTAAACAATCTAAGATTCTGACTACTACCACCTTCACTAATTCTACTAGTTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605363 Chaetogaster diastrophus water mite diet isolate 1595-BHL110116-GBD6785_10903-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTTCCACCTTCACAAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.4% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605364 Chaetogaster diastrophus water mite diet isolate 1630-BHL110116-GBD7752_12371-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAAGGACCAACTTTATAATACTCTTGTAACTGCTCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTCATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATAGCATTCCCACGAATAAACAATCTAAGATTTTGACTTCTACCACCTTCACTAACTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605365 Chaetogaster diastrophus water mite diet isolate 1633-BHL110116-GBD16017_11298-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGTTCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTTTTGTGATACCAGGATTTATTGGTGGATTTGGAAATTGAATTCTACCTTTAATACTAGGAGTCCCAGATATGGCATTCCCACGAATAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATCCTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW605366 Chaetogaster diastrophus water mite diet isolate 1634-BHL110116-GBD18608_23741-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605367 Chaetogaster diastrophus water mite diet isolate 1676-BHL110116-GBD3739_19842-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGATTTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTGCCACCTTCACTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605368 Chaetogaster diastrophus water mite diet isolate 9333-BHL032417-GBD27700_21276-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATATTAATTCGAATTGAATTATCTCAACCAGGATCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAATTTTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCTCGAATAAACAATATAAGATTTTGACTACTTCCCCCTTCACTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605369 Chaetogaster diastrophus water mite diet isolate 10857-BHL101516-GBD5522_12460-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.3% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605370 Chaetogaster diastrophus water mite diet isolate 10913-BHL101516-GBD23849_8330-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATTCTACTAATTTCATCCGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.9% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605371 Chaetogaster diastrophus water mite diet isolate 10937-BHL101516-GBD16048_3250-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605372 Chaetogaster diastrophus water mite diet isolate 10952-BHL101516-GBD16417_22506-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTTACTGCACACGCATTTCTAATAATTTTTTTTATAGTTATACCAGTACTTATTGGTGGATTTGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGAATAAACAATCTAAGATTTTGACTACTTCCACCTTCACTAATACTACTAATATCATCTGCAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605373 Chaetogaster diastrophus water mite diet isolate 10960-BHL101516-GBD18359_22970-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCATCCACCTTCACTAATACTACTAAATTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.1% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605374 Chaetogaster diastrophus water mite diet isolate 10964-BHL101516-GBD18413_19040-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTTGTAACGGCCCACGCATTTCTAATAATTTTTTTTATAGTTATACCAGTATTAATTGGAGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGAATAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAACTCTACTAATTTCAACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605375 Chaetogaster diastrophus water mite diet isolate 10968-BHL101516-GBD11659_24085-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGATCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCACACGCATTTCTAATAATTTTCTTTCTAGTTATACCAGTATTTATTGGTGGATTTGGAAACTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGACTAAACAATCTAAGATTTTGACTACTACCACCATCTCTAATCCTACGAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW605376 Chaetogaster diastrophus water mite diet isolate 10976-BHL101516-GBD19820_20724-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTTACTGCC CACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGAGGATTTGGAAATTGAATACTACCTTTAATACTAG GAGCCCCAGATATGGCATTCCCACGAATAAACAATCTAAGATTTTGACTACTACCACCATCTCTAATTCTACTAATTTCAT CTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605377 Chaetogaster diastrophus water mite diet isolate 10983-BHL101516-GBD16132_28718-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCTTAGGAAGGGATCAACTATATAATACTCTAGTTACTGCC CACGCATTCCTAATAATTTTCTTTCTAGTTATACCAGTATTTATTGGTGGATTCGGAAATTGATTTCTACCTTTAATACTAG GAGCCCCAGATATAGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTGCCACCTTCACTAATTCTACTAATATCAT CTGCAGCAGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.6% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605378 Chaetogaster diastrophus water mite diet isolate 10984-BHL101516-GBD13391_6294-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGGAACTGCC CACGCATTTCTAATAATTTTCTTTTTAGTTAAACCAGAATTTATTGGGGGATTAGGAAAATGAATTCTACCTTTAATACTA GGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATTCTACTAATTTCA TCTGCTGCAGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605379 Chaetogaster diastrophus water mite diet isolate 10987-BHL101516-GBD4547_12821-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAAGGACCAACTATATAATACTCTAGTAACTGCC CACGCATTTATAATAATTTTCTTTTTAGTTATACCAGTATTAATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTAG GAGCCCCAGATATGGCATTCCCACGAATAAACAATCTAAGATTTTGACTTCTTCCCCCTTCACTAACTCTACTAATTTCAA CTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605380 Chaetogaster diastrophus water mite diet isolate 10996-BHL101516-GBD13976_28837-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTAAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTTGTAACTGCC CACGCATTCCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAG GAGCCCCAGACATGGCATTCCCACGAATAAACAATATAAGATTTTGACTTCTTCCCCCTTCACTAACTCTACTAATTTCAT CTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605381 Chaetogaster diastrophus water mite diet isolate 11007-BHL110116-GBD27513_21195-Lq74 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGTGACCAACTATATAATACTCTAGTAACTGCC CACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAG GAGCCCCAGATATGGCATTCCCACGAATAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATTCTACTAATATCAT CTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605382 Chaetogaster diastrophus water mite diet isolate 11421-BHL101516-GBD19449_25697-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCC CACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAG GAGCACCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTTCCCCCTTCACTAATTCTACTAATTTCAT CTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605383 Chaetogaster diastrophus water mite diet isolate 11441-BHL101516-GBD20242_8024-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCC CACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAG GAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATTCTACTAATTTCAT CTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.3% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605384 Chaetogaster diastrophus water mite diet isolate 11505-BHL101516-GBD23455_24034-Lq80 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTAAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCC CACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAG GAGCCCCAGATATGGCATTCCCACGAATAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATACTACTAATTTCAA CTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605385 Chaetogaster diastrophus water mite diet isolate 11582-BHL101516-GBD27435_9909-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAAATTTATAATACTCTAGTAACTGCC CACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTCGGAAATTGAATTCTACTTTTAATACTAG GAGCCCCAGATATGGCATTCCCACGACTAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATTCTACTAATTTCAT CTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW605386 Chaetogaster diastrophus water mite diet isolate 11799-BHL101516-GBD12254_8905-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTCGGGAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.9% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW605387 Chironomidae sp. water mite diet isolate 495-BHL040517-GBD28407_10899-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTAGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTAGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTGTAATAATTTTTTTTATACTTATACCAATCTTAAATGGAGGAATTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGTCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605388 Chironomidae sp. water mite diet isolate 499-BHL040517-GBD20114_20431-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATAATATAAGTTTTTGATTACTTCCCCTGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605389 Chironomidae sp. water mite diet isolate 512-BHL040517-GBD20629_15993-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGAATCTTGCCATTAATAATATGAGCCCCAGATATAGCTTTTCCTCGAATAAAAAAAATAAGGTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605390 Chironomidae sp. water mite diet isolate 591-BHL072216-GBD24943_14206-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGACTTGCTCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTTCTTCTTTCGAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID KR287333, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605391 Chironomidae sp. water mite diet isolate 650-BHL072216-GBD23180_7111-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGGACTTTATATTTAATTGCAGGTGCTTGGGCAGGATTAATTGGTACAGGTTTAAGTTTAATTATTCGTCTTGAGTTAGGACAACCAGGATCTCTTCTACAAGATGACCAAATTTATAATGTAGTAGTAACTGCGCATGCCTTTATTATAATTTTTTTTATGGTAATACCAATTTTAATTGGGGGTTTTGGTAATTGACTTGTGCCTTTAATATTAGGATCCCCAGACATAGCTTTTCCACGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTATTTCTTTCGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.9% identical to accession ID GU565708, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605392 Chironomidae sp. water mite diet isolate 676-BHL072216-GBD29150_17399-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTACCCCGTATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605393 Chironomidae sp. water mite diet isolate 683-BHL072216-GBD6798_7865-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGACTTTATACTTCTTATTTGCTGTTTTAGCTGGTATTGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGAAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTCATAGCTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACAGAGGTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCATCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605394 Chironomidae sp. water mite diet isolate 696-BHL072216-GBD9178_9227-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTGTATTCGGAGCCTGATCAGGTATAGTAGGTACTTCCCTTAGTATTCTAGTACGAGCTGAATTAGGACACCCCGGGGCATTAATTGGAGACGATCAAACTTATAACGTAATCGTTACAGCTCATGCCTTTGTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTACCACTAATATTAGGTGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605395 Chironomidae sp. water mite diet isolate 719-BHL072216-GBD14461_12367-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTAGTTTAATTGGAGGGTTCGGAAATTGATTAGTTCCTCTTATACTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACATCCCCCATCCCTTACCCTGCTTCTTTCAAGATCAATTGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID KM991708, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605396 Chironomidae sp. water mite diet isolate 725-BHL072216-GBD24916_14228-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATTATATTTATTTTTGGGACTTGCTCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGTACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCTCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTACTACTTTCGAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.9% identical to accession ID JF412134, identified in GenBank as Paracladopelma camptolabis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605397 Chironomidae sp. water mite diet isolate 756-BHL040916-GBD7474_24403-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCATTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605398 Chironomidae sp. water mite diet isolate 814-BHL100916-GBD26306_16073-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605399 Chironomidae sp. water mite diet isolate 852-BHL100916-GBD7886_4803-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTTCTACCCCCATCATTAACTCTTTTGCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605400 Chironomidae sp. water mite diet isolate 858-BHL100916-GBD17235_16161-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGAACATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGGAATTGATTAGTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605401 Chironomidae sp. water mite diet isolate 864-BHL100916-GBD22011_18825-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KM102730, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605402 Chironomidae sp. water mite diet isolate 875-BHL100916-GBD2506_12712-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTCTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTGCATTAACCTTACTTTTATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605403 Chironomidae sp. water mite diet isolate 878-BHL100916-GBD19959_25649-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACAAAAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTCACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCAGTAACTTTACAATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605404 Chironomidae sp. water mite diet isolate 886-BHL100916-GBD18815_16301-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACCAGAACTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTATTATTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605405 Chironomidae sp. water mite diet isolate 917-BHL100916-GBD27548_14770-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGAACTTCTTTAAGTATTTTAATTCGAGTAGAATTAGGACACCCTGGATCATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGAAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605406 Chironomidae sp. water mite diet isolate 927-BHL100916-GBD15312_10355-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAGTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGAGATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATCATTACCCCCTACATCAACCTTACATAAAGCAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605407 Chironomidae sp. water mite diet isolate 932-BHL100916-GBD24704_5559-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTCATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTACCCCCATCATTAACTCTTTTGCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605408 Chironomidae sp. water mite diet isolate 933-BHL100916-GBD25453_25334-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGATCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTATTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605409 Chironomidae sp. water mite diet isolate 946-BHL100916-GBD10473_8727-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGGGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID JF412118, identified in GenBank as Glyptotendipes tokunagai. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605410 Chironomidae sp. water mite diet isolate 951-BHL100916-GBD18907_20847-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGTCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGAGAAAGCTTTTCCGCGAATAAAAAAAAAAAGAATTTGAATATTACCCCCTTCAATAACCGTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605411 Chironomidae sp. water mite diet isolate 962-BHL100916-GBD16149_20658-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCGGGAATAGTAGGCACTTCCTTAAGAATTTTAATTCGAGTAGAATTAGGACACCCTGGCTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTCTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605412 Chironomidae sp. water mite diet isolate 967-BHL100916-GBD29648_16449-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTCGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCAGTAACCGGACGGGGAGCAAGAGCAAGAGGAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605413 Chironomidae sp. water mite diet isolate 992-BHL100916-GBD25527_22236-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGCACTTTATATTTTATTTTTGGCGCTTGATCGGGGATAGTAGGTACTTCTTTAAGTATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGTCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTACTCTCACCTTACTTCTTGCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID JF412069, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605414 Chironomidae sp. water mite diet isolate 1049-BHL100916-GBD19669_13333-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGTATTTTAATTCGACTTGAATTAGGACACCCAGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTCTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605415 Chironomidae sp. water mite diet isolate 1063-BHL100916-GBD9539_17211-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCCGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGATCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTCATAGTGATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTGATATTTGGAGCTCCTGATATAGCTCTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCCTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605416 Chironomidae sp. water mite diet isolate 1073-BHL100916-GBD14935_23966-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTCGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGAAGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGTCTCCTGATAAAGCTTTTCCGCGAATAAATAATAAAAGATTTTGAATATCACCCCCTACATTAACCTTACTTTCATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605417 Chironomidae sp. water mite diet isolate 1081-BHL100916-GBD26036_22015-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTCGGCACTTCTTTAAGTATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTGCCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605418 Chironomidae sp. water mite diet isolate 1129-BHL110116-GBD26465_8237-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605419 Chironomidae sp. water mite diet isolate 1130-BHL110116-GBD26942_7682-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCTGGTTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCATTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTATTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605420 Chironomidae sp. water mite diet isolate 1155-BHL110116-GBD14280_12811-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605421 Chironomidae sp. water mite diet isolate 1168-BHL110116-GBD15681_21843-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAAGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCATCTTTAACCCTTCCTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605422 Chironomidae sp. water mite diet isolate 1190-BHL110116-GBD21284_7853-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAAACGATCAACTTTATAATGTACTTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATATTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTCCCGCGAATAAATAATATAAGATTTTGATTATTACCACCATCACTAACCTTACTATTATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605423 Chironomidae sp. water mite diet isolate 1195-BHL110116-GBD25914_14409-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTGTATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTATTGCCCCCATCATTAACTTTATTATTATCTGGATCAATTGGGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605424 Chironomidae sp. water mite diet isolate 1204-BHL110116-GBD24154_16294-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATTATATTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGGGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGAGCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID JF412118, identified in GenBank as Glyptotendipes tokunagai. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605425 Chironomidae sp. water mite diet isolate 1209-BHL110116-GBD29470_16014-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTCGGCACTTCCTTAAGTATTTTAATTCGACTAGAATTAGGACACCCAGGATCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGTAATTGATTAGTTCCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605426 Chironomidae sp. water mite diet isolate 1216-BHL110116-GBD6281_22744-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTCGGACACCCTGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTGATATTGGGTGCTCCTGATATAGCATTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGATCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605427 Chironomidae sp. water mite diet isolate 1218-BHL110116-GBD11366_26265-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605428 Chironomidae sp. water mite diet isolate 1219-BHL110116-GBD4375_22332-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTTGAATTAGGACACCCAGGCTCATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTACTCCCCCCTTCATTAACCTTACTTCTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605429 Chironomidae sp. water mite diet isolate 1249-BHL110116-GBD21780_23273-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605430 Chironomidae sp. water mite diet isolate 1259-BHL110116-GBD16357_28114-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAACCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605431 Chironomidae sp. water mite diet isolate 1280-BHL110116-GBD13964_15595-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605432 Chironomidae sp. water mite diet isolate 1299-BHL110116-GBD9583_13868-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGACTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATGGATTAGTACCTTTGATATTAGTGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605433 Chironomidae sp. water mite diet isolate 1320-BHL110116-GBD13749_17923-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605434 Chironomidae sp. water mite diet isolate 1335-BHL110116-GBD17792_23075-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTCATCGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTACCTCTGATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCCTCATTAACCTTACTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605435 Chironomidae sp. water mite diet isolate 1337-BHL110116-GBD24470_5602-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAGTCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605436 Chironomidae sp. water mite diet isolate 1341-BHL110116-GBD18269_27492-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTAGGACACCCAGGCTCAGTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATAATAATTTTTTTATAGTGATACCAATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATCATCAAGAACAATAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605437 Chironomidae sp. water mite diet isolate 1385-BHL110116-GBD17548_22623-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTGTTATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAACTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCACTAACCTTACTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605438 Chironomidae sp. water mite diet isolate 1402-BHL110116-GBD8905_18853-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTCGGTCACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTGGGTGCTCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCTTCATTAACCTTACTATTATCAAGATCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605439 Chironomidae sp. water mite diet isolate 1445-BHL110116-GBD9152_8200-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTATAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605440 Chironomidae sp. water mite diet isolate 1461-BHL110116-GBD6347_18127-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGCACTTCTTTAAGTATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTTATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTTATGCCTATTTTAATTGGAGGTTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTACTACCCCCTTCATTAACCTTATTTTTATCAAGATCAATAGTAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605441 Chironomidae sp. water mite diet isolate 1462-BHL110116-GBD15476_23145-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605442 Chironomidae sp. water mite diet isolate 1483-BHL110116-GBD5511_14127-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGGGCTTGATCGGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGAGTAGAATTAGGACACCCAGGCTCTTTAATCGGAGACGATCAAATTTATATTGTGATTGTTATAGAAAATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605443 Chironomidae sp. water mite diet isolate 1507-BHL110116-GBD28563_13650-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCGCCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605444 Chironomidae sp. water mite diet isolate 1517-BHL110116-GBD17375_6768-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATCAATTCGAGCAGAACTTGGTCACCCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTC-ACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID KR166401, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605445 Chironomidae sp. water mite diet isolate 1529-BHL110116-GBD20803_26877-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTTATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTGGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605446 Chironomidae sp. water mite diet isolate 1537-BHL110116-GBD26092_15770-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGACTTCGGCCACCCCGGTTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCATTCCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605447 Chironomidae sp. water mite diet isolate 1575-BHL110116-GBD4723_17407-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACATGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTGATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATCATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605448 Chironomidae sp. water mite diet isolate 1586-BHL110116-GBD26343_10823-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTCGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTGATCTCTTCTTCTGTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605449 Chironomidae sp. water mite diet isolate 1589-BHL110116-GBD17141_21546-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGGGCTTGATCGGGAATAGTAGGTACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGTAGCTCCTGATATAGCTTTCCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605450 Chironomidae sp. water mite diet isolate 1590-BHL110116-GBD19510_18628-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTTAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATAGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605451 Chironomidae sp. water mite diet isolate 1600-BHL110116-GBD23030_8146-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTAATTTTAGGAGTTTGAGCAGGAATAATTGGTACAGGTACTAGAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTTGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATACAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605452 Chironomidae sp. water mite diet isolate 1612-BHL110116-GBD25955_21313-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACATCCAGGCTCATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTGTTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGGGCTCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCATCATTAACCTTACTATTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605453 Chironomidae sp. water mite diet isolate 1613-BHL110116-GBD17054_10751-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605454 Chironomidae sp. water mite diet isolate 1617-BHL110116-GBD8370_3503-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACCTGGTCACCCCGGAACTTTTCTTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCATTTCTAATAATTTTCTTTCTAGTTATACCAGTATTTATTGGTGGATTCGGAAATTGAATTCTACCTTGAATACTAGGAGCCCCAGATATGGCATTCCCACGACTAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATTCTACTAATTAC-ATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KR757074, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605455 Chironomidae sp. water mite diet isolate 1631-BHL110116-GBD21455_15024-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTTGAATTAGGACACCCAGGCTCATTTATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAATACCTTTGATATTAGGGGGTCCTGATATAGCTTTTCCGCGAATAAAAAATATAAGATTTTGATTATTACCCCCTACATTAACCTTACTTATATCAAAAACAATAGGAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605456 Chironomidae sp. water mite diet isolate 1637-BHL110116-GBD5531_19143-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCGGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGACTAGAACTCGGACACCCTGGCTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTGGGAGCTCCTGATATAGCTTTCCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605457 Chironomidae sp. water mite diet isolate 1685-BHL110116-GBD7627_10096-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTC-TAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605458 Chironomidae sp. water mite diet isolate 1768-BHL110116-GBD23457_14488-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAGTCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCAAGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605459 Chironomidae sp. water mite diet isolate 1787-BHL110116-GBD10058_16388-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTATTTTATTTTCGGGGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACAAGCAGGCTCATTCATTGGAGACGATCAAATTTATATTGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTCCCTTTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGTTTTTGATTGTTACCCCCCTCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605460 Chironomidae sp. water mite diet isolate 1792-BHL101516-GBD16225_26500-Ldc85 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTCTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGCATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605461 Chironomidae sp. water mite diet isolate 1813-BHL101516-GBD25296_7527-Ldc86 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGATTTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGTTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605462 Chironomidae sp. water mite diet isolate 1830-BHL022317-GBD22070_6313-Ldc88 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGTATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACGAATACCCCCATCCCTTAACCGTCTTCGGTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.7% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605463 Chironomidae sp. water mite diet isolate 1861-BHL072216-GBD19382_12788-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATAAAGATATTGGAACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTTTTCATAGTTATGCCTATTTTAATTGGGGGGGTTGGGAATTGATTAGTTCTCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACGATCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.6% identical to accession ID DQ648215, identified in GenBank as Kiefferulus brevibucca. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605464 Chironomidae sp. water mite diet isolate 1870-BHL022317-GBD15729_8317-Ldc89 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGTACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCTTCGAATAAATAATACAAGATTTTGATTACTTCCCCCATCCCATACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.3% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605465 Chironomidae sp. water mite diet isolate 1901-BHL022317-GBD7525_23566-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGTATGCTTATTCGGGCAGAATTAGGACGACCAGGGACATTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGTTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTAACCCTTCTTCTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.3% identical to accession ID DQ648229, identified in GenBank as Riethia stictoptera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605466 Chironomidae sp. water mite diet isolate 1908-BHL022317-GBD27523_7930-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATGATGTGATTGTAACAGCCCACGCATTTATAATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCATCCCTAACCCTACTTCTTGCAAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.3% identical to accession ID KM991708, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605467 Chironomidae sp. water mite diet isolate 1909-BHL022317-GBD13726_7168-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTTTATACTTTATTTTTGGTGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATTTATAATGTGATTGTTACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTACTTCTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.5% identical to accession ID GU944724, identified in GenBank as Chironomus circumdatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605468 Chironomidae sp. water mite diet isolate 1910-BHL022317-GBD26830_22968-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGAACCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTTACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGGTCCTCTTATACTAGTGGCTCCTGATATAGCATTCCCTCGAATAAATAATAAAAGATTTTGATTACTTCCCCCAACCCTTACCCTTCTTCTTTCAAGATCAGTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.0% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605469 Chironomidae sp. water mite diet isolate 1913-BHL022317-GBD13609_21024-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGCACATCTTTAAGAACGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACGTCCCCCATCCCTTACCCTTCTTCTGTCAAGAGCAATGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.3% identical to accession ID KR287333, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605470 Chironomidae sp. water mite diet isolate 1918-BHL022317-GBD15426_3360-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGACTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAAGTAGGACGACCCGTGACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTACTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTCCCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 89.5% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605471 Chironomidae sp. water mite diet isolate 1922-BHL022317-GBD10762_10774-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTCAACAAATCATAAAGATATTGGCACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATACTTATTCGGGCAGAATTAGGACGACCAGGGACTTTTATTGGAGATGACCAAATTTATAATGTGCTTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTTCCTCTTTCAAGAGCAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.2% identical to accession ID DQ648229, identified in GenBank as Riethia stictoptera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605472 Chironomidae sp. water mite diet isolate 1927-BHL022317-GBD27981_19342-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGTCGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTACCTCTAATACTAGGGGCTCCTGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTACTACTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.8% identical to accession ID HQ846349, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605473 Chironomidae sp. water mite diet isolate 1928-BHL022317-GBD22955_15248-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCTGGCAGATTTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATACAAGATTTTGATTACTTCCCCCATCCCTTACCCATCATCAATCAAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.4% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605474 Chironomidae sp. water mite diet isolate 1932-BHL022317-GBD28327_16795-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATACTTATTCGGGCAGAGTTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTCACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTTATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTTCTACTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.3% identical to accession ID KR287333, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605475 Chironomidae sp. water mite diet isolate 1934-BHL022317-GBD15964_25182-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACATTTATAGGAGATGACCAAATTTATAATGTGCTTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCCAATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTAACCCTACTACTTTCAAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.7% identical to accession ID KR627995, identified in GenBank as Paracladopelma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605476 Chironomidae sp. water mite diet isolate 1937-BHL022317-GBD6701_24693-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGTTCTGGAATAGTGGGAACTTCTTTAAGATTGCTTATTGGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGAAAATTGATTAGTTCCTCTTATACTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCATCCCTTACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.3% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605477 Chironomidae sp. water mite diet isolate 1938-BHL022317-GBD18899_12244-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTTACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGGAATTGATTAGTTCCTTTAATACTAGGGGCACCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCATCCCTTACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID JF412122, identified in GenBank as Glyptotendipes tokunagai. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605478 Chironomidae sp. water mite diet isolate 1939-BHL022317-GBD5824_18039-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGATCAGGAATAGTGGGAACATCCTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGAACATTTATTGGAGATGACCAAATTTATAATGTGATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTGCCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.3% identical to accession ID DQ648229, identified in GenBank as Riethia stictoptera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605479 Chironomidae sp. water mite diet isolate 1943-BHL022317-GBD25410_9095-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCTTTAAGTATGCTTATTCGGGCAGAAATAGGACGACCCGGTACTTTTATTGGAGATGACCAAATTTATAACGTGATTGTAACAGCCCATGCTTTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTAATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCGTACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.3% identical to accession ID DQ648229, identified in GenBank as Riethia stictoptera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605480 Chironomidae sp. water mite diet isolate 1948-BHL022317-GBD16659_28664-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCATGATCTGGAATAGTGGGAACAGCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACATTTATTGGAGATGACCAACTTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTAACCCTTCTAATTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.2% identical to accession ID GU944724, identified in GenBank as Chironomus circumdatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605481 Chironomidae sp. water mite diet isolate 1949-BHL022317-GBD28873_14227-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACATTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCTCACGCATTTATTATAATTTTTTTCATAGTAATACCAATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTAATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCATCCCTTACCCTACTTCGATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.8% identical to accession ID JF412134, identified in GenBank as Paracladopelma camptolabis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605482 Chironomidae sp. water mite diet isolate 1952-BHL022317-GBD22165_22510-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCTTTAATAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTAACCCTTCTTCGATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID KM991708, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605483 Chironomidae sp. water mite diet isolate 1953-BHL022317-GBD24027_11117-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGGGCAAAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGAGCTCCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGATTGCTGCCCCCATCCCTAACCCTACTACTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID KM991708, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605484 Chironomidae sp. water mite diet isolate 1956-BHL022317-GBD29321_15075-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACAACCCGGTACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCACACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTGATACTAGTGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCACTTACCCTGCTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.7% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605485 Chironomidae sp. water mite diet isolate 1962-BHL022317-GBD20768_23819-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGAGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAGGATTTTGATTACTTCCCCCATCCCTTACCCAGCTTCTTTCAAGATCAAGTGTAGAAAATGGCGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 88.9% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605486 Chironomidae sp. water mite diet isolate 1963-BHL022317-GBD16396_22305-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATTATATTTTATTTTTGGGACTTGATCTGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGTGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCCCTAACCCTTCTACTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.1% identical to accession ID JF412134, identified in GenBank as Paracladopelma camptolabis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605487 Chironomidae sp. water mite diet isolate 1964-BHL022317-GBD23894_14577-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAGCAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGAATGTGATTACGTCCCCCAGCCCTTACCCTTCTGCTTTCAAGATCAAGTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.4% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605488 Chironomidae sp. water mite diet isolate 1967-BHL022317-GBD14938_14190-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTATGACGACCCGGAACTTTTATTGGAGATGACCAGATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTAATACTAGGTGCTCCTGATACAGCATTCCCTCGAATAAATAATATAAGATCTTGATTACTTCCCCCATCCCTTACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.5% identical to accession ID JF412134, identified in GenBank as Paracladopelma camptolabis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605489 Chironomidae sp. water mite diet isolate 1968-BHL022317-GBD4288_22212-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAATGGGAACTTCTTTAAGAATGCTTATTCGGGCAGAATTCGGACGACCCGGGTCTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACCGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTAATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTACTACTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.6% identical to accession ID HQ846349, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605490 Chironomidae sp. water mite diet isolate 1970-BHL022317-GBD7332_21374-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTGTGGGACTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATCCGGGCAGAATTAGGACGACTCGGGACTTTTATTGGAGATGACCAAATTTGTAATGTGATTTTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAGATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.4% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605491 Chironomidae sp. water mite diet isolate 1972-BHL022317-GBD15276_10406-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCAACCCTAACCAAGCTTCTTTCAAGAACAAGAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.7% identical to accession ID KM991708, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605492 Chironomidae sp. water mite diet isolate 1980-BHL022317-GBD28601_11662-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTTTGAATGTTTATTCGGGTTGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAACAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCATCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.7% identical to accession ID KM991708, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605493 Chironomidae sp. water mite diet isolate 1982-BHL022317-GBD20773_20928-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGCACTTTATATTTTATTTTTGGGGCTTGATCTGGAATAGTTGGAACTTCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTTCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTTCTTCTTTCAAAATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.8% identical to accession ID JF412134, identified in GenBank as Paracladopelma camptolabis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605494 Chironomidae sp. water mite diet isolate 1983-BHL022317-GBD16356_3055-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCATGACTTTTATTGGAGATGACCAAATTTATAATGTCATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCCTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCATCCCTTACCCTTCTTCTTTCAAGATCAATTGTAGCAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID KM991708, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605495 Chironomidae sp. water mite diet isolate 1986-BHL022317-GBD16951_11904-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGGTCTGGAATAGTGGAAACCTCTTTAAGAATGCCTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAGATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTACTTCTTTCAAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.4% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605496 Chironomidae sp. water mite diet isolate 1994-BHL022317-GBD9005_10440-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACTGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCACTTATACTAGGGGCTCCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGATTACTACCCCCATCCCTTACCCTACTTCCTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID JF286707, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605497 Chironomidae sp. water mite diet isolate 1996-BHL022317-GBD10899_11712-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATCATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTAATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTTTAATACTGGGGGCACCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTACTTCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.1% identical to accession ID JF412134, identified in GenBank as Paracladopelma camptolabis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605498 Chironomidae sp. water mite diet isolate 1998-BHL022317-GBD26169_12203-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGTCAGAATTAGGACGACCCGGGACTTTTCTTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCAAGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAAATGGAGGCTTCGGAAATTGATTAGTTCCTCGTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTACTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.7% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605499 Chironomidae sp. water mite diet isolate 2000-BHL022317-GBD7835_10088-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGTACTTCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCTGGGACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTTTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCATCCCTTACCCTTCTTCTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID JF412134, identified in GenBank as Paracladopelma camptolabis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605500 Chironomidae sp. water mite diet isolate 2002-BHL022317-GBD14287_22859-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCCCTTATACTTGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTCTGATTACTACCCCCCTCCCTTACCCTTCTTCTTTCAAGATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID KR287333, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605501 Chironomidae sp. water mite diet isolate 2003-BHL022317-GBD16309_9538-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAACACCTATTTTAATTGGGGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCTTCGAATAAATAATATAAGATTGTGATTACGGCCCCCATCCCTTACCCATCATAAAGCAAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.5% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605502 Chironomidae sp. water mite diet isolate 2004-BHL022317-GBD10342_15007-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTGTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGTGGCTCCTGATATAGCATTCTCTCGAATAAATAATATAAGAATTTGATTACTTCCCCCATCCCTTGCCCTACTGCTTTCAAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.4% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605503 Chironomidae sp. water mite diet isolate 2005-BHL022317-GBD14293_5185-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTCTATTTTTGGGGCTTGATCAGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGTGACTTTTATTGGATATGACCAAATTTATAATGTGATTGTAACAGCCCACTCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGTGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTTCTTCTTTCAAGATCACTTGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 89.5% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605504 Chironomidae sp. water mite diet isolate 2006-BHL022317-GBD25915_17641-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAATTTCTTTATGAATGCTTATTCGGGCAGAATTAGGACGACTCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTAATACTAGGAACTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCAGCCCTTACCCTTCTACTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.2% identical to accession ID JF412134, identified in GenBank as Paracladopelma camptolabis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605505 Chironomidae sp. water mite diet isolate 2009-BHL022317-GBD21100_23509-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGACTTGATCTGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTTGGAAAATGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCATCCCTAACCCTTCTTCTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID KM991708, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605506 Chironomidae sp. water mite diet isolate 2010-BHL022317-GBD4159_20976-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTGTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCTTCGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCATTAACATTATTATTAGCAAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.2% identical to accession ID HQ846349, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605507 Chironomidae sp. water mite diet isolate 2012-BHL022317-GBD14823_21503-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTAACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGGGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCATCCCTTACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.1% identical to accession ID GU944724, identified in GenBank as Chironomus circumdatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605508 Chironomidae sp. water mite diet isolate 2013-BHL022317-GBD19515_27578-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGTGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGACCACGCATTTATGATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAAGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTTCTACTTTCAAAATCAATTGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 88.9% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605509 Chironomidae sp. water mite diet isolate 2015-BHL022317-GBD28409_13081-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGCATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCACACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAGATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCGTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID KR287333, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605510 Chironomidae sp. water mite diet isolate 2016-BHL022317-GBD5385_16785-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGACTTGATCTGAAATAGTGGGAACATCTTTAAGAATGTTTATTCGGGCAGAATTAGGACGACCCGGGACCTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATGTAAGATTTTGATTACTTCCCCCATCCCTTACCCTTCTTCTTTCAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.4% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605511 Chironomidae sp. water mite diet isolate 2017-BHL022317-GBD28666_13819-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTTAGTATGCTTATTCGGGCAAAATTAGGACTACCCGGGAATTTTTTTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAAATTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID DQ648229, identified in GenBank as Riethia stictoptera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605512 Chironomidae sp. water mite diet isolate 2018-BHL022317-GBD6942_16877-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGACTTGATCTGGAATAGTGGGAACACCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCAGGGACATTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGTGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGAGTACTTCCCCCATCCCTTACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID KM991708, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605513 Chironomidae sp. water mite diet isolate 2020-BHL022317-GBD24565_24065-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAAGTGGAGGATTCGGAAATTGATTAGTTCCTCTTATACTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCATACCCTTTTACTTTCAAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID KM991708, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605514 Chironomidae sp. water mite diet isolate 2025-BHL022317-GBD4590_15067-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTCGGAAATTGATTAGTTCCTCTGATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAACAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTACTTTCATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.3% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605515 Chironomidae sp. water mite diet isolate 2028-BHL022317-GBD6867_19847-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGGACATTTATTGGAGATGACCAAATTTATAATGTGATTGTTACAGCCCATGCTTTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCATCCCATACCCTTCTTCTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.9% identical to accession ID DQ648229, identified in GenBank as Riethia stictoptera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605516 Chironomidae sp. water mite diet isolate 2029-BHL022317-GBD11036_21227-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCGGAATTAGGACGACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGACTAGTTCCCCTAATACTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTCTGATTTCCTCCCCCATCCCTTACCCTTCTTCTTTCAAGATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID JF412134, identified in GenBank as Paracladopelma camptolabis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605517 Chironomidae sp. water mite diet isolate 2030-BHL022317-GBD20728_28295-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGTACTTTTATTGGAAATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAACTGATTAGTTCCTCTTATACTAGTGACACCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.7% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605518 Chironomidae sp. water mite diet isolate 2032-BHL022317-GBD4641_9374-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACAACCAGGGACATTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTCTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGAGCTCCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTACTTCTTTCAAGAGCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.0% identical to accession ID KM991708, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605519 Chironomidae sp. water mite diet isolate 2037-BHL022317-GBD13851_4544-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATGATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGTGACTTTTATTGGAGATGACCATATTTATAATGGGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGCAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCTTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCCTACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGCGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 88.2% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605520 Chironomidae sp. water mite diet isolate 2038-BHL022317-GBD11809_23059-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGCACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCAATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGAGGCTCCTGATATAGCATTCCATAGAATAAATAATATAAGAGTTTGATTACTTCCCCCATCCCATACCCTGCTACTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID HQ846349, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605521 Chironomidae sp. water mite diet isolate 2039-BHL022317-GBD10870_2678-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTCAACAAATCATAAAGATATTGGAACTCTTTACTTTGTTTTTGGAGCATGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.0% identical to accession ID DQ648229, identified in GenBank as Riethia stictoptera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605522 Chironomidae sp. water mite diet isolate 2042-BHL022317-GBD19917_24402-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAAGAAATAAAATAAGAAATTGATTACATCCCCCAGCCCCTACCCGACTTCTGTCAAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.5% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605523 Chironomidae sp. water mite diet isolate 2044-BHL022317-GBD20070_16967-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGTGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGAATTTTATTGGAGATGACCAAATTTATAATGTGTCTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGTGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTACTTCTTTCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.7% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605524 Chironomidae sp. water mite diet isolate 2045-BHL022317-GBD16225_17771-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGATCTGGAGTAGTGGGAACTTCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGGTTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGACTAGTTCCTCTTATACTAGGAGCTCCTGATATAGCATTCCCTCGAACAAATAGTATAAGATTTTGATTATTTCCCCCATCCCTTACCCTTCTTCTTTCAAGATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.2% identical to accession ID JF412134, identified in GenBank as Paracladopelma camptolabis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605525 Chironomidae sp. water mite diet isolate 2047-BHL022317-GBD28436_15314-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACATCCTTAAGAATGCTTATTCGGGCAGAATTAGGACTACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCTCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTCTTATACTAGGGACTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCACTAACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.8% identical to accession ID JF412121, identified in GenBank as Glyptotendipes tokunagai. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605526 Chironomidae sp. water mite diet isolate 2049-BHL022317-GBD5298_12542-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTTGGGGCCTGATCTGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCTCATGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGTGCTCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACCTCCCCCATCCCTTACCCTTCTTCTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KM991708, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605527 Chironomidae sp. water mite diet isolate 2050-BHL022317-GBD27112_9811-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGACATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATATTAATACCTATTTTAATTGGAGGTTTCGGAAATTGATTAGTTCCTCTTATACTAGTGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCATCTTCTTTCAAAATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.0% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605528 Chironomidae sp. water mite diet isolate 2054-BHL022317-GBD25998_19853-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGGACTTGATCTGGAATAGTGGGTACATCTTTTAGAATGCTTATTCGGGCATCATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTTACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCGTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.3% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605529 Chironomidae sp. water mite diet isolate 2055-BHL022317-GBD29549_15754-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACAGCCAACGCATTTATTATAATTTTTTTCATAGTAATACCTAGTTTAATTGGAGGTTTTGGAAATTGATTAGTTCCTCTAATACTAGGTGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATGCCTTACTCATCTTCTTTCAAGATCAATTGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605530 Chironomidae sp. water mite diet isolate 2057-BHL022317-GBD14698_16103-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACTTCTTTAAGAATTCTTATTCGGGCAGAATTAGGACGCCCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACCGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGGTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTACTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID KR494970, identified in GenBank as Paracladopelma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605531 Chironomidae sp. water mite diet isolate 2060-BHL022317-GBD23006_10897-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGGGCAGAATTAGGACATCCCGGCACATTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTGTTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGTGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTACTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.2% identical to accession ID GU565721, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605532 Chironomidae sp. water mite diet isolate 2071-BHL072216-GBD21114_9728-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATCGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTGCCACCTTCTCTTACCTTATTACTTTTGGTTGGAAGGGCA---GTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605533 Chironomidae sp. water mite diet isolate 2075-BHL072216-GBD1947_17634-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATTATATTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGGGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTGCTTCCCCCTTCTTTAACTC-TCTTACTTCCAGTTGGTAGGGCTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.2% identical to accession ID JF412118, identified in GenBank as Glyptotendipes tokunagai. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605534 Chironomidae sp. water mite diet isolate 2088-BHL072216-GBD10688_4537-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTTCTTCTTTCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KR285214, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605535 Chironomidae sp. water mite diet isolate 2098-BHL072216-GBD17407_16403-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTCCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID KR288116, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605536 Chironomidae sp. water mite diet isolate 2105-BHL072216-GBD20477_4966-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTATTGCCTCTTATACTCGGGGCTCCCGACATAGCCTTTCCTCGAATAAATAACATGAGATTCTGATTGCTTCCCCCATCTATTTCTTTACTTCTTTCTAGATCAATTGCTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.0% identical to accession ID KR966081, identified in GenBank as Tanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605537 Chironomidae sp. water mite diet isolate 2111-BHL072216-GBD10561_4643-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATAACCAAATCTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTTATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605538 Chironomidae sp. water mite diet isolate 2114-BHL072216-GBD25717_22391-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGTAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTAATTGGTGACTACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGTCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAGCAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.6% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605539 Chironomidae sp. water mite diet isolate 2118-BHL072216-GBD20203_5682-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCT-TTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM991192, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605540 Chironomidae sp. water mite diet isolate 2125-BHL072216-GBD15328_7846-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605541 Chironomidae sp. water mite diet isolate 2131-BHL072216-GBD13417_10860-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTCCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID KR638998, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605542 Chironomidae sp. water mite diet isolate 2139-BHL072216-GBD10317_15260-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGGCATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTCCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR287756, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605543 Chironomidae sp. water mite diet isolate 2140-BHL072216-GBD13392_16392-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGGCATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605544 Chironomidae sp. water mite diet isolate 2142-BHL072216-GBD4604_12119-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR638998, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605545 Chironomidae sp. water mite diet isolate 2145-BHL072216-GBD10633_11193-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACACTATATTTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605546 Chironomidae sp. water mite diet isolate 2151-BHL072216-GBD22352_15021-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGGCATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605547 Chironomidae sp. water mite diet isolate 2167-BHL072216-GBD11653_4532-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGGGGCTTTGGGAATTGATTAGTTCCCCTAATATTAGGAGCACCAGATACGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTACCTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KX051982, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605548 Chironomidae sp. water mite diet isolate 2169-BHL072216-GBD25402_10254-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTCATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGTTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTGCAGCTCATGCTTTTGTAATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTT-CTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KM991192, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605549 Chironomidae sp. water mite diet isolate 2173-BHL072216-GBD15091_28865-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACGCCCAGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTCAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTGCCACCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KP041078, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605550 Chironomidae sp. water mite diet isolate 2179-BHL072216-GBD23905_20588-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGCACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGAGCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGAGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAATAATATAAGCTTCTGACTACTTCCCCCTTCTTTAACTCTCTTACTATCTAGATCAATAGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.3% identical to accession ID DQ648215, identified in GenBank as Kiefferulus brevibucca. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605551 Chironomidae sp. water mite diet isolate 2180-BHL072216-GBD16236_25706-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGTGCATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605552 Chironomidae sp. water mite diet isolate 2182-BHL072216-GBD9808_17063-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGGCATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTAATACCTATTTTAATTGGGGGCTTTGGAAATTGATTATTGCCTCTTATACTCGGGGCTCCCGACATAGCCTTTCCTCGAATAAATAACATGAGATTCTGATTACTTCCCCCATCTATTTCTTTACTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605553 Chironomidae sp. water mite diet isolate 2185-BHL072216-GBD15657_9564-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGCGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGGCATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605554 Chironomidae sp. water mite diet isolate 2191-BHL072216-GBD20249_26091-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGTTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACTTTATTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605555 Chironomidae sp. water mite diet isolate 2202-BHL072216-GBD16900_12273-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCA---GTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KM993864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605556 Chironomidae sp. water mite diet isolate 2206-BHL072216-GBD8146_20039-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACGTTATATTTTATTTTAGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGGGCTGAATTAGGACATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTCGTTACATCACATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605557 Chironomidae sp. water mite diet isolate 2208-BHL072216-GBD23331_16005-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTATTATAATTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTACCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605558 Chironomidae sp. water mite diet isolate 2210-BHL072216-GBD4778_14962-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGCTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTTTACCACCCTCTTTAACTCTTTTACTTTCAAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605559 Chironomidae sp. water mite diet isolate 2215-BHL072216-GBD19210_3016-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACCTTATACTTTATTTTCGGAGCTTGATCTGGAATAGTCGGAACTTCTTTAAGTATATTAATTCGAGCAGAACTAGGACACCCTGGAACTTTAATCGGAGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCATTTATTATAATTTTTTTATAGTGATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTCTTCTTCTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605560 Chironomidae sp. water mite diet isolate 2218-BHL072216-GBD7765_8129-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTCCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTGCCACCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605561 Chironomidae sp. water mite diet isolate 2224-BHL072216-GBD6032_10302-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGGCATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTTTAATTGGGGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605562 Chironomidae sp. water mite diet isolate 2229-BHL072216-GBD17422_16540-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTAGGACGCCCAGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTATGGTTATGCCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KP049657, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605563 Chironomidae sp. water mite diet isolate 2235-BHL072216-GBD6374_14365-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATAAAGATATTGGAACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGAGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCGTTCCCGCGAATAAATAATATAAGCTTCTGACTTCTTCCCCCTTCTTGAACGCGCTTACTTACTAGATCAATTGTCGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.3% identical to accession ID DQ648215, identified in GenBank as Kiefferulus brevibucca. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605564 Chironomidae sp. water mite diet isolate 2237-BHL072216-GBD13265_24842-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGGCATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAGTAATATAAGTTTTTGACTTTTACCACCCTCTTTAACTCTTTTACTTTCAAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605565 Chironomidae sp. water mite diet isolate 2239-BHL072216-GBD22475_10650-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACGCCCAGGTACTTTTATTGGTGATGATCAATTTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAATAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KP049657, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605566 Chironomidae sp. water mite diet isolate 2248-BHL072216-GBD26378_21383-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KT604449, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605567 Chironomidae sp. water mite diet isolate 2250-BHL072216-GBD28233_9550-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTATACTTTATTTTCGGAGCTTGATCTGGAATAGTCGGAACTTCTTTAAGTATATTAATCCGTGCAGAATTAGGACACCCGGGAACTTTAATCGGAGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR638998, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605568 Chironomidae sp. water mite diet isolate 2264-BHL072216-GBD1919_14301-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGGCGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGGGGCTTTGGGAATTGATTAGTTCCCCTAATATTAGGAGCACCAGATACGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605569 Chironomidae sp. water mite diet isolate 2270-BHL072216-GBD21789_26579-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGTCCAGGAACTTTTATTGGAGATGACCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATGGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTGCCACCTTCTCTTAC-CTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR281212, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605570 Chironomidae sp. water mite diet isolate 2271-BHL072216-GBD19003_11753-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAGGAATATTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCCTCTTCTTTCTAGTTCTAATGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR647156, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605571 Chironomidae sp. water mite diet isolate 2272-BHL072216-GBD27840_18500-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATGGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATGGCCTTCCCGCGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR287035, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605572 Chironomidae sp. water mite diet isolate 2281-BHL072216-GBD19149_24196-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATCGGGGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KM993864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605573 Chironomidae sp. water mite diet isolate 2284-BHL072216-GBD18830_21310-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR287035, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605574 Chironomidae sp. water mite diet isolate 2289-BHL072216-GBD14452_13328-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACACTTTATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACATCTTTAAGTATACTTATTCGTGCAGAATTAGGTCATCCAGGCACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCCCATGCTTTTATCATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAGTAAATAATATAAGTTTTTGATTATTGCCACCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID GU565719, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605575 Chironomidae sp. water mite diet isolate 2292-BHL072216-GBD17270_18255-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTTATGGTTATGCCTATTTTAGTTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTTTACCACCCTCTTTAACTCTTTTACTTTCAAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR287756, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605576 Chironomidae sp. water mite diet isolate 2298-BHL072216-GBD25056_20126-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACGCCCAGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCGCCGTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR274005, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605577 Chironomidae sp. water mite diet isolate 2302-BHL072216-GBD19063_14146-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAGAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605578 Chironomidae sp. water mite diet isolate 2312-BHL072216-GBD28044_12239-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTACTTTTGTAGCCTGAGCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTTATTGCTATAACTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCACTCGAATAAATAATATAAGTTTTTGATTATTGCCACCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605579 Chironomidae sp. water mite diet isolate 2315-BHL072216-GBD19564_5733-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACCTATTCGAGCTGAATTAGGGCATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTTCTTCTTTCTAGATCAATTGTAGAGAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR285214, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605580 Chironomidae sp. water mite diet isolate 2317-BHL072216-GBD17544_27399-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATAAAGATATTGGAACCTTATACTTTATTTTCGGAGCTTGATCTGGAATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGAGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAATAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID DQ648215, identified in GenBank as Kiefferulus brevibucca. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605581 Chironomidae sp. water mite diet isolate 2323-BHL072216-GBD26315_21949-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACCCTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGTACCCCCCTTAGTATCCTTATTCGTACAGAATTGGGTCACCCAGGAGCATTAATTGGAGACGATCAAATCTATAATGTAATTGTAACGGCACATGCTTTTGTTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTGCCACCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KR284737, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605582 Chironomidae sp. water mite diet isolate 2332-BHL072216-GBD25765_8725-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGTTTATTCGAGCAGAATTAGGACGAACTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTTATAGTTATGCCTATTTTAATTGGGGGCTTTGGGAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTTCTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAATAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605583 Chironomidae sp. water mite diet isolate 2336-BHL072216-GBD3532_9409-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATTGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGGATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KM991192, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605584 Chironomidae sp. water mite diet isolate 2337-BHL072216-GBD4037_18376-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACACTTTATTTTATTTTTGGAGCTTGATCTGGTATAGTATGTACATCTTTAAGTATACTTATTCGTGCAGAATTAGGTCATCCAGGCACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCCCATGCTTTTATCATAATTTTTTTTATAGTTATACCTATCTTAATTGGTGGCTTTGTTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATGACCCCCCTCTTTAACTCTACTTTTGGTTGGAAGGGCA---GTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID GU565716, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605585 Chironomidae sp. water mite diet isolate 2349-BHL072216-GBD26535_15561-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAATAATATGAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.9% identical to accession ID KT251040, identified in GenBank as Polypedilum vanderplanki. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605586 Chironomidae sp. water mite diet isolate 2352-BHL072216-GBD10837_16455-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATAAAGATATTGGAACATTATATTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACTACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTTTTCATAGTTATGCCTATTTTAATTGGAGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAATAATATCAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACATTCTAGATCAATAGTCGAAAATGGCGCCGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.9% identical to accession ID DQ648215, identified in GenBank as Kiefferulus brevibucca. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605587 Chironomidae sp. water mite diet isolate 2362-BHL072216-GBD26464_11654-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGTACCTCCCTTAGTATCCTTATTCGTACAGAATTCGGTCACCCAGGATCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTAACGGCACATGCTTTTGTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGTGGATTTGGTAATTGACTAGTACCCCTTATACTAGGAGCCCCAGATATAGCATTTCCACGAATAAATAATAAAAGATTTTGATTATTACCACCATCACTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KP043430, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605588 Chironomidae sp. water mite diet isolate 2364-BHL072216-GBD24370_9076-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGTACCTCCCTTAGTATCCTTATTCGTACAGAATTAGGTCACCCAGGAGCTTTAATTGGAGACGATCAAATCTATAATGTAATTGTAACGGCACATGCTTTTGTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGTGGATTTGGTAATTGGTTATTACCACTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID KP043430, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605589 Chironomidae sp. water mite diet isolate 2367-BHL072216-GBD7168_22408-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATAAAGATATTGGAACATTATATTTATTTTTGGAGCCTGATCAGGCATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTTTTCATAGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCCCTAATGTTAGGAGCACCCGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTGCTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID DQ648215, identified in GenBank as Kiefferulus brevibucca. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605590 Chironomidae sp. water mite diet isolate 2381-BHL072216-GBD26322_12570-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGCACATTATATTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTTTTCATAGTTATGCCTATTTTAATTGGGGGCTTTGGGAATTGAATAGTTCCCCTAATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCATCTTTAACTCTCTTACTATCTAGAAGAATAGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.2% identical to accession ID JF412118, identified in GenBank as Glyptotendipes tokunagai. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605591 Chironomidae sp. water mite diet isolate 2385-BHL072216-GBD9188_24057-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTGCCACCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605592 Chironomidae sp. water mite diet isolate 2386-BHL072216-GBD28308_15667-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATTATATTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACACCCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTGTCATAATTTTTTTCATAGTTATGCCTATTTTAATTGGGGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCATTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCGTCTTTAACTCTCTTACTATCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.2% identical to accession ID JF412118, identified in GenBank as Glyptotendipes tokunagai. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605593 Chironomidae sp. water mite diet isolate 2403-BHL072216-GBD25427_21296-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTAATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTAACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.4% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605594 Chironomidae sp. water mite diet isolate 2408-BHL072216-GBD26703_23534-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATCCGAGCTGATTTAGGGCAGTGTGGCAGACTTATTGGTGATGACCATATTTATAATGTTATTGTAACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATAAAAGTTTTTGATTATTACCTCCTTCTCATACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605595 Chironomidae sp. water mite diet isolate 2412-BHL072216-GBD26155_12635-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATCTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTACTACTATCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605596 Chironomidae sp. water mite diet isolate 2413-BHL072216-GBD5127_6877-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCAGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGTGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAATAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID KX051982, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605597 Chironomidae sp. water mite diet isolate 2417-BHL072216-GBD10148_5623-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACACTATATTTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGTGGATTTGGTAATTGACTAGTACCCCTTATACTAGGAGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTACTACCCCCTTCTTTAACCTTACTATTATCTAGCTCTATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID MF826164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605598 Chironomidae sp. water mite diet isolate 2419-BHL072216-GBD25727_13914-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGACAGGAACTTTTATTGGAGATGACCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR281212, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605599 Chironomidae sp. water mite diet isolate 2426-BHL072216-GBD14197_28604-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATTATATTTTATTTTTGGAGCCTGATCGGGTATAGTCGGAACTTCTTTAAGCATGTTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTTTTCATAGTTATGCCTATTTTAATTGGGGGCTTTGGGAATTGATTAGTTCCCCTAATATTAGGAGCCCCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTATTACTATCTAGATCACTTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID JF412118, identified in GenBank as Glyptotendipes tokunagai. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605600 Chironomidae sp. water mite diet isolate 2429-BHL072216-GBD21192_2638-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTCAATTCGAGCTGAATTAGGGCATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605601 Chironomidae sp. water mite diet isolate 2430-BHL072216-GBD6379_14383-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATAAAGATATTGGAACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGAGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGAACCAGATATGGCTTTCCCGCGAATAAATAATATAAGCTTCTGACTTCATACCCCTTCTTTAACACTCTGACGGTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.0% identical to accession ID DQ648215, identified in GenBank as Kiefferulus brevibucca. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605602 Chironomidae sp. water mite diet isolate 2432-BHL072216-GBD17640_25979-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGCACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATCATAATTTTCTTCATAGTTATACCTATTTTAATTGGGGGCTTTGGGAATTGATTAGTTCCCCTAATATTAGGAGCACCAGATATAGCTTTCCCGCGAATAAACAATAAAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACAAACTAGATCAATTGTCGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.2% identical to accession ID JF412122, identified in GenBank as Glyptotendipes tokunagai. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605603 Chironomidae sp. water mite diet isolate 2447-BHL072216-GBD8125_16905-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATAAAGATATTGGAACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACTTCTTTAAGCATGCTTATTCGAGCAAAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATCATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAATTGATTAGTTCCCCTAATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATAGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID DQ648215, identified in GenBank as Kiefferulus brevibucca. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605604 Chironomidae sp. water mite diet isolate 2448-BHL072216-GBD3355_9056-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGACGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTGTTTTAATTGGAGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAATAATATAAGTTTTTGATTATTGCCACCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID KY846150, identified in GenBank as Kiefferulus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605605 Chironomidae sp. water mite diet isolate 2454-BHL072216-GBD11051_26336-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGTTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACCCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM991192, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605606 Chironomidae sp. water mite diet isolate 2455-BHL072216-GBD12333_28913-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACGCCCAGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGGGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTGCTGACTTCTTCCCCCTTCTTTAACCCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KP049657, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605607 Chironomidae sp. water mite diet isolate 2462-BHL072216-GBD3856_8723-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGTAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCATCATTAACCTTATTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605608 Chironomidae sp. water mite diet isolate 2464-BHL072216-GBD7656_6982-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGACGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTT-CTTTCTAGTTCGATCGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605609 Chironomidae sp. water mite diet isolate 2467-BHL072216-GBD21092_2967-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGGGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACGTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.0% identical to accession ID KR279055, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605610 Chironomidae sp. water mite diet isolate 2476-BHL072216-GBD16876_21730-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGTACCTCCCTTAGTATCCTTATTCGTACAGAATTAGGTCACCCAGGTGCTTTAATTGGAGACTATCAAATCTATAATGTAATTGTAACGGCACATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCCT-TTGGATGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.8% identical to accession ID KR775767, identified in GenBank as Tanypodinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605611 Chironomidae sp. water mite diet isolate 2494-BHL072216-GBD26543_10014-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGCATGCTTATTCGAGCAGAATCAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGGGGCTTTGGGAATTGGTTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.1% identical to accession ID JF412118, identified in GenBank as Glyptotendipes tokunagai. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605612 Chironomidae sp. water mite diet isolate 2497-BHL072216-GBD15410_12770-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGTCATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTTGTTACTGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGTAATTGATTAGTACCATTAATATTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTACTACCCCCCTCATTAACACTACTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605613 Chironomidae sp. water mite diet isolate 2516-BHL072216-GBD13915_27996-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACAACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605614 Chironomidae sp. water mite diet isolate 2519-BHL072216-GBD18100_20194-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTGCTATAATTTTTTTATAGTTATACCTATCTTAATTGGGGGATTTGGAAATTGACTTTTACCATTAATGCTTGGAGCACCAGATATAGCTTTCCCCCGAATGAATAATATAAGTTTTTGACTTCTTCCCCCATCTCTAACCCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605615 Chironomidae sp. water mite diet isolate 2527-BHL072216-GBD11668_19628-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCA---GTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID KR278599, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605616 Chironomidae sp. water mite diet isolate 2530-BHL072216-GBD17925_13041-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTACATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCTGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCATTTATCATAATTTTTTTCATAGTTATGCCTATTTTAATTGGAGGCTTTGGGAATTGATTATTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGAACAATAGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.3% identical to accession ID KR294880, identified in GenBank as Xenochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605617 Chironomidae sp. water mite diet isolate 2539-BHL072216-GBD16219_20827-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGATCATCTTTAAGAATACTTATCCGAGCAGAATTAGGTCATCCAGGTACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATCTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR638998, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605618 Chironomidae sp. water mite diet isolate 2542-BHL072216-GBD21301_12895-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGTACCTCCCTTAGTATCCTTATTCGTACAGAATTAGGTCACCCAGGAGCTTTAATTGGAGACGATCAAATCTATAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KP043430, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605619 Chironomidae sp. water mite diet isolate 2556-BHL072216-GBD12533_24232-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGTTTATTCGAGCAGAATTAGGACAACCTGGTTCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGAGGGTTTGGGAATTGATTAGTTCCCCTAATATTAGGAGCACCAGATACAGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTACTTCCCCCTTCTTTAACTCTCTTACTATCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.3% identical to accession ID KP045212, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605620 Chironomidae sp. water mite diet isolate 2575-BHL072216-GBD17367_20556-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAGCGGAATTAGGGCAGTGTGGCAGACTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID KR647156, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605621 Chironomidae sp. water mite diet isolate 2576-BHL072216-GBD9287_12883-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATTTTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTAGAGATGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTATCATAATTTTTTTCATAGTTATGCCTATTTTAATTGGAGGCTTTGGAAAATGATTAGTTCCCCTAATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCGTCTTTAACTCTCTTACTATCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID KP045212, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605622 Chironomidae sp. water mite diet isolate 2580-BHL072216-GBD22336_25199-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTCGTTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTTAGTATACTTATTCGAGCAGAATTAGGTCGACCGGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTGCCACCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605623 Chironomidae sp. water mite diet isolate 2582-BHL072216-GBD3268_17795-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATAAAGATATTGGAACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACTTCTTTAAGAATGTTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTTTTCATAGTTATGCCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTCTTATATTGGGAGCACCTGATATGGCATTCCCTCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID DQ648215, identified in GenBank as Kiefferulus brevibucca. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605624 Chironomidae sp. water mite diet isolate 2586-BHL072216-GBD22431_8110-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATAAAGATATTGGCACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTTAGCATGTTTATTCGAGCAGAATTATCACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATACCAATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGAGCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.9% identical to accession ID DQ648215, identified in GenBank as Kiefferulus brevibucca. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605625 Chironomidae sp. water mite diet isolate 2590-BHL072216-GBD24636_22415-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCGGGGATAGTAGGAACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTGCCACCTTCTCTAACCTTATTACTTTCGAGTACAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605626 Chironomidae sp. water mite diet isolate 2593-BHL072216-GBD18200_14137-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGAGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAATAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID KM993864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605627 Chironomidae sp. water mite diet isolate 2608-BHL072216-GBD3217_16442-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAGTGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCTTCTTTAACCTTACTATTATCTAGCTCTATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM991192, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605628 Chironomidae sp. water mite diet isolate 2621-BHL072216-GBD24559_10739-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCATGATACGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGGGGCTCTGGGAATTGACTAGTTCCCCTAATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605629 Chironomidae sp. water mite diet isolate 2623-BHL072216-GBD17963_21461-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCTTTAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTAACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605630 Chironomidae sp. water mite diet isolate 2625-BHL072216-GBD22655_16557-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGAAGCCTGATCAGGAATAGTAGGCACTTCTTTAAGAGTTTTAATTCGAGCTGAATTAGGGCATACTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTTGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGAGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTTCTTCTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605631 Chironomidae sp. water mite diet isolate 2626-BHL072216-GBD20353_26307-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGATCTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGAGTTTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGTAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCCTCATTAACTCTTCTACTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605632 Chironomidae sp. water mite diet isolate 2634-BHL072216-GBD13004_6912-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGCATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCATCTTTATCTCTTCTTCTATCAAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR647156, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605633 Chironomidae sp. water mite diet isolate 2635-BHL072216-GBD13134_6600-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACCGCTCACGCTTCTATCATAATTTTTTTCATAGTTATGCCTATTTTAATTGGGGGATTTGGAAATTGATTAGTTCCCCTAATATTAGGAGCACCAGACATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCCTCCCCCGTCTTTAACTCTCTTACTATCTAGATCAATAGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID KR684831, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605634 Chironomidae sp. water mite diet isolate 2638-BHL072216-GBD2738_13429-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGATCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCCCACGCTTTTATCTTAATTTTCTTCATAGTTATGCCTATTTTAATTGGAGTCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.8% identical to accession ID GU944724, identified in GenBank as Chironomus circumdatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605635 Chironomidae sp. water mite diet isolate 2643-BHL072216-GBD16606_16256-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCGGGGATAGTAGGCACTTCTTTAAGAATCTTAATTCGACTTGAATTAGGACATGCTGGCTCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCTCCTTCACTTACCTTATTACTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605636 Chironomidae sp. water mite diet isolate 2645-BHL072216-GBD5435_13930-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGTGGCTTTGGAAATTGATTAGTTCCCCTAATATTAGGAGCACCAGATACGGCTTTCCCGCGAATAAACAATATAAGCTGCTGACTTCTTCCCCCTTCTTTAAATCTCTGACGTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.3% identical to accession ID KR751162, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605637 Chironomidae sp. water mite diet isolate 2656-BHL072216-GBD15268_23360-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTCATAGTTATGCCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCCCTAATATTAGGAGCACCAGATATAGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTTCTTTCTAGATCAATCGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID JF412121, identified in GenBank as Glyptotendipes tokunagai. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605638 Chironomidae sp. water mite diet isolate 2664-BHL072216-GBD6813_15268-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGTACCTCCCTTAGTATCCTTATTCGTACAGAATTAGGTCACCCGGGAGCTTTAATTGGAGACGATCAAATCTATAATGTAATTGTAACGGCACATGCTTTTGTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGTGGATTTGGTAATTGACTAGTACCCCTTATACTAGGAGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTACTACCCCCATCTATTTCTTTACTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KP043430, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605639 Chironomidae sp. water mite diet isolate 2667-BHL072216-GBD4463_18431-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATCTATAATGTAATTGTAACGGCACATGCTTTTGTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGTGGATTTGGTAATTGACTAGTACCCCTTATACTAGGAGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTACTACCCCCTTCTTTAACCTTACTATTATCTAGCTCTATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR288057, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605640 Chironomidae sp. water mite diet isolate 2670-BHL072216-GBD11145_11897-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTGATTGAAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGATTACTCCCACCTTCTCTAACCCTTTTACTACCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605641 Chironomidae sp. water mite diet isolate 2673-BHL072216-GBD10400_13268-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACACTTTATTTTATTTTCGGAGTATGGTCTGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGGGGCTTTGGGAATTGATTAGTTCCCCTAATATTAGGGGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.8% identical to accession ID JF412118, identified in GenBank as Glyptotendipes tokunagai. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605642 Chironomidae sp. water mite diet isolate 2677-BHL072216-GBD8938_26502-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATTATATTTTATTTTTGGAGCCTGATCAGGTACAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATAATAATTTTCTTCATAGTTATGCCTATTTTAATTGGAGGCTTTGGGAATTGATTATTTCCCCTAATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTCTAACTCTCTTACTTTCTAGATCAATAGTCGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 88.2% identical to accession ID JF412118, identified in GenBank as Glyptotendipes tokunagai. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605643 Chironomidae sp. water mite diet isolate 2693-BHL072216-GBD27935_8605-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGTGGATTTGGTAATTGACTAGTACCCCTTATACTAGGAGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTACTACCCCCTTCTTTAACCTTACTATTATCTAGCTCTATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID MF826164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605644 Chironomidae sp. water mite diet isolate 2841-BHL032417-GBD22775_14054-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATGCCAATTTTAGTTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGATATATCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTTACATTATTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.9% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605645 Chironomidae sp. water mite diet isolate 2898-BHL032417-GBD21538_7574-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATATTTCTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATGCTTATTCGAGCAAAACTAGGACGACCCGGAACTTTCATTAGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605646 Chironomidae sp. water mite diet isolate 2910-BHL032417-GBD9727_14518-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAACAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCATTCGTCTTTCTAGTTCCTTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605647 Chironomidae sp. water mite diet isolate 2957-BHL032417-GBD18496_3335-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTCTTTACATTATTTTAGGTGCTTGATCAGGAATGGTAGGGACTTCTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605648 Chironomidae sp. water mite diet isolate 3017-BHL032417-GBD15758_28721-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTTTTTTGGAGTTTGATCAGGTATAGGAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATGGGTGATGCCCAAATTTATAATGTAATTGTTACTTCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTATTACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID KR756187, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605649 Chironomidae sp. water mite diet isolate 3580-BHL032417-GBD24374_23464-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTTGAGCTGAATTAGGACACCCCGGGGCATTAATTGGAGACGATCAAATTTATAACGTAATGGTTACAGCTCATGCCTTTGTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTACCACTAATATTATGTGCACCAGATATAGCTTTCCCTCGAATAAATAATATATGCTTTTGATTATTACCCCCATCTTTAACATTACTAATAGCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605650 Chironomidae sp. water mite diet isolate 3657-BHL032417-GBD6232_5476-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTGTATTCGGAGCCTGATCAGGTATAGTAGGTACTTCCCTTAGTAATCTAGTACGAGCTGAATTAGGACACCCCGGGGCATTAATTGGAGACGATCAAATTTATAACGTAATGGTTACAGCTCATGCCTTTGTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTACCACTAATATTAGGTGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACATACATTACTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605651 Chironomidae sp. water mite diet isolate 3707-BHL032417-GBD27410_10219-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTGTATTCGGAGCCTGATCAGGTATAGTAGTTACTTCCCTTAGTAATCTAGTACGAGCTGAATTAGGACACCCCGGAGCATTAATTGGATACGATCAAATTTATAACGTAATGGTTACAGCTCATGCCTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605652 Chironomidae sp. water mite diet isolate 3737-BHL032417-GBD7475_14179-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTACCAGTAATATTAGGTGCACCAGATATAGCTTTCCCTCGAATAAATAATATATGCTTTTGATTATTACCCCCATCTTTAACATTACTATTAGCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.5% identical to accession ID KR941561, identified in GenBank as Chironomus quinnitukqut. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605653 Chironomidae sp. water mite diet isolate 3750-BHL032417-GBD17284_18265-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTGTATTCGGAGCCTGATCAGGTATAGTAGGTACTTCCCTTAGTAATCTAGTGCGAGCTGAATTAGGACACCCCGGGGCATTAATTGGAGACGATCAAATTTATAACGTAATGGTTACAGCTCATGCCTTTGTAATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605654 Chironomidae sp. water mite diet isolate 3781-BHL032417-GBD9425_11639-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCCTTATTTTGTATTCGGAGCCTGATCAGGTATAGTAGGTACTTCCCTTAGTAATCTAGTACGAGCTGAATTAGGACACCCCGGGGCATTAATTGGAGACGATCAAATTTATAACGTAATGGTTACAGCTCATGCCTTTGTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTACCACTAATACTAGGTGCACCAGATATAGCTTTCGCTCAAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCTCTTACATTACTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACGGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605655 Chironomidae sp. water mite diet isolate 3859-BHL032417-GBD9489_20274-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACTTTATACATTATGTTTGGGGCTTGTTCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGATGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCCCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGACTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.5% identical to accession ID GU944724, identified in GenBank as Chironomus circumdatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605656 Chironomidae sp. water mite diet isolate 3861-BHL032417-GBD8130_20259-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTACGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTATAACGTAATGGTTACAGCTCATGCCTTTGTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTACCACTAATATTAGGTGCACCAGATATAGCTTTCCCTCGAATAAATAATATATGCTTTTGATTATTACCCCCATCTTTAACATTACTATTAGCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605657 Chironomidae sp. water mite diet isolate 3865-BHL032417-GBD17325_5554-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATCTTATTTTTGGGGCTTGATCCGGAACAATGGGAACGTCTTTAAGTATGCTAATTCGAGCAGAAATAGGACGACCTGTAACTTTTATTGGAGATGACCGTATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATATTATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.8% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605658 Chironomidae sp. water mite diet isolate 3896-BHL032417-GBD25740_11398-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAACGATATTGGAACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTCTAAGTATGCTTATTCGAGCAGAATTAGGACGACCGGGATCTTTTGTTGGCGACGACCAGATTTATAATGTAGTTGTTACAGCTCATGCATTTATTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605659 Chironomidae sp. water mite diet isolate 3901-BHL032417-GBD18328_14627-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACTTTATACTTTATGTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTGGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCTCTTACATTACTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.8% identical to accession ID KR941561, identified in GenBank as Chironomus quinnitukqut. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605660 Chironomidae sp. water mite diet isolate 3929-BHL032417-GBD18767_11711-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTGTATTCGGAGCCTGATCAGGTATAGTAGGTACTTCCTTTAGTAATCTAGTACGAGCTGAATTAGGACACCCCGGAACATTAATTGGAGACGATCAAAATTATAACGTAATGGTTACAGCTCATGCCTTTGCAATAATTTTCTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCACTAATATTAGGTGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGCTTTTGATTATTACCCCCATCTTTAACATTACTATTAGCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605661 Chironomidae sp. water mite diet isolate 3937-BHL032417-GBD7316_12916-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTGTTTTCGGAGCCTGATCAGGTATAGTAGGTACTTCCTTTAGTATTCTAGTTCGAGCTGAATTAGGACACCCAGGGTCATTAATTGGAGACGATCAAATTTATAATGTAATGGTTACAGCTCATGCCTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTACCTCTAATATTAGGTGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGCTTTTGATTATTACCCCCATCATTAACCTTACTATTAGCTAGCCCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605662 Chironomidae sp. water mite diet isolate 3949-BHL032417-GBD11730_5798-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCCTTAGTAATCTAGTACGAGCTGAATTAGGACACCCCGGGGCATTAATTGGAGACGATCAAATTTATAACGTAATGGTTACAGCTCATGCCTTTGTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGGTTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605663 Chironomidae sp. water mite diet isolate 3954-BHL032417-GBD19812_15037-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTTAGAATTTTAATTCGAGCTGTATTAGGACATGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTATGGTTATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTCCACCTAATACTTGAAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTGCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605664 Chironomidae sp. water mite diet isolate 3963-BHL032417-GBD19003_21206-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTGTATTCGGAGCCTGATCAGGTATAGTAGGTACTTCCCTTAGTATTTTAGTTCGAGCTAAATTAGGACACCCCGGGACATTAATTGGAGACGATCAAATTTATAACGTAATGGTTACAGCTCATGCCTTTGTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAACTGATTAGTACCACTAATATTAGGAGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGCTTTTGACTATTACCCCCATCTTTAACATTACTATTAGCTAGCACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605665 Chironomidae sp. water mite diet isolate 3966-BHL032417-GBD26149_23210-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTGTTTTCGGAGCCTGATCAGGTATAGTAGGTACTTCCCTTAGTATTCTTGTTCGAGCTGAATTAGGACACCCCGGAGCATTAATTGGAGACGATCAAATTTATAACGTGATGGTTACAGCTCATGCCTTTGTAATAATTTTCTTTATAGTAATACCGATTTTAATTGGTGGATTTGGAAATTGATTAGTACCACTAATATTAGGTGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGCTTTTGATTATTACCCCCATCTTCAACATTACTATTGGCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605666 Chironomidae sp. water mite diet isolate 3993-BHL032417-GBD26449_17591-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTGTTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCCCTTAGTATTCTTGTACGAGCCGAATTAGGACACCCCGGGGCGGTAATTGGAGACGATCAAATTTATAACGTAATGGTTACAGCTCATGCCTTTGTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTACCACTAATATTAGGTGCACCAGATATAGCTTTCCCTCGAATAAATAAAATATGCTTTTGATTATTACCCCCATCTTTAACATTACTATTAGCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605667 Chironomidae sp. water mite diet isolate 4007-BHL032417-GBD4751_19204-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTATTTTTGGAGCTTTATCAGGAATAGTAGTTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACACCCCGGGGCATTAATTGGAGACGATCAAATTTATAACGTAATCTTTACAGCTCGTGCCTTTGTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTACCACTAATATTAGGTGCACCAGATATAGCTTTCCCTCGAATAAATAATATATGCTTTTGATTATTACCCCCATCTTTAACATTACTATTAGCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605668 Chironomidae sp. water mite diet isolate 4131-BHL032417-GBD3610_16480-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTGTATTTTATTTTTTGGAGCTTGATCGGGAATAGTATGCACTTCTTTAAGATTTTTAATTCGACTTGAGTTAGTACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACAAGCTTTTGTAATAATTTTTTTTATAGTGACACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAAATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605669 Chironomidae sp. water mite diet isolate 4137-BHL032417-GBD23959_5683-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGCGCTTGATCAGGAATAGATGTAACTTCTTTAAGAATTCTAATTCGCGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAACTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAAAAAATAATATAAGGTTTTGATTGTTGCCCCCATCATTAACTTTAGTATTAGCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605670 Chironomidae sp. water mite diet isolate 4154-BHL032417-GBD23286_14220-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGTATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGTCACCCTGGATCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605671 Chironomidae sp. water mite diet isolate 4161-BHL032417-GBD19080_3927-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCATCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605672 Chironomidae sp. water mite diet isolate 4167-BHL032417-GBD18203_12155-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTCTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCTGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGTTATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCTCTTCATTAAC---TCTTTTACTTTCAAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605673 Chironomidae sp. water mite diet isolate 4170-BHL032417-GBD23445_8369-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGAACATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTTGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605674 Chironomidae sp. water mite diet isolate 4177-BHL032417-GBD3218_10174-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGTAGAATTCGGTCACCCAGGTTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGGGCTCCTGATATAGCATTCCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTATTATCAAGATCAATAGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605675 Chironomidae sp. water mite diet isolate 4190-BHL032417-GBD28825_12682-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTTGGAGCTTGATCAGGTATAGTTGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCATGCAGGTTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605676 Chironomidae sp. water mite diet isolate 4202-BHL032417-GBD29332_18486-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAACTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGACTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCAGTAACCGGACGGGGAGCAAGAGCAAGAGGAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605677 Chironomidae sp. water mite diet isolate 4204-BHL032417-GBD25874_16656-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCCTTAAGTATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGGAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAACATAAGATTTTGATTATTACCCCCATCATTAACCTTACTTTTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605678 Chironomidae sp. water mite diet isolate 4224-BHL032417-GBD18006_2837-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGATGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATTCAGGCTCATTAATTGGAGGCGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605679 Chironomidae sp. water mite diet isolate 4229-BHL032417-GBD7019_15731-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAACAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAAGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGAAAAGGCTTTCCCACGAATAAAAAAAAAAAGGTTTCGAATGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605680 Chironomidae sp. water mite diet isolate 4244-BHL032417-GBD22287_3887-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGACTCATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGGACATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTATTACCCCCTTCATTAACCCTACTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605681 Chironomidae sp. water mite diet isolate 4246-BHL032417-GBD25065_10490-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTTATTCGAGCAGAATTAGGACATGCAGGCACACTAATTGGAGACGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTGTTACCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605682 Chironomidae sp. water mite diet isolate 4257-BHL032417-GBD26427_8971-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTATTTTATTTTTGGAGCTTGATCAGGTATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGACATGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCTATCATTAACTTTATTATTATCTAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605683 Chironomidae sp. water mite diet isolate 4260-BHL032417-GBD19476_5645-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTTGGAGCTTGTCCGGGAATAGTAGGCACTTCTTTAAGATTTTTAATTGGACTGGAATTGGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATCGGAGGCTTTGGAAACTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCTAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605684 Chironomidae sp. water mite diet isolate 4266-BHL032417-GBD23344_20073-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCAGGAATAGTTGGCACTTCTTTAAGTATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605685 Chironomidae sp. water mite diet isolate 4268-BHL032417-GBD9156_14801-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCGGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGTAGAATTAGGACATCCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTATTACCCCCATCATTAACCTTACTATTATCAAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605686 Chironomidae sp. water mite diet isolate 4270-BHL032417-GBD14864_29054-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGTCACCCAGGCTCATTAATGGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCGCGAATAAATAAAATAAGATTTTGATTATTACCCCCATCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605687 Chironomidae sp. water mite diet isolate 4271-BHL032417-GBD28119_20575-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGTGCTCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTATTACCCCCCTCATTAACCTTACTACTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605688 Chironomidae sp. water mite diet isolate 4303-BHL032417-GBD6974_7804-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCACTAATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTGTGATTATTACCACCATCACTAACCTTACTATTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605689 Chironomidae sp. water mite diet isolate 4307-BHL032417-GBD9016_23984-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGATCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGCTATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTGCTGCCCCCATCATTAACTTTATTATTATCTAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605690 Chironomidae sp. water mite diet isolate 4312-BHL032417-GBD12421_24090-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAAAATTAAGTCAACCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605691 Chironomidae sp. water mite diet isolate 4316-BHL032417-GBD3741_8980-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAACTTGATCAGGAATAGTTGGAACTTCTTTAAGATTTCTAATTCGAGCAGCATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAAGATTTGGAAACTTACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAAAAATATAAGGTTTTGAATGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605692 Chironomidae sp. water mite diet isolate 4319-BHL032417-GBD12119_13945-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTCGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACCTTATTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605693 Chironomidae sp. water mite diet isolate 4320-BHL032417-GBD19087_24326-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGTAGAACTCGGACACGCTGGTTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGATCAAAAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605694 Chironomidae sp. water mite diet isolate 4327-BHL032417-GBD16503_27826-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATTGGAGATGATCAACTTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCATCACTAACCTTACTATTATCAAGAACAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605695 Chironomidae sp. water mite diet isolate 4348-BHL032417-GBD18707_25456-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTTTTTTCGGAGCTTGATCCGGAATTGTTGGAACTTCTTTTAGAATTCTTATTTGGGCAGGATTTGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605696 Chironomidae sp. water mite diet isolate 4349-BHL032417-GBD26932_21750-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGTATTTTAATTCGACTAGAATTAGGACATCCAGGCACATTTATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAACATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605697 Chironomidae sp. water mite diet isolate 4357-BHL032417-GBD21704_9677-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTATTACGCGAATAAATAATATAAGATTTTGAATATTAACCAATACAAGAACCTTACGTTGAACAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605698 Chironomidae sp. water mite diet isolate 4360-BHL032417-GBD26145_10683-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCTTGAGCGGGAATAGTTGGCACTTCTTTAAGAATTTTAATTCGACTTGAATTATGACACCCAGGCTCATTAATCGGAGACGATCAACTTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCAATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTGCATTAACCTTACTTTTATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605699 Chironomidae sp. water mite diet isolate 4362-BHL032417-GBD25312_15786-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATACTTATTCGAGCAGAACTAGGACATCCTGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605700 Chironomidae sp. water mite diet isolate 4364-BHL032417-GBD25291_22773-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATGCAGGCTTATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTATTGCCCCCATCATTAACTTTATTATCATCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605701 Chironomidae sp. water mite diet isolate 4365-BHL032417-GBD28274_13210-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTATTTTATTTTCGGAGCTTGATCAGTAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGATCATTTATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCCGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605702 Chironomidae sp. water mite diet isolate 4366-BHL032417-GBD18550_18097-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTACTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGACATCCAGGCTCATTCATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605703 Chironomidae sp. water mite diet isolate 4376-BHL032417-GBD8777_11122-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACACGCAGGTTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGATGGTTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTATTGCCCCCGTCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605704 Chironomidae sp. water mite diet isolate 4380-BHL032417-GBD25367_8552-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTATTTTCGGAGCTTGGTCAGGAATAGTTGGAACTTCTTTAAGTATTCTAATTCGAGCAGAATTAGGGCATCCTGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTACTTCCTTTAATATTAGGAGCACCCGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACCTTATTATTATCTAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605705 Chironomidae sp. water mite diet isolate 4394-BHL032417-GBD15846_11026-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATTCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGATGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTATTGCCACCATCATTAACTTTATTATTATCAAGAACAATTATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605706 Chironomidae sp. water mite diet isolate 4396-BHL032417-GBD24668_9428-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGAACTTCTTTAAGAATTTTTATTCGACTAGAATTAGGACACCCAGGATCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTCATAGTGATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTGATATTAGGAGGTCCTGATATAGTTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605707 Chironomidae sp. water mite diet isolate 4399-BHL032417-GBD8898_4713-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCCGGTATAGTTGGAACTTCTTTTAGAATTCTAATTCGAGCAGAATTTGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGACATGGCTTTCCCACGAATAAATAATATAAGTTATGGATTGTGGCCCCCATCATTAACTTTATTATTATCTAGAGCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605708 Chironomidae sp. water mite diet isolate 4401-BHL032417-GBD25041_19328-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTCGGAGCTTGATCAGGTATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAACTAGGACATGCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605709 Chironomidae sp. water mite diet isolate 4403-BHL032417-GBD11333_4903-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATACTAATTCGAGTAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAACTTTATAATATAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGATTGTTGCCCCCATCATTAACCTTATTATTATCTAGAGCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605710 Chironomidae sp. water mite diet isolate 4407-BHL032417-GBD28792_18302-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGCATTAGGACTTGCAGGCTCATTAATTGGAGACGATCAGATTTATAATGTAATTGGTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATATGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAAAAAAAAAAAGTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605711 Chironomidae sp. water mite diet isolate 4409-BHL032417-GBD10134_7821-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCTTTTATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCCTTTGTTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCACCAGATATAGCATTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605712 Chironomidae sp. water mite diet isolate 4411-BHL032417-GBD27178_20988-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGTACTTCTTTAAGAATTTTAATTCGAATAGAATTAGGACACGCAGGTTCATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGTTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGAATATTACCCCCTTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605713 Chironomidae sp. water mite diet isolate 4421-BHL032417-GBD24855_23152-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAGTTCGAGTAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATATTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605714 Chironomidae sp. water mite diet isolate 4426-BHL032417-GBD24214_17867-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTTAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAAGAGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCAATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGGGCTCCTGATATAGCTTTTCCGAGAATAAATAATATAAGATTTTGATTATTACCCCCTTCACTAACCTTACTATTATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605715 Chironomidae sp. water mite diet isolate 4427-BHL032417-GBD19120_22736-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGTAGAATTAGGACATGCAGGCTCATTAATCGGGGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTCCCGCGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACTTTAATATTATCTAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM994396, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605716 Chironomidae sp. water mite diet isolate 4432-BHL032417-GBD24472_22494-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTATAAGAATTCTAATTCGAGTAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATAAGACTTTCCCACGAATAAAAAAAAAAAAGTTTTGATTATTGCCCCCATCATTAACCTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605717 Chironomidae sp. water mite diet isolate 4448-BHL032417-GBD16481_15372-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCATTGATATTAGGTGCTCCTGATATAGCTTTTCCGAGAATAAATAATATAAGATTTTGATTATTACCACCATCACTTACCTTACTTCTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605718 Chironomidae sp. water mite diet isolate 4449-BHL032417-GBD15031_16360-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATCTTTGGAGCTTGATCGGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTGTCATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605719 Chironomidae sp. water mite diet isolate 4457-BHL032417-GBD10271_26911-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGACACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTAACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTGGGAGCACCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTGACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605720 Chironomidae sp. water mite diet isolate 4460-BHL032417-GBD24077_13691-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATCTTTGGAGCTTGATCGGCAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTTATTAATCGGAGAAGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCAATTTTAATTGGAGGCTTTGGAAATTGATTATTACCTTTAATATTAGGAGCTCCAGATATAGCTTTCCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605721 Chironomidae sp. water mite diet isolate 4461-BHL032417-GBD23676_6851-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGTAGAATTAGGACATCCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTACTTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGATCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTACCCCCATCATTAACCTTACTATTATCTAGAGCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605722 Chironomidae sp. water mite diet isolate 4466-BHL032417-GBD20414_28071-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTTAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCACTAATTGGAGACGATCAAATTTATAGTGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATGCCATTTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTTTTACCTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.9% identical to accession ID GU565715, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605723 Chironomidae sp. water mite diet isolate 4468-BHL032417-GBD16032_3395-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTGTGTTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATTCATTCTCATTAATTGGAGACGATCCAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGATGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTACCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605724 Chironomidae sp. water mite diet isolate 4473-BHL032417-GBD15645_24093-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATATTAATTCGAGCAGAATTAGGACATGCTGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTAGTACCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTATTACCCCCATCATTAACTTTATTATTATCTAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605725 Chironomidae sp. water mite diet isolate 4476-BHL032417-GBD10958_17499-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTACTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCGTTAAGAATACTAATTCGAGTAGAATTATGACATCCAGGCTCATTAATTGGAGACGATCAACTTTATAATGTACTTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605726 Chironomidae sp. water mite diet isolate 4479-BHL032417-GBD17760_18788-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTTGAATTAGGACACCCAGGCACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTCATTAGTACCTTTAATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605727 Chironomidae sp. water mite diet isolate 4480-BHL032417-GBD24986_6909-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGAGCAGGAATAGTTGGAACTGCTTTAAGAATTCTAATTCGAGCAGAATTATGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCTAGTTATACCAGTCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAACAATATAAGATTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATCGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605728 Chironomidae sp. water mite diet isolate 4483-BHL032417-GBD13230_3586-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTGATACCCATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605729 Chironomidae sp. water mite diet isolate 4484-BHL032417-GBD25211_18403-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCTGGATCATTTATTGGTGACGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCGTTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605730 Chironomidae sp. water mite diet isolate 4485-BHL032417-GBD17199_20317-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATGCAGGTTTATTAATTGGAGACGATCAGATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605731 Chironomidae sp. water mite diet isolate 4489-BHL032417-GBD26143_16080-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTACGTATTCTAATTCGAGCTGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACTTTATTAAAATCTAGAGCAAGAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605732 Chironomidae sp. water mite diet isolate 4493-BHL032417-GBD3346_13380-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACTCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGGA	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605733 Chironomidae sp. water mite diet isolate 4559-BHL032417-GBD18069_5629-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGGGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCA--TCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.8% identical to accession ID KR764064, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605734 Chironomidae sp. water mite diet isolate 4565-BHL032417-GBD14049_11530-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.6% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605735 Chironomidae sp. water mite diet isolate 4662-BHL032417-GBD16140_13711-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTAATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605736 Chironomidae sp. water mite diet isolate 4699-BHL032417-GBD26360_9244-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGTAGAATTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605737 Chironomidae sp. water mite diet isolate 4815-BHL032417-GBD19131_23439-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGATACATCTTTAAGAATTTTAATTCGAGCAAAACTAGGTCACGCTGGTTCTTTAATCGGAGACGTTCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTCATAGTGATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605738 Chironomidae sp. water mite diet isolate 4889-BHL032417-GBD25843_11353-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATGGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACTTTATTATTATCAAGCACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605739 Chironomidae sp. water mite diet isolate 4904-BHL032417-GBD27770_20112-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGCACATCTTTAAGAATTTTAATTCGACTAGAACTAGGTCACGCTGGCTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCGCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605740 Chironomidae sp. water mite diet isolate 4935-BHL032417-GBD19474_9561-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCAATTTTAATTGGAGGGTTGGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTGGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.4% identical to accession ID GU565715, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605741 Chironomidae sp. water mite diet isolate 5045-BHL032417-GBD4124_16955-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTGCAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAGTTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.1% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605742 Chironomidae sp. water mite diet isolate 5053-BHL032417-GBD25325_15269-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTAATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCGCGAATAAATAATATACGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605743 Chironomidae sp. water mite diet isolate 5085-BHL032417-GBD24854_11533-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTAGTCCCTCTAATATTAGGAGCCCCAGATATAGCTTTCCCCCGAATAAATAATATAAGATTTTGGCTTCTACCCCCGTCATTAACTTTACTACTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605744 Chironomidae sp. water mite diet isolate 5097-BHL032417-GBD15262_20411-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCATGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATACATTTTTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605745 Chironomidae sp. water mite diet isolate 5104-BHL032417-GBD4400_22735-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTACGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605746 Chironomidae sp. water mite diet isolate 5125-BHL032417-GBD5293_23255-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTCTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTGGGAAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTATACCCTCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KM990292, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605747 Chironomidae sp. water mite diet isolate 5133-BHL032417-GBD14358_2418-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAATTATACCAATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTT-TCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605748 Chironomidae sp. water mite diet isolate 5139-BHL032417-GBD6890_10178-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCTTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATCTTAATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCA--TCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.6% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605749 Chironomidae sp. water mite diet isolate 5140-BHL032417-GBD5673_11796-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACATCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATATTTTTTTTATAGTTATACCTATTTTAATTAGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCTCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KM992253, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605750 Chironomidae sp. water mite diet isolate 5152-BHL032417-GBD15133_5644-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAAGTAGGACGACCCGGAACTTTCATTGGTGACGACCTAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAGATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605751 Chironomidae sp. water mite diet isolate 5155-BHL032417-GBD23815_18066-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCTGAACTTTCATTGGTGACGACCAAATTTATAACTTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.2% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605752 Chironomidae sp. water mite diet isolate 5176-BHL032417-GBD15866_6079-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGTACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTGGTTTCTTCTGCTGCCGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605753 Chironomidae sp. water mite diet isolate 5185-BHL032417-GBD15880_12279-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCTATGCTTTTATTATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAAATGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605754 Chironomidae sp. water mite diet isolate 5202-BHL032417-GBD20303_9446-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGATCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTGGGAAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTATACCCTCGTCATTAACTTTACTTCTTGCTAGTTCAAGTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KM990292, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605755 Chironomidae sp. water mite diet isolate 5209-BHL032417-GBD16148_3234-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTGTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGTCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATATTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605756 Chironomidae sp. water mite diet isolate 5234-BHL032417-GBD9703_24672-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATACTGTAGTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAGTTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCA---GTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605757 Chironomidae sp. water mite diet isolate 5237-BHL032417-GBD24992_21889-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAGTCGGGACTTCTCTAAGAATGCCTATTCGAGCAGAATTAGGACAACCCGGAACTTTCATTGGTGACGACCAATTTTATAACGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605758 Chironomidae sp. water mite diet isolate 5272-BHL032417-GBD9537_7171-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGCATTAGGTCATGCGGGTTCTTTAATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCACGTATAAATAATATAAGGTTTTGGCTTTTACCCCCGTCATTATCTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID KM990292, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605759 Chironomidae sp. water mite diet isolate 5273-BHL032417-GBD5737_6659-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTATATTTTATTTTTGGAGCCTGATCTGGGATAGTCGGGACTTCTCTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGATCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605760 Chironomidae sp. water mite diet isolate 5275-BHL032417-GBD13149_26555-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATACCGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCATCACTAATTCTATTAGTTTCATCGGCTGCA---GTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605761 Chironomidae sp. water mite diet isolate 5277-BHL032417-GBD26053_9056-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTTTAAGAATGCTTGTTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGACGACCAAATTTATAACGTTATTGTTACTGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTAATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605762 Chironomidae sp. water mite diet isolate 5293-BHL032417-GBD9321_9936-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATGAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605763 Chironomidae sp. water mite diet isolate 5297-BHL032417-GBD18567_7246-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605764 Chironomidae sp. water mite diet isolate 5303-BHL032417-GBD11723_20623-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCA--GTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.5% identical to accession ID KM569758, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605765 Chironomidae sp. water mite diet isolate 5307-BHL032417-GBD23229_13808-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCCTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCACTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KM990292, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605766 Chironomidae sp. water mite diet isolate 5334-BHL032417-GBD26754_20731-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATATTTTATTTTTGGAGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGGACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGGCATTAACTTTACTTCTAGCTAGTGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605767 Chironomidae sp. water mite diet isolate 5344-BHL032417-GBD26388_14878-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACATGCAGGCTCATTTATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTGTTTGACTGTTGCCCCCTTCATTAACTTTATTGTTATCAAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605768 Chironomidae sp. water mite diet isolate 5347-BHL032417-GBD7765_25912-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGTTTATTCGAGCAGAATTCGGACGCCCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACCGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCATTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605769 Chironomidae sp. water mite diet isolate 5352-BHL032417-GBD5716_23561-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCTTGATCTGGGATAATCGGGACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGCACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTAATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGACTTTTGCCCCCATCATTAACTTTACTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605770 Chironomidae sp. water mite diet isolate 5360-BHL032417-GBD19723_13899-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGTACTTCTCTAAGAATGTTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAAGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGGTTTTGACTTTTACCCCCGTCATTAACTTTACTTCTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605771 Chironomidae sp. water mite diet isolate 5369-BHL032417-GBD22272_10796-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCCGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGAAGGATTTGGGAACTGATTATTGCCTTTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTGGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGGACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605772 Chironomidae sp. water mite diet isolate 5380-BHL032417-GBD9898_13370-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCCCGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACCTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605773 Chironomidae sp. water mite diet isolate 5382-BHL032417-GBD6576_10790-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTCGGAAATTGATTAGTTCCTTTGATATTGGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAGGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605774 Chironomidae sp. water mite diet isolate 5400-BHL032417-GBD15898_21453-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTTCCTTTAATATTAGGAGCGCCAGATATGGCCTTCCCTCAAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.1% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605775 Chironomidae sp. water mite diet isolate 5412-BHL032417-GBD5341_22059-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGCTGACAACCAGTTTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAAGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTATCTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605776 Chironomidae sp. water mite diet isolate 5418-BHL032417-GBD5362_17088-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605777 Chironomidae sp. water mite diet isolate 5428-BHL032417-GBD8958_26960-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTTAGAATTCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCTTTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTACCTCTTATATTAGGAGCACCAGACATAGCTTTCCCCCGTATAAATAATATAAGATTTTGACTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605778 Chironomidae sp. water mite diet isolate 5433-BHL032417-GBD18213_23905-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTTAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAATTTTATAACGTAATTGTTACAGTCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTCACTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605779 Chironomidae sp. water mite diet isolate 5454-BHL032417-GBD8322_18070-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTATATTTTATTTTTGGCGCCTGATCTGGTATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGCCCAGGAACTTTCATTGGTGACGATCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTGGTCCCTCTAATATTAGGAGCCCCAGACATAGCTTTCCCCCGAATAAATAATATAAGTTTTTGACTTTTACCCCCGTCATTAACTTTACTACTATCTAGTTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605780 Chironomidae sp. water mite diet isolate 5464-BHL032417-GBD16548_11808-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGATGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTGGTCCCTCTAATATTAGGAGCCCCAGACATAGCTTTCCCCCGGATAAATAATATAAGTTTTTGGCTATTACCCCCGTCATTATCTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605781 Chironomidae sp. water mite diet isolate 5467-BHL032417-GBD27778_15315-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATATTTTATTTTTGGAGCCTGATCTGGGATAATAGGGACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGAACCGGAACTTTCATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCTGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTATCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605782 Chironomidae sp. water mite diet isolate 5470-BHL032417-GBD14741_25953-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGACTATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCTCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGCATAAATAATATAAGTTTTTGGCTTTTACCCCCGACATTAACTTTACATCTTTCTAATTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605783 Chironomidae sp. water mite diet isolate 5476-BHL032417-GBD22176_11431-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGTATAATCGGTACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGGACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACCGCCCATGCTTTTATTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTGGTCCCTCTAATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGTTTTTACCCCCGTCATTAACTTTACTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605784 Chironomidae sp. water mite diet isolate 5484-BHL032417-GBD27628_12347-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGCCCCGGAACTTTAATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGAATAAATAATATAAGTTTTTGGCTATTACCCCCGTCATTAACCTTACTTCTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605785 Chironomidae sp. water mite diet isolate 5485-BHL032417-GBD24188_19221-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTATCTCTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605786 Chironomidae sp. water mite diet isolate 5493-BHL032417-GBD20505_10314-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTATACTTTATTTTTGGCGCTTGATCTGGGATAGTCGGGACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGATGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTGTAGTTATACCTATTTTAATTGGAGGGTTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605787 Chironomidae sp. water mite diet isolate 5509-BHL032417-GBD24845_11557-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGAATAATCGGGACTTCTCTAAGAATTTTTATTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGAGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATATTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTAGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGAATAAATAATATAAGTTTTTGACTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605788 Chironomidae sp. water mite diet isolate 5529-BHL032417-GBD25060_25491-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTATATTTTATTTTTGGCGCCTGATCTGGAATAATCGGGACTTCTCTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCGTTGGTGACGATCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAAAGATAGCTTTCCCCCGTATAAATAATATAAGTTTCTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605789 Chironomidae sp. water mite diet isolate 5541-BHL032417-GBD8616_10464-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTCATTTCTGGTGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGGCGACCAATTTTATAACGTAATTGTTACAGCCCATGCTTTTATTATATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTGGGAAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTATACCCTCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605790 Chironomidae sp. water mite diet isolate 5569-BHL032417-GBD28264_11161-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGATCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTCTTCTTCTTATTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.6% identical to accession ID KR287035, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605791 Chironomidae sp. water mite diet isolate 5603-BHL032417-GBD20091_8945-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605792 Chironomidae sp. water mite diet isolate 5610-BHL032417-GBD24396_16296-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGATCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTATTTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCCAAAAAAATATATTAAATTTTGGCTTCTTCCCCCGTCTCTTACTCTTCTTCTTTCTAGTTGAATTGTTGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR287035, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605793 Chironomidae sp. water mite diet isolate 5631-BHL032417-GBD3235_18995-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATAAAGATATTGGAACATTATACTTCATTTTTGGGCCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAAAATTAGGACGGCCAGGAACTTTTATTGGAGATGATCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID DQ648211, identified in GenBank as Dicrotendipes pseudoconjunctus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605794 Chironomidae sp. water mite diet isolate 5632-BHL032417-GBD13139_14152-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATGTTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605795 Chironomidae sp. water mite diet isolate 5635-BHL032417-GBD4438_15536-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGATCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAACTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR165695, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605796 Chironomidae sp. water mite diet isolate 5647-BHL032417-GBD16457_7623-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTCTATTGGAGATGATCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGTGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCACCTGACATAGCTTCCCCGCGAATAAATAATATAAGATTTTGGCTTCATCCAACGTCTCTTACTCGTCGTATTTCTAGTTCAATTGTTGAAAATGGAGTTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR287035, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605797 Chironomidae sp. water mite diet isolate 5648-BHL032417-GBD10911_24939-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGCTTAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAAAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR171593, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605798 Chironomidae sp. water mite diet isolate 5660-BHL032417-GBD27033_10956-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGATCAAAATTAGGACGGCCAGGAACTTTTATTGGAGATGATCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCGGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR287035, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605799 Chironomidae sp. water mite diet isolate 5661-BHL032417-GBD21259_22317-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAAATCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605800 Chironomidae sp. water mite diet isolate 5673-BHL032417-GBD7850_6473-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCTGAATTAGGACGGCCAGGAACTTTTATTGGAGATGATCAAATCTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGTAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACAGAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTTCACCGTCTCTTACTCTTCTTCTTTCTAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR287035, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605801 Chironomidae sp. water mite diet isolate 5687-BHL032417-GBD8506_16596-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATAAAGATATTGGAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTGTACTTATTCGAGCAGGATTAGGACGGCCAGGAACTTTTATTGGAGATGATCAAATCTATAATGTAATTGTAACTGCACACGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.2% identical to accession ID DQ648211, identified in GenBank as Dicrotendipes pseudoconjunctus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605802 Chironomidae sp. water mite diet isolate 5693-BHL032417-GBD22347_23616-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGTCCAGGAACTTTTATTGGAGATGATCAAATCTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTACTACCACCGTCTCTTACTCTACTTCTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR287035, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605803 Chironomidae sp. water mite diet isolate 5695-BHL032417-GBD16941_11017-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCATGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCATCATTAACTTTATTATGATCTAGCCCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605804 Chironomidae sp. water mite diet isolate 5723-BHL032417-GBD26231_7575-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGACACTTTACTTTATTTTTGGAGCTTGATCCGGAGTAGTAGGAACATCTTTAAGAATACTAATTCGAGCAGAATTAGGACATCCAGGAACATTGATTGGGTATGATCAAATTTACAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATTAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605805 Chironomidae sp. water mite diet isolate 5728-BHL032417-GBD10958_19989-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605806 Chironomidae sp. water mite diet isolate 5768-BHL032417-GBD3711_19723-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGCATTTTAATTCGAGCAGAACTCGGTCACTCTGGTTCTTTAATCGGAGAAGATCAAATTTATAATGTAATCGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGGGATACCTACTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGAATACTTCCCCCGTCATTAACTTTATTATTATCTAACGCTCTAGTTGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605807 Chironomidae sp. water mite diet isolate 5782-BHL032417-GBD12682_19080-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCGATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGGGCCCCTGATATAGCCTTCCCGCGAATAAATAATATAAGATTGTGACTTCTCCCACCGTCTCTTTCTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KM900037, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605808 Chironomidae sp. water mite diet isolate 5783-BHL032417-GBD28745_17290-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGAACAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605809 Chironomidae sp. water mite diet isolate 5784-BHL032417-GBD7445_25881-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGCTCAGGTGTAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCGGAACTCGTTCACGCTGGTTCTTTAATCATAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGGTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCACGCTAGTTGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605810 Chironomidae sp. water mite diet isolate 5798-BHL032417-GBD19435_5121-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTAACCGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCGATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGTGGCCCCTGATATAGCCTTCCCGCGAATAAATAATATAAGATTTTGACTTCTCCCACCATCTCTTTCTCTTCTTCTATCTAGTTCAATTGTTGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.0% identical to accession ID KJ209337, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605811 Chironomidae sp. water mite diet isolate 5801-BHL032417-GBD21779_15626-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGAAAATGCCATCCCCCCAAAAAAAAATAAAAGGTTTTGATTTCCTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605812 Chironomidae sp. water mite diet isolate 5803-BHL032417-GBD24336_23676-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTCGGAGCTTGATCAGGTATAGTAGGTACTTCCTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGCTGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605813 Chironomidae sp. water mite diet isolate 5805-BHL032417-GBD27031_10824-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGTTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCATGATAAACCATCCCCTCAAAAAAAAATATAATTTTTTGTTTCCTCCCCCCGCCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605814 Chironomidae sp. water mite diet isolate 5823-BHL032417-GBD13913_8469-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCTTGATCTGGTAAAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAACGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAACAATATAAGTTTCTGACTTTTACCCCCTTCTCTTACTCTTCTTCTTTCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605815 Chironomidae sp. water mite diet isolate 5827-BHL032417-GBD29501_15548-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCACGCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCCCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605816 Chironomidae sp. water mite diet isolate 5830-BHL032417-GBD23329_17621-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGAAAAAGCATTCCCCCAAAAAAATAAAATAAGGTTTTGAATACCTCCCCCGTCCTTAACCTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605817 Chironomidae sp. water mite diet isolate 5837-BHL032417-GBD7699_12910-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGCTCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGTTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAAATGATTAGTTCCTTTAATATTGGGAGTCCCTGATACAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACGTTATTATTATCGAGCACGCTAGTTGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605818 Chironomidae sp. water mite diet isolate 5841-BHL032417-GBD17274_9246-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTATGCACTTCTTTAAGAATTTTAATTCGACTAGAATTCGGTCACGCAGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACCTTATTATTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605819 Chironomidae sp. water mite diet isolate 5842-BHL032417-GBD4692_9127-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCAGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTATTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605820 Chironomidae sp. water mite diet isolate 5847-BHL032417-GBD20176_6160-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGCACTTCTTTAAGAATTTTAATTCTACTAGAATTAGGACACCCTGGTTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCATTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605821 Chironomidae sp. water mite diet isolate 5849-BHL032417-GBD26179_23215-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGCACTTCCTTAAGTATACTTATTCGAGCCGAGTTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTAACCGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCGATTTTAATTGGTGGTTTTGGAAATTGATTAGTACCTTTAATGTTAGGGGCCCCTGATATAGCCTTCCCGCGAATAAATAATATAAGATTTTGACTACTCCCACCGTCTCTATCTCTTCTTCTTGCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ208847, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605822 Chironomidae sp. water mite diet isolate 5853-BHL032417-GBD27082_21927-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGACACCCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCATTCCCGCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTATTAGTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605823 Chironomidae sp. water mite diet isolate 5856-BHL032417-GBD6264_16011-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAAAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCACCCCCACAAAAAAATAATATAATTTTTTTATTCCTCCCCCCGCCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACGGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605824 Chironomidae sp. water mite diet isolate 5857-BHL032417-GBD10400_14868-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTGGGAGCCCCTGATATAGCTTTCCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCTTTAACTTTATTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605825 Chironomidae sp. water mite diet isolate 5860-BHL032417-GBD18796_6090-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAACGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCGATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGGGCCCCTGATATAGCCTTCCCGCGAATAAATAATATAAGATTTTGACTTCTCCCACCGTCTCTTTCTCTTCTTCTTTCCAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KJ208847, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605826 Chironomidae sp. water mite diet isolate 5861-BHL032417-GBD6650_25930-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGTGCCTGATCAGGTATAGTAGGAACTTCTTTAAGAGTTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGATGAGCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCAAGCACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605827 Chironomidae sp. water mite diet isolate 5862-BHL032417-GBD2707_18146-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCATGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGACACGCTGGTTCTTTAATCTGAGACGATCAAATTTATAATGTAATTGTTACCGTTAATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGAGAGCCCCTGATATAGCATTCCCTCGAATAAAAAATATAAGTTTTTGATTACTTCCCCCGTCAGTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605828 Chironomidae sp. water mite diet isolate 5863-BHL032417-GBD12087_19681-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGTATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACCCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTTATTGTTACCGCTCACGCTTTTGTTATAATTTTTTTATAGTGATACCCATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACCTTATTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605829 Chironomidae sp. water mite diet isolate 5870-BHL032417-GBD23160_21795-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACACTGGTTCTTTTATTGGTGACGATCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605830 Chironomidae sp. water mite diet isolate 5871-BHL032417-GBD6598_11501-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGTCACGCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCACTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTGCTGCCCCCGTCATTAACTTTATTATTATCTAGCTCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605831 Chironomidae sp. water mite diet isolate 5878-BHL032417-GBD15799_3456-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGTGACGATCTAATTTATAATTTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATATTGATACCTATTTTAATTGGAGGGTTTCGACATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGCATAAATAATATATGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGCGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605832 Chironomidae sp. water mite diet isolate 5884-BHL032417-GBD25062_7851-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGAATAGTAGGTACTTCTTTAAGAATTTTAATTCGACTAGAACTAGGACACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCTCCTGATATAGCATTCCCGCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACCTTATTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605833 Chironomidae sp. water mite diet isolate 5885-BHL032417-GBD19211_28591-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCTTTAAGTATTTTAATTCGAGCAGAACTTGGTCACGCTGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCATTAACTTTATTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605834 Chironomidae sp. water mite diet isolate 5886-BHL032417-GBD7099_8204-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCATGCTGGCTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCACCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KM102730, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605835 Chironomidae sp. water mite diet isolate 5888-BHL032417-GBD13651_20360-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGTATAGTAGGCACTTCTTTAAGAATTTTAATTCGACCAGAATTCGGTCACACTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTTATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACCTTATTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605836 Chironomidae sp. water mite diet isolate 5895-BHL032417-GBD16129_12367-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACTTCTTTAAGTATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGAGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAGATAACATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTATTATTATCTAGAACACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605837 Chironomidae sp. water mite diet isolate 5897-BHL032417-GBD28925_17965-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGTCACGCTGGTTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTGGGGGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCATTAACCTTATTATTATCAAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID KM102730, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605838 Chironomidae sp. water mite diet isolate 5898-BHL032417-GBD27880_19402-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCTGAACTCGGACACGCTGGATCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCGTCTTTAACTTTATTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605839 Chironomidae sp. water mite diet isolate 5900-BHL032417-GBD19042_13924-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATAGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTGATATTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACCTTATTATTATCAAGATCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605840 Chironomidae sp. water mite diet isolate 5902-BHL032417-GBD19922_18252-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGTAGAATTCGGTCACCCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCATCATTAAATTTATTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605841 Chironomidae sp. water mite diet isolate 5907-BHL032417-GBD10026_6943-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTCATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGATCCCCTTATATAGCTTCCCCTCAAAAAAAAAATATAAGTTTTTGATCCCTCCCCCCGCCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605842 Chironomidae sp. water mite diet isolate 5909-BHL032417-GBD9662_18493-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGTGACGATCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCATTAATATTGGGAGCCCCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACTTTATTACTATCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605843 Chironomidae sp. water mite diet isolate 5910-BHL032417-GBD21596_22340-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAAAGTTAGGACGGCCAGGAACTTTTATTGGAGACGACCAAATTTATAACGTAATTGTAACCGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCGATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGGGCCCCTGATATAGCCTTCCCGCGAATAAATAATATAAGATTTTGACTTCTCCCACCGTCTCTTTCTCTTCTTCTTTCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ208847, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605844 Chironomidae sp. water mite diet isolate 5913-BHL032417-GBD23834_12539-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGTATTTTAATTCGAGCTGAACTCGGTCACCCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTGATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTACCTTTAATATTGGGAGCCCCTGATATAGCATTCCATCGAATAAATAATATAAGTTTTTGATTACTACCCCCGTCATTAACTTTATTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605845 Chironomidae sp. water mite diet isolate 5915-BHL032417-GBD27992_11977-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGTTTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGATCATTAATCGGAGACGATCAACTTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCGCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605846 Chironomidae sp. water mite diet isolate 5916-BHL032417-GBD17493_14980-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGGACTTCTTTAAGTATTTTTATTCGAGCAGAACTCGGTCAAGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTCTATTATTATCTAGATCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605847 Chironomidae sp. water mite diet isolate 5918-BHL032417-GBD24880_22992-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATAGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTGCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACATTATTATTATCAAGAACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605848 Chironomidae sp. water mite diet isolate 5926-BHL032417-GBD29315_18134-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGTCACACTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTATTATTATCTAGATCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605849 Chironomidae sp. water mite diet isolate 5928-BHL032417-GBD17810_28257-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGTCATCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTAATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGTAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID KM102730, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605850 Chironomidae sp. water mite diet isolate 5929-BHL032417-GBD24609_13529-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCCCCTGATATAGCATTCCCGCGAATAAATAATATAAGATTTTGATTATTTCCCCCGTCATTAACCTTATTATTATCTAGCACACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605851 Chironomidae sp. water mite diet isolate 5932-BHL032417-GBD28139_19864-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTCTTAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATTGGAGATGGTCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACATTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605852 Chironomidae sp. water mite diet isolate 5933-BHL032417-GBD22550_22051-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCATTAACTTTATTACTATCTGGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605853 Chironomidae sp. water mite diet isolate 5938-BHL032417-GBD27982_20015-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTTGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCATGCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTGCTGCCCCCATCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605854 Chironomidae sp. water mite diet isolate 5940-BHL032417-GBD20395_4715-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAAAACTCGGTCATCCTGGTACTTTTATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605855 Chironomidae sp. water mite diet isolate 5942-BHL032417-GBD19447_26560-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATACTTATTCGAGCAGAGTTAGGACGGACAGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTACCCGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCGATTTTAATTGGTGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGGGCCCCTGATATAGCCTTCCCGCGAATAAATAATATAAGATTTTGACTTCTCCCACCGTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KJ208847, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605856 Chironomidae sp. water mite diet isolate 5943-BHL032417-GBD8130_23724-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTAGGAGCATGATCAGGTATAGTAGGTACTGCTTTAAGAATTTTAATTCGAGCAGAATTAGGTCACGCTGGTTCTTTAATCGGAAAAGATCAACTTTATAACGTAATTGTTACCGCTCACGCTTTTTTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605857 Chironomidae sp. water mite diet isolate 5945-BHL032417-GBD22998_26439-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTACTTCCTTTAATATTGGGAGCTCCTGATATAGCATTCCCCCGAATAAATAACATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTATTATTATCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605858 Chironomidae sp. water mite diet isolate 5948-BHL032417-GBD25645_21554-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGTAGAACTAGGACACGCTGGTTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTATTATTATCAAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605859 Chironomidae sp. water mite diet isolate 5950-BHL032417-GBD14008_5481-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACTCTGTTGCTTTAATCGTCGACTATCAAATTTATAATGGAATTGTTACCGCGCTCGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTTGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605860 Chironomidae sp. water mite diet isolate 5952-BHL032417-GBD19953_9419-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGTATTTTAATTCGAGCAGAACTCGGTCACCCTGGTTCTTTTATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATCTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTATTACTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605861 Chironomidae sp. water mite diet isolate 5953-BHL032417-GBD25730_12989-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGAATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACCCTGGTTCTTTAATTGGTGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTACTATCTAGCACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605862 Chironomidae sp. water mite diet isolate 5954-BHL032417-GBD21854_22419-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACTGCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCAAGCTGGTTCTTTAATCGGGGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCGTCATTAACCTTATTATTATCTAGCACACTAGCTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605863 Chironomidae sp. water mite diet isolate 5955-BHL032417-GBD27526_17576-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTTAGAATTTTAATTCGAGTAGAATTCGGTCACGCTGGTTCATTAATCGGAGACGATCAAATTTATAATGTTATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCATTAACTTTATTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605864 Chironomidae sp. water mite diet isolate 5957-BHL032417-GBD13055_6095-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTATTTTTGGAGCCTGGTCAGGAATAGTCGGTACTTCTTTAAGTATTTTAATTCGAGCAGAATTCGGTCACACTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTATTATTATCAAGAACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605865 Chironomidae sp. water mite diet isolate 5958-BHL032417-GBD16714_17766-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGTATAGTCGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTACTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCCCGAATAAATAACATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTATTATTATCTAGCACACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605866 Chironomidae sp. water mite diet isolate 5959-BHL032417-GBD8626_25958-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTTATCGGTGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATGCCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGGTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605867 Chironomidae sp. water mite diet isolate 5961-BHL032417-GBD6313_19811-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTTGGTCACGCTGGTTCTTTAATCGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTATTAATATCTAGCACACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605868 Chironomidae sp. water mite diet isolate 5962-BHL032417-GBD6277_18340-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGTTTTGGAAATTGATTAGTACCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACCTTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605869 Chironomidae sp. water mite diet isolate 5964-BHL032417-GBD14976_4193-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGTTCACTCTTTATCTTTAATCGGAGACGATCTAATTTATAATGGAATTGTTACCGTACACGCATTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605870 Chironomidae sp. water mite diet isolate 5965-BHL032417-GBD4250_16848-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTATTGGAGCCTGATCAGGTATAGTTGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCAATTTTAATTGGAGGATTTGGAGATTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCATTCCCTCGAATAAATAATATAAGTTTTTGATTGCTGCCCCCGTCATTAACTTTATTATTATCTAGCTCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605871 Chironomidae sp. water mite diet isolate 5967-BHL032417-GBD22386_27195-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTATGTCATGCTGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGTTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTATTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605872 Chironomidae sp. water mite diet isolate 5968-BHL032417-GBD26091_7167-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTTCTTCTTTAAGATTTTTAATTCGAGCAGTACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGTTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACTTTATTATTATCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605873 Chironomidae sp. water mite diet isolate 5973-BHL032417-GBD13980_27884-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGTCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGTCACGCTGGATCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCTTTAACTTTATTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605874 Chironomidae sp. water mite diet isolate 5976-BHL032417-GBD23094_25752-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATATTAATTCGAGCAGAACTAGGTCACGCTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTACTATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACATTATTATTATCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605875 Chironomidae sp. water mite diet isolate 5979-BHL032417-GBD27805_17164-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCAGAACTCGGTCACGCTGGTACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGTTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCTTTAACTTTATTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605876 Chironomidae sp. water mite diet isolate 6049-BHL032417-GBD11781_4383-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACACTATACTTGATCTTAGGAGTATGAGCAGGAATACTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAACCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605877 Chironomidae sp. water mite diet isolate 6078-BHL032417-GBD7844_8606-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTGCTTCTTTCTAGTTGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR647156, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605878 Chironomidae sp. water mite diet isolate 6125-BHL032417-GBD2373_12941-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAAGTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605879 Chironomidae sp. water mite diet isolate 6133-BHL032417-GBD21986_8048-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGTACGGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCAAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCATTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.0% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605880 Chironomidae sp. water mite diet isolate 6193-BHL032417-GBD12604_21859-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACCTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605881 Chironomidae sp. water mite diet isolate 6238-BHL032417-GBD25294_19296-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATAATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR647156, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605882 Chironomidae sp. water mite diet isolate 6258-BHL032417-GBD23969_23580-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTACTTTATCCCTTCTTCGTTCTAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR647156, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605883 Chironomidae sp. water mite diet isolate 6348-BHL032417-GBD26793_11443-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGTATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAACATAAGATTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR647156, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605884 Chironomidae sp. water mite diet isolate 6381-BHL032417-GBD11962_8038-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAACACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTT-TCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605885 Chironomidae sp. water mite diet isolate 6404-BHL032417-GBD14828_27069-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTCTTATTGGTGACGACTATATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR647156, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605886 Chironomidae sp. water mite diet isolate 6592-BHL032417-GBD23176_21518-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGAACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGATCAACTATATAATACCTTAGTTACTGCACATGCATTT------------TTAATAGTTATATCCATTTTCATTGGAGGGTTTGGAAATTGATTAGATCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 80.6% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605887 Chironomidae sp. water mite diet isolate 6609-BHL032417-GBD6464_14897-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTGGGTACTTCTTTAAGAATTTTTATTCGAGCAGAACTCGGTCAAGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATACTGGGAGCCCCTGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTGTTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605888 Chironomidae sp. water mite diet isolate 6620-BHL032417-GBD11349_2314-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTAGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605889 Chironomidae sp. water mite diet isolate 6659-BHL032417-GBD15928_15219-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTGGGAGCCTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTATTTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605890 Chironomidae sp. water mite diet isolate 6702-BHL032417-GBD14261_24411-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605891 Chironomidae sp. water mite diet isolate 6765-BHL032417-GBD19173_4496-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTATGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605892 Chironomidae sp. water mite diet isolate 6875-BHL032417-GBD15035_12483-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGTTTTGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCCTCTTTCTAGATTATTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605893 Chironomidae sp. water mite diet isolate 6927-BHL032417-GBD16242_19233-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTACAAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATATAATTGTTACAGCTCATGCTTATATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCTCCTGACAAAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCCTCTTTCTAGTTTTCTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605894 Chironomidae sp. water mite diet isolate 7162-BHL032417-GBD8622_26024-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTCCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTGCCTTTAATATTGGGAGCCCTTGAGATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605895 Chironomidae sp. water mite diet isolate 7608-BHL040517-GBD18639_6221-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTATTCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605896 Chironomidae sp. water mite diet isolate 7714-BHL040517-GBD16647_5515-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACATCCCTAAGAATACTAATTCGGGCTGAATTAGGTCACCCAGTAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAGGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605897 Chironomidae sp. water mite diet isolate 7730-BHL040517-GBD11410_23172-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGACCCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTACTTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCTTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KM993958, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605898 Chironomidae sp. water mite diet isolate 7765-BHL040517-GBD18536_20764-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCATGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605899 Chironomidae sp. water mite diet isolate 7800-BHL040517-GBD27171_11711-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCAGGCTGAATTAGGTCACCCAGGAACATTAATTGATGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACTTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605900 Chironomidae sp. water mite diet isolate 7841-BHL040517-GBD19091_14814-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGGCATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605901 Chironomidae sp. water mite diet isolate 7855-BHL040517-GBD12686_9264-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTATCCCCCTCTCTTACTCTTCCTCTTTCTAGATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605902 Chironomidae sp. water mite diet isolate 7863-BHL040517-GBD10967_17389-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGGGCCTGATCGGGGATAGTAGGGACTTCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTTTACCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGATTACTCCCCCCTTCTCTTACTCTTTTACTTTCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605903 Chironomidae sp. water mite diet isolate 7940-BHL040517-GBD9174_25866-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGGGCCTGATCGGGGATAGTAGGGACTTCCCTAAGAATACTAATTCGTGCTGAATTAGGACACCCAGGAACATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTGTTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTAACCCTATTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605904 Chironomidae sp. water mite diet isolate 8002-BHL040517-GBD12049_22306-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCGGGGATAGTAGGGACTTCCTTAAGAATACTTATTCGTGCTGAATTAGGTCAACCAGGAACATTAATTGGTGACAACCAAATTTATAATGTTATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAAAATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTACCTCCTTCTCTTACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605905 Chironomidae sp. water mite diet isolate 8062-BHL040517-GBD23351_20404-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATATTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTATAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACATGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605906 Chironomidae sp. water mite diet isolate 8085-BHL040517-GBD11811_23039-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGAACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAAGATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGGTTCGGAAATTGACTGTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGGTTCTGATTACTACCTCCTTCTCTAACTCTTTTACTGTCTAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605907 Chironomidae sp. water mite diet isolate 8094-BHL040517-GBD7421_21608-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATACATTATTTCTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCAGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTACTCTTTTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605908 Chironomidae sp. water mite diet isolate 8142-BHL040517-GBD7198_14271-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACTTCTTTAAGAATATTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTCGGAAATTGGCTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGATTACTCCCTCCTTCTCTTACTCTATTACTTTCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605909 Chironomidae sp. water mite diet isolate 8165-BHL040517-GBD23788_15454-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGACTTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGATTACTACCACCTTCTCTTACTCTACTACTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605910 Chironomidae sp. water mite diet isolate 8173-BHL040517-GBD5786_20594-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR278209, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605911 Chironomidae sp. water mite diet isolate 8190-BHL040517-GBD13353_28747-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGGGCTGAATTAGGACACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605912 Chironomidae sp. water mite diet isolate 8219-BHL040517-GBD28945_13050-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGTGCCTGATCGGGGATAGTAGGGACTTCCCTAAGAATACTAATTCGTGCTGAATTAGGTCAACCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCCTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTTCCTCCTTCTCTAACTCTTTTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR278209, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605913 Chironomidae sp. water mite diet isolate 8230-BHL040517-GBD4691_22343-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCTTGATCGGGGATAGTAGGGACTTCTTTAAGTATACTAATTCGTGCTGAATTAGGTCACCCAGGAACTTTAATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTATTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605914 Chironomidae sp. water mite diet isolate 8252-BHL040517-GBD27239_10495-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACTTCTTTAAGAATACTAATTCGTGCAGAATTAGGACACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTCGGAAATTGACTATTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGATTACTCCCTCCTTCTCTATCTCTTTTACTTTCCAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR278209, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605915 Chironomidae sp. water mite diet isolate 8302-BHL040517-GBD14886_6660-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGTTACATCCCTTAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGTTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCAGTCACTTGCTAGTACAAGAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605916 Chironomidae sp. water mite diet isolate 8320-BHL040517-GBD14116_28766-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGTGCCTGATCGGGGATAGTAGGGACTTCCTTAAGAATGCTAATTCGTGCTGAATTAGGACAACCAGGAACTTTAATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTTGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCCCCTTCTCTAACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605917 Chironomidae sp. water mite diet isolate 8336-BHL040517-GBD11563_21259-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACTTCCTTAAGAATACTTATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGACGACCAAATTTATAATGTTATTGTTACTGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTCTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCCCCTTCTCTTACTCTTTTACTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605918 Chironomidae sp. water mite diet isolate 8345-BHL040517-GBD22121_22234-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGGGCTTGATCGGGGATAGTAGGGACTTCCTTAAGAATACTTATTCGTGCTGAATTAGGACACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTGTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605919 Chironomidae sp. water mite diet isolate 8350-BHL040517-GBD11307_27875-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTGGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605920 Chironomidae sp. water mite diet isolate 8564-BHL101416-GBD20141_10239-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605921 Chironomidae sp. water mite diet isolate 8613-BHL101416-GBD20508_26676-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATAGGAGACGATCAAATTTATAATGTCATTGCTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACCTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605922 Chironomidae sp. water mite diet isolate 8628-BHL101416-GBD21080_23157-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTCGTCCCCCTAATACTTGGAGCACCTGACGTAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCGGCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605923 Chironomidae sp. water mite diet isolate 8635-BHL101416-GBD21464_5759-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTAGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATGTAAGTTTTTGACTTTTACCCCCTTCATTATCTTTACTTCTTTCTAGTTCAATCGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID KR293527, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605924 Chironomidae sp. water mite diet isolate 8647-BHL101416-GBD20936_24779-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATGGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTCATTATAATTTTCTTTATAGTTATACCAGTTTTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATGGCCTTCCCACGACTTAACAATATAAGATTTTGACTTCTACCACCTTCACTAATCCTACTGGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.1% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605925 Chironomidae sp. water mite diet isolate 8658-BHL101416-GBD15073_15616-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCGTGATCGGGAATAGTAGGAACTTCTCTTAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAAATTTAATTGGAGATGATCAAATTTATAATGTTATTGTAACAGCCCATGCCTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTGCCATTAAAATTAGGAGCACCTGCTATGGCATTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCTCTTACTCAT--CTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR754220, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605926 Chironomidae sp. water mite diet isolate 8674-BHL101416-GBD28066_18005-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGTAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCATCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.4% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605927 Chironomidae sp. water mite diet isolate 8692-BHL101416-GBD24763_18061-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGTACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605928 Chironomidae sp. water mite diet isolate 8695-BHL101416-GBD22184_13206-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCGGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGCTATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTGCCATTAATATTAGGAGCACCTGATATGGCATTTCCTCGAATAAATAATATAAGATTTTGACCTTTACCCCCTTCCTTAACATTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID KR754220, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605929 Chironomidae sp. water mite diet isolate 8711-BHL101416-GBD28930_12312-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACCTTATTATTATCTAGCGCTGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605930 Chironomidae sp. water mite diet isolate 8720-BHL101416-GBD23647_8163-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605931 Chironomidae sp. water mite diet isolate 8732-BHL101416-GBD7271_6281-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGTATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATGCTTGGAGCACCAGATAAGGCCTTCCCACGACTTAACAATTTAAGATTTTGACTTCTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCA---GTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.2% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605932 Chironomidae sp. water mite diet isolate 8795-BHL101416-GBD27950_14764-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATACTTAATCTTAGTAGTATGAGCAGGAATAGTTGGTACACGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAAAGACCAACTATATAATACCTTAGTTACCGCACATGCATTTTTAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATAATTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605933 Chironomidae sp. water mite diet isolate 8800-BHL101416-GBD24836_12348-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTGTATTTTATTTTTGGAGCGTGATCGGGAATAGTAGGAACTTCTCTTAGAATATTAATTCGAGCTGAATTAGAACATCCTGGAAATTTAATTGGAGATGATCAAATTTATAATGTTATTGTAACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGGCTAGTGCCATTAATATTAGGAGCACCTGATATGGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR754220, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605934 Chironomidae sp. water mite diet isolate 8830-BHL101416-GBD14275_26255-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605935 Chironomidae sp. water mite diet isolate 9550-BHL032417-GBD18626_5106-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAACGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605936 Chironomidae sp. water mite diet isolate 9573-BHL032417-GBD25641_9185-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCATATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605937 Chironomidae sp. water mite diet isolate 9581-BHL032417-GBD9228_18362-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGGGGGTTTGGAAACTGACTAGTTCCCTTAATATTAGGAGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCTTTAACTCTTCTTTTATCAAGCTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR161705, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605938 Chironomidae sp. water mite diet isolate 9596-BHL032417-GBD23266_9070-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605939 Chironomidae sp. water mite diet isolate 9625-BHL032417-GBD5232_10386-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGCACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACAGGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTATTGCCCCCATCATTAACTTTACTGTTATCAAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605940 Chironomidae sp. water mite diet isolate 9749-BHL040517-GBD14396_5684-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCTAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAAC---TCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605941 Chironomidae sp. water mite diet isolate 9751-BHL040517-GBD6932_10996-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGTATATTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTCATTGTAGACGATCAAATTTATAATGTAATTGTTACAGCACACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605942 Chironomidae sp. water mite diet isolate 9778-BHL040517-GBD9041_17328-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTCTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605943 Chironomidae sp. water mite diet isolate 9782-BHL040517-GBD8209_14813-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTAGGAGCTTGATCGGGAATAGTATGCACTTGTTTAAGAATTTTAATTCGACTAGAATTAGGTCACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCATTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCACTAACCTTACTTTTATCATGAGCAAAAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605944 Chironomidae sp. water mite diet isolate 9791-BHL040517-GBD4720_11884-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGTATATTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCGATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605945 Chironomidae sp. water mite diet isolate 9795-BHL040517-GBD28340_13758-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGATCATTCATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGAATAGTACCTCTGATATTTGGGACTCCTTATATAGCTTTTCCGCGAATAAAAAAAATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605946 Chironomidae sp. water mite diet isolate 9796-BHL040517-GBD7312_12111-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCGGGTATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCCCCTGATATAGCATTCCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605947 Chironomidae sp. water mite diet isolate 9857-BHL040517-GBD14888_21077-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605948 Chironomidae sp. water mite diet isolate 9919-BHL040517-GBD3500_20719-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTCTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605949 Chironomidae sp. water mite diet isolate 9920-BHL040517-GBD18548_4282-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCCTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605950 Chironomidae sp. water mite diet isolate 9957-BHL040517-GBD11608_28230-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGTTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605951 Chironomidae sp. water mite diet isolate 9966-BHL040517-GBD12405_13445-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605952 Chironomidae sp. water mite diet isolate 9982-BHL040517-GBD19707_13220-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTCTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605953 Chironomidae sp. water mite diet isolate 9985-BHL040517-GBD15700_7042-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTCGGTGTCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCGAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605954 Chironomidae sp. water mite diet isolate 10012-BHL040517-GBD22042_6852-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTCGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605955 Chironomidae sp. water mite diet isolate 10013-BHL040517-GBD7353_12236-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTTATAATTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCGCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605956 Chironomidae sp. water mite diet isolate 10034-BHL040517-GBD19520_5750-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAACTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605957 Chironomidae sp. water mite diet isolate 10044-BHL040517-GBD12204_15280-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGATATGACCAAATTTATAATGTTGTAGTTACCGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTCGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605958 Chironomidae sp. water mite diet isolate 10046-BHL040517-GBD19646_14221-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTGATTGGAGGCTTTGGAAGTTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCTCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605959 Chironomidae sp. water mite diet isolate 10050-BHL040517-GBD3019_14827-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATCTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTGTTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605960 Chironomidae sp. water mite diet isolate 10059-BHL040517-GBD20896_14919-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGTATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTACTTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTATGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTACCGAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605961 Chironomidae sp. water mite diet isolate 10066-BHL040517-GBD26549_8922-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGACTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605962 Chironomidae sp. water mite diet isolate 10080-BHL040517-GBD10071_12209-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCGAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605963 Chironomidae sp. water mite diet isolate 10085-BHL040517-GBD17463_26636-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGAACATTCCTAGGAAGAGATCAACTATATAATACTGTAGTAACTGCACATGCATTCATAATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.3% identical to accession ID KR765094, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605964 Chironomidae sp. water mite diet isolate 10086-BHL040517-GBD14078_26677-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACATTTATTGGTGATGACCAAATTTATAACGTAATAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTC-TATTAGTTGTA--TCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.3% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605965 Chironomidae sp. water mite diet isolate 10093-BHL040517-GBD8982_10450-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGACACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605966 Chironomidae sp. water mite diet isolate 10094-BHL040517-GBD4550_11144-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATAATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATGGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605967 Chironomidae sp. water mite diet isolate 10140-BHL040517-GBD23041_9568-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAGCCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605968 Chironomidae sp. water mite diet isolate 10149-BHL040517-GBD17013_18689-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.9% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605969 Chironomidae sp. water mite diet isolate 10176-BHL040517-GBD19708_17584-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGACACCTATTTTAATTGGAGGCTTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605970 Chironomidae sp. water mite diet isolate 10179-BHL040517-GBD10584_26086-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCACATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605971 Chironomidae sp. water mite diet isolate 10187-BHL040517-GBD14968_21508-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AATCATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTCGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.4% identical to accession ID KP697533, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605972 Chironomidae sp. water mite diet isolate 10201-BHL040517-GBD22554_9242-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605973 Chironomidae sp. water mite diet isolate 10203-BHL040517-GBD9588_4056-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAATAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATATACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605974 Chironomidae sp. water mite diet isolate 10208-BHL040517-GBD10429_13902-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAACTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCCTTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605975 Chironomidae sp. water mite diet isolate 10209-BHL040517-GBD19361_13207-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAGGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAGTATTTATTGGTAGATTTGGAAATTGACTTCTACCTCTAATACTCGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605976 Chironomidae sp. water mite diet isolate 10227-BHL040517-GBD19410_21773-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605977 Chironomidae sp. water mite diet isolate 10228-BHL040517-GBD21776_20505-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAACACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.7% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605978 Chironomidae sp. water mite diet isolate 10238-BHL040517-GBD24726_20552-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCGAATTTATAATGTTGTAGTTACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAACACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCGATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605979 Chironomidae sp. water mite diet isolate 10242-BHL040517-GBD10477_27350-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCCTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605980 Chironomidae sp. water mite diet isolate 10245-BHL040517-GBD14571_4816-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605981 Chironomidae sp. water mite diet isolate 10260-BHL040517-GBD23261_12960-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACGTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATACGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605982 Chironomidae sp. water mite diet isolate 10265-BHL040517-GBD20762_19402-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KM992253, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605983 Chironomidae sp. water mite diet isolate 10285-BHL040517-GBD24902_16541-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACAACCCGGGACATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605984 Chironomidae sp. water mite diet isolate 10295-BHL040517-GBD22951_24064-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTCTTTCTGGTTATACCAGTACTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCCCCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605985 Chironomidae sp. water mite diet isolate 10300-BHL040517-GBD6552_14866-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGCACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCGCATGCATTTTTAATAATTTTTTTCTTAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGTCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCGAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.9% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605986 Chironomidae sp. water mite diet isolate 10320-BHL040517-GBD23158_12548-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.1% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605987 Chironomidae sp. water mite diet isolate 10327-BHL040517-GBD12101_4484-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGTGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCAACTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605988 Chironomidae sp. water mite diet isolate 10337-BHL040517-GBD9858_25212-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTGCCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605989 Chironomidae sp. water mite diet isolate 10365-BHL040517-GBD11686_6328-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAGTACCTTAGTTACTGCACATGCATTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTGCCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605990 Chironomidae sp. water mite diet isolate 10377-BHL040517-GBD10616_12337-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAATAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACCATTACCCCCATCACTAA---TTCTATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.5% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605991 Chironomidae sp. water mite diet isolate 10386-BHL040517-GBD20069_22938-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGCCCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605992 Chironomidae sp. water mite diet isolate 10415-BHL040517-GBD19405_26237-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACACTATACTTAATCTTAGGAGTATGAGCAGGACTAGTTGGTACAGGAACAAGACTATTAATTCGTATTAAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATACAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605993 Chironomidae sp. water mite diet isolate 10514-BHL040517-GBD9893_23201-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAGGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTGACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGTTTTTCCTCGAATAATTAATATAAGTTCCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605994 Chironomidae sp. water mite diet isolate 10521-BHL040517-GBD8310_18357-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTTCATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTACTTTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID GU565708, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605995 Chironomidae sp. water mite diet isolate 10533-BHL040517-GBD11447_22687-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGAACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW605996 Chironomidae sp. water mite diet isolate 10540-BHL040517-GBD22407_26278-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGGATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605997 Chironomidae sp. water mite diet isolate 10547-BHL040517-GBD15064_25280-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATCTTTTTTATAGTGATGCCTATTTTAATTGGAGGCTATGGAAATTGATTAGTACCTTGGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCGAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.0% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605998 Chironomidae sp. water mite diet isolate 10560-BHL040517-GBD21049_14779-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGACTAGAACTAGGACATCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCATTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW605999 Chironomidae sp. water mite diet isolate 10601-BHL040517-GBD5407_20903-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTGTAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606000 Chironomidae sp. water mite diet isolate 10666-BHL040517-GBD18083_10912-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAAATTTATAATGTAATTGTTACAGCACATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.2% identical to accession ID KR757714, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606001 Chironomidae sp. water mite diet isolate 10670-BHL040517-GBD28769_15213-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACCAGAATTAGGACACCCTGGCACATTTATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCATCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606002 Chironomidae sp. water mite diet isolate 10673-BHL040517-GBD14813_9253-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGCACTTCTTTTAGAATTTTAATTCGAGTAGAATTAGGACATCCAGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCATTTCCGCGAATAAATAACATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606003 Chironomidae sp. water mite diet isolate 10683-BHL040517-GBD13813_1863-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAGTATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCCACTACTATCTAGTACATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606004 Chironomidae sp. water mite diet isolate 10717-BHL101516-GBD11135_4015-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTCTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.1% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606005 Chironomidae sp. water mite diet isolate 10749-BHL101516-GBD27373_11025-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTCTTTATTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCCTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.1% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606006 Chironomidae sp. water mite diet isolate 10770-BHL101516-GBD16105_28020-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGTCCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGGTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTGGTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606007 Chironomidae sp. water mite diet isolate 10772-BHL101516-GBD8668_11675-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACTGG	Using NCBI BLASTN in June 2018, this sequence was 86.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606008 Chironomidae sp. water mite diet isolate 10781-BHL101516-GBD8123_5449-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAACCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGACCAAATTTATAACGTAATTGTAACCGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCGATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGGGCCCCTGATATAGCCTTCCCGCGAATAAATAATATAAGATTTTGACTTCTCCCACCGTCTCTTTCTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ208847, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606009 Chironomidae sp. water mite diet isolate 10789-BHL101516-GBD24176_9105-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCGATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGGGCCCCTGATATAGCCTTCCCGCGAATAAATAATATAAGATTTTGACTTCTCCCACCGTCTCTTTCTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KJ208847, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606010 Chironomidae sp. water mite diet isolate 10815-BHL101516-GBD7774_15008-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGACATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCCGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606011 Chironomidae sp. water mite diet isolate 10821-BHL101516-GBD23213_10871-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGCACTTCCTTAAGTATACTTATTCGAGCAGAGTTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTAACCGCACATGCTTTTATTATAATTTTTTTTATAGTTGTACCGATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGGGCCCCTGATATAGCCTTCCCGCGAATAAATAATATAAGATTTTGACTTCTCCCACCATCTCTAATCT-TACTGATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KJ209337, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606012 Chironomidae sp. water mite diet isolate 10852-BHL101516-GBD8831_20496-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGCACTTCCTTAAGTATACTTATTCGAGCAGAGTTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTAACCGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATACGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCT-TACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID KJ209337, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606013 Chironomidae sp. water mite diet isolate 10884-BHL101516-GBD12799_24707-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGCTCTTCCTTAAGTATACTTATTCGAGCAGAGTTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTAACCGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCGATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCT-TACTGATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KJ209337, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606014 Chironomidae sp. water mite diet isolate 11009-BHL110116-GBD21631_25625-Lq74 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATCGGAGATGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KM102730, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606015 Chironomidae sp. water mite diet isolate 11010-BHL110116-GBD24926_21832-Lq74 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGTATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTTTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTTGGAGCTCCTGATACAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606016 Chironomidae sp. water mite diet isolate 11054-BHL110116-GBD23921_15945-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606017 Chironomidae sp. water mite diet isolate 11064-BHL110116-GBD16942_25778-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606018 Chironomidae sp. water mite diet isolate 11067-BHL110116-GBD16375_26233-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGACTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCTTCAGCAGCAGGAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606019 Chironomidae sp. water mite diet isolate 11068-BHL110116-GBD17464_16986-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606020 Chironomidae sp. water mite diet isolate 11070-BHL110116-GBD8458_14627-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGAACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606021 Chironomidae sp. water mite diet isolate 11081-BHL110116-GBD18968_6153-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606022 Chironomidae sp. water mite diet isolate 11085-BHL110116-GBD6316_10137-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAATAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606023 Chironomidae sp. water mite diet isolate 11088-BHL110116-GBD11502_24765-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTGATCGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID KT606986, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606024 Chironomidae sp. water mite diet isolate 11089-BHL110116-GBD25106_11245-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTGATCGGAGGCTTTGGAAATTGACTATTACCACTTATACTTGGAGCCCCTGATATGGCCTTTCCTCGAATAAATAACATAAGATTCTGGTTACTACCTCCGTCTATTTCTTTGCTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM919897, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606025 Chironomidae sp. water mite diet isolate 11100-BHL110116-GBD20512_19731-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCCATTTTAATCGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606026 Chironomidae sp. water mite diet isolate 11105-BHL110116-GBD17620_12381-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAA-TCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID KR276243, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606027 Chironomidae sp. water mite diet isolate 11110-BHL110116-GBD9182_12195-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGACTATTACCACTTATACTTGGAGCCCCTGATATGGCCTTTCCTCGAATAAATAACATAAGATTCTGGTTACTACCTCCGTCTATTTCTTTGCTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606028 Chironomidae sp. water mite diet isolate 11115-BHL110116-GBD17847_7034-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AATCATAAAGATATTGGAACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.2% identical to accession ID KP697581, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606029 Chironomidae sp. water mite diet isolate 11122-BHL110116-GBD21222_26050-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCATTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAAACTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606030 Chironomidae sp. water mite diet isolate 11134-BHL110116-GBD15207_10806-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGGATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KR751697, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606031 Chironomidae sp. water mite diet isolate 11144-BHL110116-GBD17819_11449-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTATGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGTAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTAACTTTGATATTAGGAGCTCCTGATATAGCATGTCCACGAATAAAAAATATAAGAGTTTGATTATTACCCCCTTCATTAACCTTACTTATATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606032 Chironomidae sp. water mite diet isolate 11152-BHL110116-GBD16660_22048-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAAAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAGTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606033 Chironomidae sp. water mite diet isolate 11156-BHL110116-GBD9540_12998-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTGATCGGAGGCTTTGGAAATTGACTATTACCTCTTATACTTGGAGCCCCTGATATAGCCTTTCCTCGAATAAATAACATAAGATTCTGGTTACTACCTCCCTCTATAACTCTGCTTCTTTCTAGAACAATAGTGGAAAATGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606034 Chironomidae sp. water mite diet isolate 11164-BHL110116-GBD20829_26403-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGTAGAATTAGGACACCCAGGTTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606035 Chironomidae sp. water mite diet isolate 11167-BHL110116-GBD16480_19250-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606036 Chironomidae sp. water mite diet isolate 11168-BHL110116-GBD10947_15987-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACATCCAGGAACTTTAATCGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTGATCGGAGGCTTTGGAAATTGACTATTACCACTTATACTTGGAGCCCCTGATATGGCCTTTCCTCGAATAAATAACATAAGATTCTGGTTACTACCTCCGTCTATTTCTTTGCTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606037 Chironomidae sp. water mite diet isolate 11173-BHL110116-GBD16302_4380-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTGATAGGAGGCTTTGGAAATTGACTATTACCACTTATACTTGGAGCCCCTGATATGGCCTTTCCTCGAATAAATAACATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606038 Chironomidae sp. water mite diet isolate 11178-BHL110116-GBD28377_14652-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGATCATTAATAGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606039 Chironomidae sp. water mite diet isolate 11182-BHL110116-GBD10221_11528-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGCAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606040 Chironomidae sp. water mite diet isolate 11187-BHL110116-GBD25875_11486-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGTACTTTAATTGGAGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTGATCGGAGGGTTTGGAAATTGACTATTACCTCTTATACTTGGAGCCCCTGATATGGCCTTTCCTCGAATAAATAACATAAGATTCTGGTTACTACCTCCGTCTATTACTTTACTACTATCTAGATCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606041 Chironomidae sp. water mite diet isolate 11197-BHL110116-GBD18581_18638-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACCTTAATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTGATCGGAGGCTTTGGAAATTGACTATTACCACTTATACTTGGAGCCCCTGATATGGCCTTTCCTCGAATAAATAACATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606042 Chironomidae sp. water mite diet isolate 11203-BHL110116-GBD21628_17447-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTATGACATCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATATTGATTGGAGGCTTTGGAAACTGACTATTACCACTAATACTTGGAGCCCCTGATATGGCCTTTCCACGAATAAATAACATAAGATTCTGGTTACTACCTCCGTCTATTACCTTGCTTCTTTCTAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606043 Chironomidae sp. water mite diet isolate 11210-BHL110116-GBD19245_13669-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATTTTCGGAGCTTGATCAGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAAAATTAGGACATCCTGGAACTTTAATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGACTATTACCACTTATACTTGGAGCCCCTGATATGGCCTTTCCTCGAATAAATAACATAAGATTCTGATTACTACCTCCGTCTATTACTTTGCTTCTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606044 Chironomidae sp. water mite diet isolate 11220-BHL110116-GBD12291_3353-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTCGGTCACCCAGGTTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTGGGAGCTCCTGATATAGCATTCCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTATTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606045 Chironomidae sp. water mite diet isolate 11224-BHL110116-GBD21134_27810-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGAAATTAGGGGCTCCTGATATAGCTTTTCCGCGAAGAAAAAAAATAAGATATTGATTAGTACCCCCGTCAGTAACCGTACATTTATCAAGAGCAAGAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606046 Chironomidae sp. water mite diet isolate 11232-BHL110116-GBD26886_19740-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTAGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCTAGCAAAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCACCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.6% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606047 Chironomidae sp. water mite diet isolate 11233-BHL110116-GBD3553_17004-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAAAACTCGGTCACGCTGGTTCCTTAACTGGTGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCGATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606048 Chironomidae sp. water mite diet isolate 11237-BHL110116-GBD27623_10298-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGTATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTCGGTCACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTAGTGGCTCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTATTATCAAGATCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606049 Chironomidae sp. water mite diet isolate 11238-BHL110116-GBD6214_21981-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGGTCGGGAATAGTCGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGATCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCATCATTAACCCTACTTTTATCAAGAAAAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606050 Chironomidae sp. water mite diet isolate 11242-BHL110116-GBD25033_11310-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGTATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTGATATTAGGAGATCCTGATATAGCTTTTCCCCGAATAAATAACATAAGATTTTGATTAATACCCCCATCATTAACCCTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606051 Chironomidae sp. water mite diet isolate 11243-BHL110116-GBD12242_16185-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACTTTATATTTTATTTTTGGAGCCTGATCGGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTGTTTTGATCGGAGGCTTTGGAAATTGACTATTACCACTTATACTTGGAGCCCCTGATATGGCCTTTCCTCGAATAAATAACATAAGATTCTGGTTACTACCTCCGTCTATTTCTTTGCTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606052 Chironomidae sp. water mite diet isolate 11265-BHL110116-GBD26063_12766-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAGTTCGACTAGAATTAGGACACCCAGGTTCCTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCATTTCCGCGAATAAATAACATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606053 Chironomidae sp. water mite diet isolate 11271-BHL110116-GBD9179_22423-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTCGGACATCCAGGTACTTTAATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTATAGTAATACCTATTTTGATTGGAGGCTTTGGAAATTGACTATTACCACTTATACTGGGAGCCCCTGATATAGCCTTCCCTCGAATAAATAATATAAGATTCTGATTACTACCTCCGTCTATTACTTTGCTACTATCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606054 Chironomidae sp. water mite diet isolate 11283-BHL110116-GBD18469_24796-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGTACTTCTTTAAGAATTTTAATTCGACCAGAATTAGGACACCCTGGCTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTAATATTTGGGGCTCCTGATATAGCATTTCCGCGAATAAATAATATAAGATTTTGATTATCACCCCCGTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606055 Chironomidae sp. water mite diet isolate 11292-BHL110116-GBD22560_13646-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTCGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACATCCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCACGAATAAATAATATAAGATTTTGATTATTGCCCCCATCATTAACCTTATTTTTATCTAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606056 Chironomidae sp. water mite diet isolate 11295-BHL110116-GBD23787_8748-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAGTTGGAACTTCTTTAAGAATTCTAGTTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606057 Chironomidae sp. water mite diet isolate 11296-BHL110116-GBD12020_27087-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAACTAGGACACCCAGGCTCATTTATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606058 Chironomidae sp. water mite diet isolate 11302-BHL110116-GBD24730_19282-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGATCTTTAATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATGATTTTTTTATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGACTAGTACCTCTTATACTTGGTGCCCCTGATATAGCCTTTCCGCGAATAAATAACATAAGATTCTGATTACTACCTCCGTCAATAACCTTGCTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR292221, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606059 Chironomidae sp. water mite diet isolate 11310-BHL110116-GBD2152_12890-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACAACCAGGCACATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTGATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTCTGACTATTACCCCCCTCATTAACCGTACTTCTATCAAGATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606060 Chironomidae sp. water mite diet isolate 11317-BHL110116-GBD27583_9245-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCGGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCCGATATAGCATTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTATTATCAAGATCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606061 Chironomidae sp. water mite diet isolate 11320-BHL110116-GBD12600_6104-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCGAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATAGTAGAGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGAGTTTGATTATTACCCCCATCATTAACCATGCCAATATCAAGAACAAGAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606062 Chironomidae sp. water mite diet isolate 11322-BHL110116-GBD15167_10320-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGTATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAACTCGGACACCCAGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCACACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCTCCTGATATAGCATTCCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606063 Chironomidae sp. water mite diet isolate 11328-BHL110116-GBD23123_12071-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGATCTTTAATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTGATTGGAGGCTTTGGAAATTGACTATTACCACTAATACTTGGAGCCCCTGATATGGCCTTTCCTCGAATAAATAACATAAGATTCTGGTTGCTACCTCCATCTATATCTTTGCTACTATCTAGATCAATTGTGGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606064 Chironomidae sp. water mite diet isolate 11341-BHL110116-GBD9402_21784-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCAACTAGAATTAGGACACCCAGGCTCATTAATCGAAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACGTCTTCCCCCCTCTTTAAC---TCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606065 Chironomidae sp. water mite diet isolate 11349-BHL110116-GBD6859_25426-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGTACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATCGGAGGCTTTGGAAATTGACTATTACCACTTATACTTGGAGCCCCTGATATAGCATTTCCTCGAATAAATAACATAAGATTATGATTACTACCTCCGTCTATAACTTTACTACTATCTAGATCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606066 Chironomidae sp. water mite diet isolate 11350-BHL110116-GBD26132_13794-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATTCTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTGATCGGAGGCTTTGGAAATTGACTATTACCACTTATACTTGGAGCCCCTGATATGGCCTTTCCACGAATAAATAACATAAGATTCTGGTTACTACCACCGTCTATTACTTTGCTTCTATCTAGAAGAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606067 Chironomidae sp. water mite diet isolate 11354-BHL110116-GBD27442_13286-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGAACTTCTTTTAGAATTTTAATTCGACTAGAATTAGGACATCCAGGTTCATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGCTTTGGAAATTGATTAGTCCCTTTGATATTAGGAGCTCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606068 Chironomidae sp. water mite diet isolate 11363-BHL110116-GBD20284_18047-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTATTACCCCCTTCATTAACCTTACTTTTATCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606069 Chironomidae sp. water mite diet isolate 11366-BHL110116-GBD16566_18315-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTCATTTTTGGTGCCTGATCAGGAATAGTAGAAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGGACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606070 Chironomidae sp. water mite diet isolate 11372-BHL110116-GBD11090_22347-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCACGAATAAATAATATAAGATTTTGATTATTGCCCCCATCATTAACCTTATTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606071 Chironomidae sp. water mite diet isolate 11374-BHL110116-GBD26150_13124-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGTATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTCGGACACCCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATAGTAGGAGCACCTGATATAGCATTCCCGCGAATAAATAATATAAGATTTTGATTATTTCCCCCGTCATTAACCTTATTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606072 Chironomidae sp. water mite diet isolate 11375-BHL110116-GBD25732_7160-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTTATTGGAGGCTTTGGAAATTGACTATTACCACTTATACTTGGAGCCCCTGATATGGCTTTTCCCCGAATAAATAACATAAGATTCTGATTACTACCTCCGTCTATTTCCCTGCTTCTTTCAAGAACATTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606073 Chironomidae sp. water mite diet isolate 11377-BHL110116-GBD15051_23970-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606074 Chironomidae sp. water mite diet isolate 11379-BHL110116-GBD23551_21682-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACAACCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATGTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCACCTGATATAGCTTTGCCGCGAATAAATAATATAAGATTTTGATTATTGCCCCCTTCATTAACCTTATTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606075 Chironomidae sp. water mite diet isolate 11382-BHL110116-GBD14266_26218-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTGATCGGAGGCTTTGGAAATTGACTATTTCCACTTATACTAGGAGCCCCTGATATAGCCTTTCCCCGAATAAATAACATAAGATTCTGATTACTACCCCCGTCTATTACCTTGCTTCTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606076 Chironomidae sp. water mite diet isolate 11386-BHL110116-GBD14053_20124-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTCGGACACCCTGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTGATATTAGGAGCTCCTGATATAGCATTTCCGCGAATAAATAATATAAGTTTTTGATTATTTCCCCCTTCATTAACCTTATTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606077 Chironomidae sp. water mite diet isolate 11499-BHL101516-GBD4473_8475-Lq80 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACTTTAATTGGAGATGATCAAATTTGTAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTATAGTAATACCTATTTTGATTGGAGGCTTTGGAAATTGACTATTACCACTTATACTTGGAGCCCCTGATATGGCCTTTCCTCGAATAAATAACATAAGATTCTGGTTACTACCCCCGTCTATTACCTTGCTTCTATCTAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606078 Chironomidae sp. water mite diet isolate 11667-BHL101516-GBD10788_7288-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTGGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTAGGAAACTGATTAGTTACTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAAAATTAATGTTATCGAGAGCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606079 Chironomidae sp. water mite diet isolate 11773-BHL101516-GBD18686_16002-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606080 Chironomidae sp. water mite diet isolate 12203-BHL040517-GBD20141_10239-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606081 Chironomidae sp. water mite diet isolate 12252-BHL040517-GBD20508_26676-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATAGGAGACGATCAAATTTATAATGTCATTGCTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACCTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606082 Chironomidae sp. water mite diet isolate 12267-BHL040517-GBD21080_23157-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTCGTCCCCCTAATACTTGGAGCACCTGACGTAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCGGCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606083 Chironomidae sp. water mite diet isolate 12274-BHL040517-GBD21464_5759-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCTCATGCATTTATTATAATTTTTTTATAGTAATACCTATTTTAATTAGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATGTAAGTTTTTGACTTTTACCCCCTTCATTATCTTTACTTCTTTCTAGTTCAATCGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID KR293527, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606084 Chironomidae sp. water mite diet isolate 12286-BHL040517-GBD20936_24779-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATGGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTCATTATAATTTTCTTTATAGTTATACCAGTTTTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATGGCCTTCCCACGACTTAACAATATAAGATTTTGACTTCTACCACCTTCACTAATCCTACTGGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.1% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606085 Chironomidae sp. water mite diet isolate 12297-BHL040517-GBD15073_15616-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCGTGATCGGGAATAGTAGGAACTTCTCTTAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAAATTTAATTGGAGATGATCAAATTTATAATGTTATTGTAACAGCCCATGCCTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTGCCATTAAAATTAGGAGCACCTGCTATGGCATTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCTCTTACTCAT--CTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR754220, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606086 Chironomidae sp. water mite diet isolate 12313-BHL040517-GBD28066_18005-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGTAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCATCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.4% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606087 Chironomidae sp. water mite diet isolate 12331-BHL040517-GBD24763_18061-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGTACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606088 Chironomidae sp. water mite diet isolate 12334-BHL040517-GBD22184_13206-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCGGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGCTATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTGCCATTAATATTAGGAGCACCTGATATGGCATTTCCTCGAATAAATAATATAAGATTTTGACCTTTACCCCCTTCCTTAACATTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID KR754220, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606089 Chironomidae sp. water mite diet isolate 12350-BHL040517-GBD28930_12312-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACCTTATTATTATCTAGCGCTGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606090 Chironomidae sp. water mite diet isolate 12359-BHL040517-GBD23647_8163-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606091 Chironomidae sp. water mite diet isolate 12371-BHL040517-GBD7271_6281-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGTATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATGCTTGGAGCACCAGATAAGGCCTTCCCACGACTTAACAATTTAAGATTTTGACTTCTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCA---GTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.2% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606092 Chironomidae sp. water mite diet isolate 12434-BHL040517-GBD27950_14764-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATACTTAATCTTAGTAGTATGAGCAGGAATAGTTGGTACACGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAAAGACCAACTATATAATACCTTAGTTACCGCACATGCATTTTTAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATAATTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606093 Chironomidae sp. water mite diet isolate 12439-BHL040517-GBD24836_12348-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTGTATTTTATTTTTGGAGCGTGATCGGGAATAGTAGGAACTTCTCTTAGAATATTAATTCGAGCTGAATTAGAACATCCTGGAAATTTAATTGGAGATGATCAAATTTATAATGTTATTGTAACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGGCTAGTGCCATTAATATTAGGAGCACCTGATATGGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR754220, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606094 Chironomidae sp. water mite diet isolate 12469-BHL040517-GBD14275_26255-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606095 Chironomidae sp. water mite diet isolate 12535-BHL040517-GBD26773_7772-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGTAGAATTAGGACACCCAGGTTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTTGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606096 Chironomidae sp. water mite diet isolate 12584-BHL040517-GBD16990_5274-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCATGAGCAGGTATAGTAGGGACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGTTCAAATTGATAATGTAATTGTTACCGCACACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606097 Chironomidae sp. water mite diet isolate 12613-BHL040517-GBD14328_9703-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGTAGAATTAGGTCACCCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCCCCTGATATAGCATTCCCGCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACCTTACTATTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606098 Chironomidae sp. water mite diet isolate 12675-BHL040517-GBD24599_19495-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTCTTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTACTTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAACTTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGAATTTGATTATTACCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGGACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606099 Chironomidae sp. water mite diet isolate 12693-BHL040517-GBD10047_23653-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAAAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTAACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGTGGATTTGGAAATTGGCTTTTACCTTTAATACTTGGAGCCCCTGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCATCTATCACATTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID KP043758, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606100 Chironomidae sp. water mite diet isolate 12694-BHL040517-GBD15139_5081-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GACACTTTACTTTATTTTTGGAGCTTGATCCGGAATAGTAGGAACACCTTTAAGAATATTAATTCGAGCAGAATTAGGGCACCCAGGAACATTGATTGGGGATGATCAAATTTACAATGGAATTGTAACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAACTGGTCGATTTGGAAATTGGCTTTTACCTTTAATACTGGGAGCCCCTGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCATCTATTTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KP043758, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606101 Chironomidae sp. water mite diet isolate 12712-BHL040517-GBD25592_25115-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGATGATCAAATTTATAATGTTATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAAGATTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606102 Chironomidae sp. water mite diet isolate 12724-BHL040517-GBD26008_15236-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCGGGAATAGTAGGTACTTCTTTAAGAATTTTAATTCGCCTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCGAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606103 Chironomidae sp. water mite diet isolate 12767-BHL040517-GBD24071_24735-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACACTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCTCCTGATATAGCATTTCCGCGAATAAATAATATAAGATTTTGATTATTTCCCCCGTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606104 Chironomidae sp. water mite diet isolate 12779-BHL040517-GBD6345_22160-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGACTCATTAATCGGAGACGATCAAATTTATAGTGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATACAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTTTCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606105 Chironomidae sp. water mite diet isolate 12781-BHL040517-GBD10394_19916-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGGTCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAACATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCATTAACTCTATTACTATCAAGCTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606106 Chironomidae sp. water mite diet isolate 12793-BHL040517-GBD24993_21079-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGTAATTGACTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTACTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606107 Chironomidae sp. water mite diet isolate 12797-BHL040517-GBD17826_8315-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GACACTTTACTTTATTTTTGGAGCTTGATCCGGAATAGTAGGAACATCTTTAAGAATATTAATTCGAGCAGAATTAGGGCACCCAGGAACATTGATTGGGGATGATCAAATTTACAATGTAATTGTAGCAGCCCATGCTTTTATTATAATTTTTTTTATACTTATACCAATTTTAATTGGTGGATTTGGAAATTGGCTTTTACCTTTAATACTTGGAGCCCCTGATATGGCCTTTCCACGAATAAATAATATAAGTTTTTGATTACTTCCCCCGT-TATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KP043758, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606108 Chironomidae sp. water mite diet isolate 12837-BHL040517-GBD17879_21613-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGGACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCAAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.6% identical to accession ID KM102730, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606109 Chironomidae sp. water mite diet isolate 12845-BHL040517-GBD27268_23102-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCATCCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTACTATCTAGGTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID KM102730, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606110 Chironomidae sp. water mite diet isolate 12868-BHL040517-GBD6295_7295-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTATTTCGAGCAGAACTCGGTCACGTTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGATCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606111 Chironomidae sp. water mite diet isolate 12882-BHL040517-GBD4214_8333-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGTCTGATCAGATATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAGTAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAACCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCATTAACTTTATTATGATCGAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606112 Chironomidae sp. water mite diet isolate 12899-BHL040517-GBD24572_25756-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGCACATCTTTAAGAATTTTAATTCGAGTAGAATTAGGTCACGCTGGTTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTGATATTAGGAGCCCCTGATATAGCATTCCCGCGAATAAATAATATAAGATTTTGATTATTTCCCCCGTCATTAACCTTACTATTATCAAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606113 Chironomidae sp. water mite diet isolate 12916-BHL040517-GBD26534_14614-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGATCAGAATTATGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATACTGTAATTGTTACATCTCATGCATTTGTACTAATTTTTTTATACTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAAAAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606114 Chironomidae sp. water mite diet isolate 12923-BHL040517-GBD5928_14450-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTACTTTATTTTTGGAGCTTGATCCGGAATAGTAGGAACATCTTTAAGAATATTAATTCGAGCAGAATTAGGACATCCAGGAACATTGATTGGGGATGATCAAATTTACAATGTAATTGTAACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KM994396, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606115 Chironomidae sp. water mite diet isolate 12937-BHL040517-GBD7269_6307-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCCTTAAGTATTCTAATTCGAGCAGAATTAGGACATGCTGGCACATTAATTGGAGACGATCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606116 Chironomidae sp. water mite diet isolate 12943-BHL040517-GBD6660_4734-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTCCCGTTAATATTAGGAGCCCCCGACACAGCATTCCCTCGAATAAATAATATAAGGTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606117 Chironomidae sp. water mite diet isolate 12947-BHL040517-GBD24287_23879-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGTACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGATCATTTATTGGAGACGATCATATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCATTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606118 Chironomidae sp. water mite diet isolate 12963-BHL040517-GBD19125_24553-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTTGGAGCTTGATCAGGCATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGCAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATAAAAGTTTTTGATTATTGCCCCTATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606119 Chironomidae sp. water mite diet isolate 12967-BHL040517-GBD6314_14699-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATCTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGTAGAATTAGGACATGCAGGCTCATTATTTGGAGACGATCAAATTTATAATGTAATTGTTACACCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTACCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606120 Chironomidae sp. water mite diet isolate 12969-BHL040517-GBD25509_23561-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606121 Chironomidae sp. water mite diet isolate 12973-BHL040517-GBD16236_14966-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTTAGAATTTTAATTCGAGCAGAATTAGGACATTCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTACCCCCATCATTAACATTATTATTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606122 Chironomidae sp. water mite diet isolate 12975-BHL040517-GBD21691_10879-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACATGATATGGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTGTTGCCCACATCATTAACTTTATGATGATCGAGAACAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606123 Chironomidae sp. water mite diet isolate 12984-BHL040517-GBD7236_13207-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTCATTGGAGAAGATCAACTTTATAATGTCCTTGTTACAGCTCATGCTTTTTTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGAATGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606124 Chironomidae sp. water mite diet isolate 12986-BHL040517-GBD5838_8509-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACAAGCAGGATCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTGTAATAATTTTTTTATAGTTATACCAGTCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTCTCCCACGAATAAATAATATAAGTTTCTGACTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606125 Chironomidae sp. water mite diet isolate 12992-BHL040517-GBD27520_8700-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTTAGAATTCTAATTCGAGTAGAATTAGGACAAGCAGGCTCATTCCTTGGAGACGATCAACTTTATAATATAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGAGCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606126 Chironomidae sp. water mite diet isolate 12994-BHL040517-GBD8019_16742-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGAATTCTTATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAGTTGTTACAGTTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606127 Chironomidae sp. water mite diet isolate 12995-BHL040517-GBD25786_6948-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGGATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGGCAGGCTGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCCCCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606128 Chironomidae sp. water mite diet isolate 12998-BHL040517-GBD26684_14635-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTATCGGAGCTTGATCATGAATAGTTGTAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACAAGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGATTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTAGGAAACTGACTAGATCATTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGATGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606129 Chironomidae sp. water mite diet isolate 12999-BHL040517-GBD20874_3387-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCTGAACTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTGCCTTTAATATTAGGAGCCCCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGACTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606130 Chironomidae sp. water mite diet isolate 13005-BHL040517-GBD6336_7733-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAAAAATAAAAGGTTTTGAATGGTGCCCCCATCATTAACCTTATTATTATCCAGAACAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606131 Chironomidae sp. water mite diet isolate 13008-BHL040517-GBD14035_18104-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAACAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGGCTTTTACCTTTAATACTCGGGGCCCCTGATATAGCCTTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCATCTATTTCATTACTTCTTTCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KP043758, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606132 Chironomidae sp. water mite diet isolate 13012-BHL040517-GBD10594_4745-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTCTATTTTCGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGTAGAATTAGGACATGCAGGCTCATTAACTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACAGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACTCTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606133 Chironomidae sp. water mite diet isolate 13014-BHL040517-GBD5260_20252-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGAGCAGGAATAGTTGGAACTGCTTTAAGAATTCTAATTCGAGCAGAATTATGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTACTTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATATTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606134 Chironomidae sp. water mite diet isolate 13023-BHL040517-GBD13100_4316-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTATTACCCCCATCATTAACTTTATTATTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606135 Chironomidae sp. water mite diet isolate 13033-BHL040517-GBD15888_10093-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTAGAACTTCTTTTAGAATTCTAATTCGAGCTGAATTATGTCATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATATCATTCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCACCATCATTAACTTTATTATTATCTAGAGCAACTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606136 Chironomidae sp. water mite diet isolate 13037-BHL040517-GBD22599_26046-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGGGCTTGATCCGGAATAGTTGGAACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACATCCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCCTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTGTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606137 Chironomidae sp. water mite diet isolate 13038-BHL040517-GBD8382_14424-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AATCATAAAGATATTGGAACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGAACATGCAGGCTCATTAATTGGAGACGATCAAGTTTATAATGTAATTGTTACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCATCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACGGG	Using NCBI BLASTN in June 2018, this sequence was 82.8% identical to accession ID KP697581, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606138 Chironomidae sp. water mite diet isolate 13039-BHL040517-GBD16994_10022-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCAGGCACTTTCATTGGAGACGATCAAATTTATAATGTTATTGTTACAGTTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606139 Chironomidae sp. water mite diet isolate 13040-BHL040517-GBD10163_8240-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTATATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCAGGAACATTGATTGGGGATGATCAAATTTACAATGTAATTGTAACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGGCTTTTACCTTTAATACTCGGGGCCCCTGATATAGCCTTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCATCTATTTCATTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KP043758, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606140 Chironomidae sp. water mite diet isolate 13041-BHL040517-GBD7283_11977-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATCCAGGATCATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCACCATCATTAACTTTATTATTATCTAGAACAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606141 Chironomidae sp. water mite diet isolate 13052-BHL040517-GBD13451_25104-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATACTAATTCGAGCAGAATTAGGTCATCCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTACTATCAAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606142 Chironomidae sp. water mite diet isolate 13066-BHL040517-GBD15207_25211-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGCATAGTTGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCGTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606143 Chironomidae sp. water mite diet isolate 13068-BHL040517-GBD25268_16872-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AATCATAAAGATATTGGAACACTTTCTTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.9% identical to accession ID KP697581, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606144 Chironomidae sp. water mite diet isolate 13074-BHL040517-GBD7470_20285-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCATGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGCATTAGGACATGCATGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGATCATGCTTTTGTAATAATTTTTTTTATAGTTAGACCAATCTTAATTGTAGGATTTGGAAACCGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCACCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606145 Chironomidae sp. water mite diet isolate 13081-BHL040517-GBD23275_18378-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGCATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAAGAGAAACTGATATGGCTTTCCCACGAATAAATAATATAAAATTTTGATTGTTGCCCCCATCATTAACGGTATTATTATCTAGAGCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606146 Chironomidae sp. water mite diet isolate 13083-BHL040517-GBD19902_22431-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGCACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCAATAACCTTATTATTATCTGGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606147 Chironomidae sp. water mite diet isolate 13085-BHL040517-GBD25201_18906-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGACATGCTGGCTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCCCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTGCCCCCGTCATTAACTTTATTATTATCTAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606148 Chironomidae sp. water mite diet isolate 13088-BHL040517-GBD28771_19369-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGATCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGACATGGCTTTCCCACGAATAAATAATATAAGTTTCTGACTGTTGCCCCCCTCACTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606149 Chironomidae sp. water mite diet isolate 13093-BHL040517-GBD21568_3380-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACATCCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACTTTATTAATATCTAGATCAATTGTGGAGAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606150 Chironomidae sp. water mite diet isolate 13095-BHL040517-GBD2830_10023-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTACTGGATTTTCGGAGATTGATCTGGAATAGTAGGAACTTCTTGAAGAATTCTAATTCGAGTAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGCTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTATTGATTGTTGCCCCCATCATTAACTTGATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606151 Chironomidae sp. water mite diet isolate 13097-BHL040517-GBD27156_10313-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATGCTAATTCGAGCAGAATTAGGACATGCAGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTTTTTCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606152 Chironomidae sp. water mite diet isolate 13100-BHL040517-GBD27161_20862-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCCTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCACATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATCTTAATTGGAGGATTTGGTAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAAAATAAGTTTTTGATTATTGCCCCCATCATTAACTTTATTATTATCTAGATCATTTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606153 Chironomidae sp. water mite diet isolate 13103-BHL040517-GBD11005_15007-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTTTATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCAGGAACATTTATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTTCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606154 Chironomidae sp. water mite diet isolate 13104-BHL040517-GBD19882_24632-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGATTTAGGCCATCCAGTCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTATTGCCCCCATCATTAACGTTATTATTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606155 Chironomidae sp. water mite diet isolate 13105-BHL040517-GBD26267_8047-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGGACATTAATTGGAGACGATAAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTGTAATATTAGGAGAACTTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACTTGATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606156 Chironomidae sp. water mite diet isolate 13107-BHL040517-GBD9986_22148-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGAATTGGAAACTGACTAGTTCCTTTAATATTAGGATCACCAGATATGGCTTTCCCACGAATAAATAATATAAGTATTTGATTGTTGCCCCAATCATTAACATTATGATTATCTAGATCAATAGTGGAAAATGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606157 Chironomidae sp. water mite diet isolate 13115-BHL040517-GBD13987_10110-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGTAATAGTTAGGACTTCTTTGAGAATTCTGATTCGAGCAGACTTAGAACATGCAGGCTTATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606158 Chironomidae sp. water mite diet isolate 13116-BHL040517-GBD22630_7204-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGCGCTTGATCAGGACTAGTTGGAACTTCTTTATGTATTCTAATTCGAGCTGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTTTAATCTAATTGTCACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGAAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606159 Chironomidae sp. water mite diet isolate 13121-BHL040517-GBD23535_4671-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACAGTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGTGCTTCTTTAAGTATTCTAATTCGAGCAGAATTAGGTCATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTATTTGTTACAGATCATGCTTTTGTAATAATTTTTCTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606160 Chironomidae sp. water mite diet isolate 13125-BHL040517-GBD22549_15102-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGAACATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATAATAATTTTTTTATAGTTATACCCATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTCTGATTGTTGCCCCCATCATTAACTTTACTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606161 Chironomidae sp. water mite diet isolate 13126-BHL040517-GBD7797_9392-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGCACATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGATTGCTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606162 Chironomidae sp. water mite diet isolate 13127-BHL040517-GBD25969_11435-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTATCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATTTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAATGGACTAGTTCCTCTAATATTAGGAGCCCCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGCTGCCCCCATCATTAACTTTATTATTATCTAGATCAACTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606163 Chironomidae sp. water mite diet isolate 13129-BHL040517-GBD22310_18614-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGAGAATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTACCCCCATCATTAACTTCATTATTATCTAGATCTATCGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606164 Chironomidae sp. water mite diet isolate 13131-BHL040517-GBD10929_11087-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACCGGATCT---AGAATCTTAATTCGAGCAGAATTAGGACATCCAGGAACATTGATTGGGGATGATCAAATTTACAATGTAATTGTAACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGGCTTTTACCTTTAATACTCGTGGCCCCTGATATAGCCTGTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCATCTATTTCATTACATCATTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KP043758, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606165 Chironomidae sp. water mite diet isolate 13137-BHL040517-GBD9695_5032-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTGGGACATGCAGGCACATTAATTGGAGACTATCAAACTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCATTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCACCATCATTAACTTTATTATTATCTAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606166 Chironomidae sp. water mite diet isolate 13138-BHL040517-GBD4572_9419-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTCGGGGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTCATTGGAGAAGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTCTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTCTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATCGTGGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606167 Chironomidae sp. water mite diet isolate 13147-BHL040517-GBD9975_6026-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTTGAACTTCTTTAAGAATTCTAATTCGTGCAGTATTATGACATGCAGTCTTATTAATTGGAGACTATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTACCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606168 Chironomidae sp. water mite diet isolate 13148-BHL040517-GBD25163_22415-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGGATTGGTGGAACTTCTTTTAGAATTCTAATTCGAGCCGGATTTGGACATGCAGGCTCATTTATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606169 Chironomidae sp. water mite diet isolate 13160-BHL040517-GBD9830_12948-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGTTTGATCAGGAATAGTTGGAACTTCATTTAGAATTCTAATTCGAGTTGAATTATGACATGCAGGCTCATTAATTGGAGGCGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAGTCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCAGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGAGCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606170 Chironomidae sp. water mite diet isolate 13161-BHL040517-GBD7579_4301-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTTTATTTTATTTTCGTAGCTTGATCTGGAATAGTTGGAACTTCTTTTAGAATTTTAATTCGAGCAGAATTAGGACATACAGGCTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606171 Chironomidae sp. water mite diet isolate 13162-BHL040517-GBD19070_17260-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGAAACTGATATGGCTTTCCCACCAATAAATAATAAAAGTTTTTGATTGTTGCCCCCATCATTAAATTTATGATTATCTAGAACAATTGGGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606172 Chironomidae sp. water mite diet isolate 13224-BHL040517-GBD28735_18045-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACTCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAATGATACCTATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606173 Chironomidae sp. water mite diet isolate 13228-BHL040517-GBD13124_12029-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGATCAGGTATGGTAGGTACATCTTTAAGAATTTTGATTCGAGCAGAACTCGGTCACGCTGTTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGGTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAAAAAAAAAAGTTTTTGATTACCTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606174 Chironomidae sp. water mite diet isolate 13235-BHL040517-GBD24354_13064-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGATCACGCTGGTTCTTTAATCGGTGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606175 Chironomidae sp. water mite diet isolate 13255-BHL040517-GBD15588_26072-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATCGTTACCGCTCACGCATTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATATCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCGTCATTAACTTTATTATTATCTAGCACACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606176 Chironomidae sp. water mite diet isolate 13258-BHL040517-GBD8077_11182-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCGGGTATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGTAGAATTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGATCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606177 Chironomidae sp. water mite diet isolate 13283-BHL040517-GBD9296_26557-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAATAGGAACATCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACTCTGGTTCTTTAATCGGAGACGATCAAATATATAATGGAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGATCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606178 Chironomidae sp. water mite diet isolate 13296-BHL040517-GBD25805_11073-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGACACGCTGGTTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTATTATTATCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606179 Chironomidae sp. water mite diet isolate 13301-BHL040517-GBD6196_9303-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTCAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTATTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTATCAAGAAGTATTATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606180 Chironomidae sp. water mite diet isolate 13302-BHL040517-GBD21476_11369-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGGACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606181 Chironomidae sp. water mite diet isolate 13310-BHL040517-GBD3279_18422-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGAGAGCCCCTTATATATCATTCCCTCCACTAAATAATATAAGTTTTTTATTATTTCCCCCTTCATTAACATTATTATTATCTAGCTCTCTAGTTGAAACTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606182 Chironomidae sp. water mite diet isolate 13313-BHL040517-GBD20813_11106-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCATGCTGGTTCTTTAATCGGTGACGATCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACTTTATTATTATCTAGCACACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606183 Chironomidae sp. water mite diet isolate 13324-BHL040517-GBD21098_16829-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGTACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGAACATGCATTCATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTAGTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCACTAACATTATTACTATCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606184 Chironomidae sp. water mite diet isolate 13330-BHL040517-GBD28096_20914-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCCTTAAGTATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTAGTGCCATTAATACTAGGAGCCCCTAATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTGCAAGAAGAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606185 Chironomidae sp. water mite diet isolate 13341-BHL040517-GBD13949_18058-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGAACAGGAATAGTTGGAACCTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCATGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTTTTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGAATATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606186 Chironomidae sp. water mite diet isolate 13345-BHL040517-GBD26035_11028-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGGGGCTTTGGGAATTGATTAGTTCCCCTAATATTAGGAGCACCAGATACGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID JF412118, identified in GenBank as Glyptotendipes tokunagai. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606187 Chironomidae sp. water mite diet isolate 13348-BHL040517-GBD25701_22207-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATTGGAGATGACCAAATTTATAATGTTATTGTTACCGCTCACGCCTTTGTTATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606188 Chironomidae sp. water mite diet isolate 13368-BHL040517-GBD13450_28030-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAAAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGTTTATTACCCCCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KM991192, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606189 Chironomidae sp. water mite diet isolate 13370-BHL040517-GBD8096_22060-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACATCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTCTGATATTAGTGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606190 Chironomidae sp. water mite diet isolate 13387-BHL040517-GBD4162_11764-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCATCCTGGTTCTTTTATCGGTGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTAGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCACTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606191 Chironomidae sp. water mite diet isolate 13394-BHL040517-GBD27351_12287-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGTATCTTTATTCGAGCAGAACTCGGTCACGCTGGTTCTTTTATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTATAATTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCATTAACTTTATTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606192 Chironomidae sp. water mite diet isolate 13395-BHL040517-GBD25097_19154-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCACGCTGGTTCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606193 Chironomidae sp. water mite diet isolate 13396-BHL040517-GBD22971_23916-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCATACTGGTTCTTTAATCGGTGACGATCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCACCGTCATTAACTTTATTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606194 Chironomidae sp. water mite diet isolate 13404-BHL040517-GBD15758_23122-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTCACTGCACATGCTTTCATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGCTACAGCTTTTCCGCGAATGAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606195 Chironomidae sp. water mite diet isolate 13415-BHL040517-GBD29225_17157-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGATTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCAGGAACGGGAGGAGGAGCGAGCGCGCGAGGGGAAAAGGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606196 Chironomidae sp. water mite diet isolate 13426-BHL040517-GBD18208_22335-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCGGGTATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCATTCCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606197 Chironomidae sp. water mite diet isolate 13432-BHL040517-GBD6774_10615-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGGACATCTTTAAGAATTTTAATTCGAGCAGAATTAGGTCACGCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGTGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACATTATTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606198 Chironomidae sp. water mite diet isolate 13434-BHL040517-GBD23791_8414-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGTAGAACTCGGACACACTAGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGCGCCCCTGATATAGCATTCCCGCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACCTTATTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606199 Chironomidae sp. water mite diet isolate 13435-BHL040517-GBD19921_20502-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGCACTTCTTTAAGAATTTTATTTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606200 Chironomidae sp. water mite diet isolate 13438-BHL040517-GBD26009_8445-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACAACCTTGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTGATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606201 Chironomidae sp. water mite diet isolate 13444-BHL040517-GBD6450_25510-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGTTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGATTAGTGCCATTAATACTAGGAGCCCCAGACGTAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTAACTTTATTACTATCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606202 Chironomidae sp. water mite diet isolate 13448-BHL040517-GBD14246_9124-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATCCCCACGAATAAATAATATAAGATTTTGATTACTACCACCGTCATTAACTTTATTATTATCTAGCACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606203 Chironomidae sp. water mite diet isolate 13450-BHL040517-GBD15929_26086-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCATGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCATTAATATTTGGAGCCCCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACTTTATTATTATCTAGATCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606204 Chironomidae sp. water mite diet isolate 13463-BHL040517-GBD6878_4624-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTATAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCACAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606205 Chironomidae sp. water mite diet isolate 13467-BHL040517-GBD18166_22374-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTTGGTACTTCTTTAAGTATTTTAATTCGAGCAGAACTCGGTCACCCTGGTTCTTTTATTGGAGACGATCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTATAGTGATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606206 Chironomidae sp. water mite diet isolate 13471-BHL040517-GBD26355_20651-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTTGGTACTTCTTTAAGTATATTAATTCGAGCTAAATTAGGACATCCTGGTACCTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGTAATTGACTCATGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCACTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606207 Chironomidae sp. water mite diet isolate 13476-BHL040517-GBD18676_13479-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGTACTTCCTTATGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGACATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGGTTTTGATTATTACCCCCATCGCTAACATTAGTAATTTCAAGAAGGAGAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606208 Chironomidae sp. water mite diet isolate 13480-BHL040517-GBD27883_20663-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGTAGAATTAGGTCACGCTGGCTCATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGTAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606209 Chironomidae sp. water mite diet isolate 13486-BHL040517-GBD18048_19362-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTCGGACATCCTGGTTCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACACGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTGCCATTAATATTGGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCATCACTAACATTATTACTATCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606210 Chironomidae sp. water mite diet isolate 13488-BHL040517-GBD26868_9614-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCATGCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTATTGCCCCCGTCATTAACTTTATTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606211 Chironomidae sp. water mite diet isolate 13491-BHL040517-GBD23525_14068-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGTACATCTTTTAGTATTTTAATTCGAGCAGAACTCGGTCACCCTGGTTCTTTTATCGGAGACGATCAAATTTATAATGTTATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGAATAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606212 Chironomidae sp. water mite diet isolate 13495-BHL040517-GBD5288_14626-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTCATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTATAGCTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606213 Chironomidae sp. water mite diet isolate 13507-BHL040517-GBD4237_23006-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGGCTCTTGCCATTAATACTAGGAGCCCCAGATATAGCCTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCATCTATAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606214 Chironomidae sp. water mite diet isolate 13510-BHL040517-GBD23771_8399-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACCCAGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGGTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606215 Chironomidae sp. water mite diet isolate 13517-BHL040517-GBD24991_6877-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGCCAACCAGGATCATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606216 Chironomidae sp. water mite diet isolate 13518-BHL040517-GBD9871_22963-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGCACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCGTACCATTAATACTAGGAGCTCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCATCACTAACATTACTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR295408, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606217 Chironomidae sp. water mite diet isolate 13526-BHL040517-GBD12961_9444-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGCTGGTTCTTTTATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTAATACTTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606218 Chironomidae sp. water mite diet isolate 13529-BHL040517-GBD4007_20432-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGGATATTAATTCGAGCAGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGTATATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTATTGCCATTAATACTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGATTATTATCCCCATCTCTAACATTATTACTATCAAGCAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606219 Chironomidae sp. water mite diet isolate 13534-BHL040517-GBD6253_22439-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCTGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCCTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGGTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606220 Chironomidae sp. water mite diet isolate 13608-BHL040517-GBD7609_24155-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTACCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACCCTTCTTCTTTCTAGATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID KR286724, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606221 Chironomidae sp. water mite diet isolate 13609-BHL040517-GBD13812_12760-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTGGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACCTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID KR961044, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606222 Chironomidae sp. water mite diet isolate 13767-BHL040517-GBD20892_16644-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGGCATGCAGGCTCATTAATTGAAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCCTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGGGGATTTGGAAACTGACTGGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAATTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTT-TCTAGATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606223 Chironomidae sp. water mite diet isolate 13798-BHL040517-GBD11710_15370-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGATACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATGATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606224 Chironomidae sp. water mite diet isolate 13848-BHL040517-GBD25810_12612-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCCCTAAGAATCTTAATTCGAGCTGAATTAGATCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KM102730, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606225 Chironomidae sp. water mite diet isolate 13922-BHL040517-GBD22573_18183-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAGTAAGATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAGTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606226 Chironomidae sp. water mite diet isolate 13952-BHL040517-GBD23934_5355-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATCTTTTATTTTTGGAGCTTGATCAGGAATAATGTGAACTTCTTTAAGAATCTTAATTCGAGCAGAATTAGGACATGCTGGTTCATTGATTGGTGACGATCAGATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATCTTAATTGTGGGATTTGGAAATTGATTAGTACCTTTAATATTAGGTGCCCCAGATATAGCTTTCCCTCGAATAAATAACATAAGTTTTTGACTTCTTCCCCCATCTTTAACACTTTTACTTTCAAGCTCAGTTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID KR512196, identified in GenBank as Smittia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606227 Chironomidae sp. water mite diet isolate 13974-BHL040517-GBD11684_2827-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTCTTCCGCTAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTAGTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606228 Chironomidae sp. water mite diet isolate 14004-BHL040517-GBD17654_8893-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGACCGGGTATAGTAGGCAATTCTTTAAGAATTTTAATTCGACTAGAATTCGGACACCCTGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATACTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAAAAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606229 Chironomidae sp. water mite diet isolate 14006-BHL040517-GBD25809_5788-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGTAGACGATAAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGTACTCCTGATATAGCTTTTCCGCGAATAAATAATATAAAAATTTGATTATTACCCCCTTCATTAGCCTTACAGTTATCAAGATCAATAGTAGAAAATGGAACTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606230 Chironomidae sp. water mite diet isolate 14013-BHL040517-GBD14319_16222-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTCGATCGGGAGTAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGCAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGAAAATTCACTAGTACCTTTGATATTAGGGGCTCCCGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTATATCGAGATCAATAGTAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606231 Chironomidae sp. water mite diet isolate 14027-BHL040517-GBD18293_26046-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCCTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTTCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTCTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606232 Chironomidae sp. water mite diet isolate 14059-BHL040517-GBD5786_16135-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCGTCATTAACTTTATTACTATCAAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606233 Chironomidae sp. water mite diet isolate 14066-BHL040517-GBD29337_16487-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACATCTTTAAGAATCTTAATTCGAGCAAAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606234 Chironomidae sp. water mite diet isolate 14088-BHL040517-GBD5794_24970-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAACTTATATTGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGAAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGAGTCTCCTGATATAGCTTTTCCGCCAATAAATAATATAAGATTTTGAATATTACCCCCTTCATTAACCTGACTTTTATCAAGAACAATAGTAGAAAATGCAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606235 Chironomidae sp. water mite diet isolate 14105-BHL040517-GBD4841_15674-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCCCGAATAAATAATATAAGAGTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606236 Chironomidae sp. water mite diet isolate 14178-BHL040517-GBD23405_9916-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACATTATTTTTGGTGCTTGATCAGGAATGATAGGGACTACTTTAAGTATGCTTATTCGAGGAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTTCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCCCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606237 Chironomidae sp. water mite diet isolate 14324-BHL040517-GBD11962_23903-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATATTTGGAGCTTGAGCGGGAATAGTAGGAACTTCTCTTAGTATTTTAATTCGAGCAGAAATAGGACATCCAGGTGCTTTAGTTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR638998, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606238 Chironomidae sp. water mite diet isolate 14433-BHL040517-GBD4363_15246-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAAACTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTTACATTACTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.0% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606239 Chironomidae sp. water mite diet isolate 14494-BHL040517-GBD9921_17475-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTCGGAGCTTGGTCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACATTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGTATAAATAACATGAGATTTTGATTACTTCCCCCTTCTTTAACCCTTCTTCTATCTAGCAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR636712, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606240 Chironomidae sp. water mite diet isolate 14514-BHL040517-GBD18191_9927-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTCTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTACTTTAAGCATGCTTATTGGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGTTTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606241 Chironomidae sp. water mite diet isolate 14606-BHL040517-GBD18664_5131-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606242 Chironomidae sp. water mite diet isolate 14711-BHL040517-GBD14322_4692-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATGGTCGGAACTTCTCTAAGAATTCTAATTAGGGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTAGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTCTGACCTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTTTTTCGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 87.7% identical to accession ID GU565715, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606243 Chironomidae sp. water mite diet isolate 14754-BHL040517-GBD6633_6786-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTCATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTAGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGTTTCGGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606244 Chironomidae sp. water mite diet isolate 14879-BHL040517-GBD9665_10297-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTAGACTAGAATTAGGACACCCAGGTTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCATGTAG---AATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606245 Chironomidae sp. water mite diet isolate 14920-BHL040517-GBD23518_12433-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGACTTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAAGTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACGTAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTTTTTCGTAGAAAATGGAGCTGGATCAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID GU565715, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606246 Chironomidae sp. water mite diet isolate 14935-BHL040517-GBD5886_23746-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAACCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTCCTAAATTAGGACACCCTGGGGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.0% identical to accession ID GU565715, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606247 Chironomidae sp. water mite diet isolate 14969-BHL040517-GBD21296_12415-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTAGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTATTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606248 Chironomidae sp. water mite diet isolate 15210-BHL040517-GBD8885_4282-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTAGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTCACAGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTCCGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTCTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606249 Chironomidae sp. water mite diet isolate 477-BHL040517-GBD19013_12389-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAGTTCTAATTCAAGCAGAATTAGGACATGCAGGCTCAATAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATATGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCAGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCAACATTAACTATATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606250 Chironomidae sp. water mite diet isolate 522-BHL040517-GBD14305_4627-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCTCCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606251 Chironomidae sp. water mite diet isolate 528-BHL040517-GBD13213_17674-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606252 Chironomidae sp. water mite diet isolate 586-BHL072216-GBD20441_25641-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTGTATTCGGAGCCTGATCAGGTATAGTAGGTACTTCCCTTAGTATTCTAGTACGAGCTGAATTAGGACACCCCGGGGCATTAATTGGAGACGATCAAATTTATAACGTAATCGTTACAGCTCATGCCTTTGTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTACCAGTAATATTAGGTGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGCTTTTGATTATTACCCCCGTCTTTAACATTACTATTAGCTAGCTCAATTGTAGAAAATGGAGCTGGAA	Using NCBI BLASTN in June 2018, this sequence was 98.4% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606253 Chironomidae sp. water mite diet isolate 747-BHL040916-GBD15229_10969-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606254 Chironomidae sp. water mite diet isolate 762-BHL040916-GBD12257_12257-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGGACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCCCCTTCTCGTACTCTTTTACTTTCTAGTAGAATCGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606255 Chironomidae sp. water mite diet isolate 777-BHL040916-GBD25455_6277-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCGGGAATAGTAGGTACTTCTCTTAGAATCTTAATTCGATCTGAATTAGCTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTGCCACCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606256 Chironomidae sp. water mite diet isolate 800-BHL100916-GBD9004_7123-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606257 Chironomidae sp. water mite diet isolate 847-BHL100916-GBD9955_23257-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGTACTTCTTTAAGAATTTTAATTCGACTAGAATTCGGTCACCCTGGTTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606258 Chironomidae sp. water mite diet isolate 851-BHL100916-GBD27129_11524-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTTCGGAGCTTGGTCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606259 Chironomidae sp. water mite diet isolate 853-BHL100916-GBD5395_17953-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCGCTTCTTTAAGAATTTTAATTCGACTTGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606260 Chironomidae sp. water mite diet isolate 863-BHL100916-GBD23532_18644-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGCACTTCTTTTAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCAATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCATTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606261 Chironomidae sp. water mite diet isolate 872-BHL100916-GBD20519_22690-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCACATTAATCGGAAAAGATCAAATTTATAATGTAATTGTTACAGCACATGCCTTTGTAATAATTTTTATATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTCACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606262 Chironomidae sp. water mite diet isolate 874-BHL100916-GBD14397_9302-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGTGATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCATCATTAACCATGCTATTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606263 Chironomidae sp. water mite diet isolate 887-BHL100916-GBD8092_23854-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGATAATCAAACTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTCTGATTATTACCCCCCTCACTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606264 Chironomidae sp. water mite diet isolate 901-BHL100916-GBD19388_27249-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGTATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTGGGACACCCTGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCACCTTCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606265 Chironomidae sp. water mite diet isolate 903-BHL100916-GBD25107_6091-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606266 Chironomidae sp. water mite diet isolate 905-BHL100916-GBD23036_18697-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTTATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGTAATTGATTTGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCATCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606267 Chironomidae sp. water mite diet isolate 907-BHL100916-GBD23939_7855-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTTATTAATCGGAGACGATCAAATTTATCATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGAAAGTAGTGACTCCTGATAGAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606268 Chironomidae sp. water mite diet isolate 920-BHL100916-GBD4773_14123-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCCTGATCGGGAATAGTAGGCACTTCTTTAGGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTGCCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTATTACCCCCTTCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606269 Chironomidae sp. water mite diet isolate 922-BHL100916-GBD8777_14041-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGACTAGAATTAGGACACCCAGGCTCACTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606270 Chironomidae sp. water mite diet isolate 924-BHL100916-GBD29667_14162-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGTAGAATTAGGACACCCAGGATCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTATTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606271 Chironomidae sp. water mite diet isolate 928-BHL100916-GBD7925_11465-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTTATTCGACTAGAATTAGGACACCCAGGCTCATTCATCGGAGACGATCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAACTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAGTAAATAATATAAGATTTTGATTATTACCCCCCTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606272 Chironomidae sp. water mite diet isolate 934-BHL100916-GBD22156_20552-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTTGAATTAGGTCGTCCAGGCTCATTAATCGGAGAAGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606273 Chironomidae sp. water mite diet isolate 935-BHL100916-GBD24338_19447-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTTATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGTGGCTTTGGAAATTGATTGGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTAGCAGGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606274 Chironomidae sp. water mite diet isolate 937-BHL100916-GBD29496_13761-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGAACTTCTTTAAGCATTTTAATTCGACTAGAATTAGGACACCCAGGATCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAACATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606275 Chironomidae sp. water mite diet isolate 945-BHL100916-GBD27683_20528-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACCTGCTTTTGTAATAATTTTTTTCTAGTGATACCTATTTTAATTGGATGCTTTGGAAATTGATTAGTACCTTTGAAATTAGGGGCTCCTGATATAGCTTTTCCGCGAAAAAAAAAAAAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606276 Chironomidae sp. water mite diet isolate 954-BHL100916-GBD8001_19778-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTTATTCGACTAGAATTAGGACCACCAGGCTCATTAATCGGAGAAGATCAAATTTATAATGTAATTGTTACAGCACATACTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTGTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606277 Chironomidae sp. water mite diet isolate 957-BHL100916-GBD7808_19713-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATCTTTTATTTTTGGAGCTTGATCGGGAATAATAGGCACTTCTTTAAGTATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGTTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAACATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTCTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606278 Chironomidae sp. water mite diet isolate 974-BHL100916-GBD9635_16148-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATATTAATTCGACTTGAATTAGGACACCCAGGCTCATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAACTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTATTACCCCCCTCATTAACCTTACTTCTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606279 Chironomidae sp. water mite diet isolate 988-BHL100916-GBD10955_23809-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGTACCTCCCTTAGTATCCTTATTCGTACAGAATTAGGTCACCCAGGAGCTTTAATTGGAGACGATCAAATCTATAATGTAATTGTAACGGCACATGCTTTTGTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGTGGATTTGGTAATTGACTAGTACCCCTTATACTAGGAGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTACTACCCCCTTCTTTAACCTTACTATTATCTAGCTCTATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KP043430, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606280 Chironomidae sp. water mite diet isolate 989-BHL100916-GBD8844_7167-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGCACTTCTTTAAGAATTTTTATTCGACTAGAATTAGGACACCCAGGATCATTAATCGGAGACGATCAAATTTATAGTGTAATTGTTACTGCACATGCTTTTATAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTCTGATATTTGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606281 Chironomidae sp. water mite diet isolate 991-BHL100916-GBD19289_28089-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTGAGAATTTTAATTCGAGTAGAATTAGGACACCCAGGCTCATTAATCGGAGAAGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGGGCTCCTGATATAGCTTTCCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCACTCACCTTACTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606282 Chironomidae sp. water mite diet isolate 996-BHL100916-GBD20177_11782-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTTATTCGACTAGAGTTAGGACACCCAGGCTCATTAATCGGTGACGATCAAATTTGTAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAACATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606283 Chironomidae sp. water mite diet isolate 1000-BHL100916-GBD25654_13633-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGACCTGGAATAGTAGGCACTTCTTTAAGTATTTTTATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAACTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606284 Chironomidae sp. water mite diet isolate 1003-BHL100916-GBD22287_9645-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATACTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAAAATAAGATTTTGATTAGTACCCCCGGCATTAACCTTAAATTTATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606285 Chironomidae sp. water mite diet isolate 1007-BHL100916-GBD15471_5872-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCACATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCATTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTTCTTTTATCAAGTTCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606286 Chironomidae sp. water mite diet isolate 1010-BHL100916-GBD21702_3543-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACAACCTGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTCACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGGTTAGTGCCTTTAATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTATTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606287 Chironomidae sp. water mite diet isolate 1015-BHL100916-GBD21402_3819-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTTATTCGACTAGAATTAGGACACCCAGGAACATTAATCGGAGAAGATCAAATTTATAATGTACTTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCAATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606288 Chironomidae sp. water mite diet isolate 1017-BHL100916-GBD25386_21773-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTCGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAGGAATTTTAATTCGACTAGAATTAGGACACCCAGGAACATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTCTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606289 Chironomidae sp. water mite diet isolate 1019-BHL100916-GBD21081_23123-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTTTATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTTATTCGACTAGAATTAGGACACCCAGGATCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTCTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606290 Chironomidae sp. water mite diet isolate 1025-BHL100916-GBD3528_12427-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGAACTTCATTAAGAATTTTTATTCGACTAGAATTAGGACACCCAGGATCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTTCTTTTATCAAGATCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606291 Chironomidae sp. water mite diet isolate 1029-BHL100916-GBD10614_27466-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATATTAGGCACTTCTTTAAGAATTTTAATTCGAGTAGAATTAGGACTCCCAGGGTCATTTATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606292 Chironomidae sp. water mite diet isolate 1033-BHL100916-GBD25437_25317-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGTTTTGGAAATTGATTAGTCCCTTTGATATTAGGGCCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTATTACCCCCTTCATTAACCCTACTTCTATCAAGATCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606293 Chironomidae sp. water mite diet isolate 1036-BHL100916-GBD27138_17148-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCATGATCAGGCATAGTAGGCACTTCTTTAAGAATATTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTGTTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAACGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606294 Chironomidae sp. water mite diet isolate 1037-BHL100916-GBD22824_8718-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGCACTTTTTTTAGAATTTTATTTCGACTCGAATTTGGACACCCAGGAACATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606295 Chironomidae sp. water mite diet isolate 1040-BHL100916-GBD20970_24951-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTTATTCGACTAGAATTAGGACACCCAGGCTCATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACCGCACATGCTTTTGTTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606296 Chironomidae sp. water mite diet isolate 1058-BHL100916-GBD16368_6549-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCCTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTTGAATTAGGACACCCTGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTGTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606297 Chironomidae sp. water mite diet isolate 1062-BHL100916-GBD24741_17193-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGGGCTTGGTCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATCAACCATACTTTTAGCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606298 Chironomidae sp. water mite diet isolate 1068-BHL100916-GBD23109_26648-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTATATTTTATCTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATATTAATTCGAGTAGAATTAGGACAACCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606299 Chironomidae sp. water mite diet isolate 1069-BHL100916-GBD9226_19121-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGTATTTTAATTCGACTAGAATTAGGACACCCGGGTTCATTAATCTGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGAGACTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTGCCTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606300 Chironomidae sp. water mite diet isolate 1080-BHL100916-GBD20181_22871-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGGATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTTATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTCGGAAATTGATTTGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGAATATTACCCCCTTCACTAACCTGACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606301 Chironomidae sp. water mite diet isolate 1082-BHL100916-GBD23065_6627-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTGAGAATTTTAATTCGACTAGCATTTGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATACAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTATATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606302 Chironomidae sp. water mite diet isolate 1084-BHL100916-GBD4971_23414-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTCATCGGAGAAGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTTGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGTGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606303 Chironomidae sp. water mite diet isolate 1086-BHL100916-GBD27098_22877-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGGACTTCTTTAAGAATTTTAATTCGAGTAGAATTAGGACACCCAGGTTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTTCCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606304 Chironomidae sp. water mite diet isolate 1090-BHL100916-GBD9076_23010-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTTAGAATTTTAATTCGACTAGAATTAGGTCACACAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGAAAATTGATTAGTACCTTTGATATTAGTGGCTCCTGATATAGCATTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTACCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606305 Chironomidae sp. water mite diet isolate 1093-BHL100916-GBD14598_13516-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTATGACACCCAGGATCATTAATCGGAGAAGATCAAATTTATAATGTCATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTCCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606306 Chironomidae sp. water mite diet isolate 1100-BHL100916-GBD12663_17953-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTCGGAGCTTGGTCGGGAATAGTCGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606307 Chironomidae sp. water mite diet isolate 1101-BHL100916-GBD21301_13261-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGACCAGCATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTATTAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCGTTGATATTAGTAGCTCCTGATATAGCATTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606308 Chironomidae sp. water mite diet isolate 1103-BHL100916-GBD9663_3680-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCAAGCTAAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTGCCACCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606309 Chironomidae sp. water mite diet isolate 1105-BHL100916-GBD24333_26235-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGATTAGAATTAGGACACCCAGGCTCATTAGTTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606310 Chironomidae sp. water mite diet isolate 1106-BHL100916-GBD20352_4567-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAAAATTAGGTCATCCAGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAGATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606311 Chironomidae sp. water mite diet isolate 1121-BHL110116-GBD23423_5456-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTTAGACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGTGGCTCCTGATAGAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTGACTTTGATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606312 Chironomidae sp. water mite diet isolate 1125-BHL110116-GBD6941_7997-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGCATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAACTGATTAGTACCTTTGATATTAGGTGCTCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606313 Chironomidae sp. water mite diet isolate 1126-BHL110116-GBD13413_6182-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGACCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATGGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTCCATTAACCTTTCTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606314 Chironomidae sp. water mite diet isolate 1127-BHL110116-GBD22652_21521-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCATTAAGAATTTTAATTCGAGTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606315 Chironomidae sp. water mite diet isolate 1131-BHL110116-GBD18499_25349-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAACATAAGATTTTGATTATGACCCCCTTCATTAACCGTACATTTATCAAGAGCAAGAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606316 Chironomidae sp. water mite diet isolate 1136-BHL110116-GBD15260_21935-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATATCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTCGGGTGTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAGCAATAGTAGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606317 Chironomidae sp. water mite diet isolate 1140-BHL110116-GBD19948_27899-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGATTTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTTATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGTTTTGGAAATTGATTAGTACCTTTGATATTAGAGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606318 Chironomidae sp. water mite diet isolate 1141-BHL110116-GBD20457_15870-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCCGGAATAGTAGGCGCTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATACAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCAATTTTAATTGGAGGCTTTGGAATTTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606319 Chironomidae sp. water mite diet isolate 1142-BHL110116-GBD11229_9622-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606320 Chironomidae sp. water mite diet isolate 1145-BHL110116-GBD13507_3548-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTGAATGCGACTAGAATTAGGACACCCATGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATACTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGCGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606321 Chironomidae sp. water mite diet isolate 1153-BHL110116-GBD19911_20070-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGACTTATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGTCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606322 Chironomidae sp. water mite diet isolate 1154-BHL110116-GBD10335_3144-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGCACTTCTTTAGGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGATGCTCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATCATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCATCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606323 Chironomidae sp. water mite diet isolate 1158-BHL110116-GBD3867_21152-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTAGACTAGAATTAGGACACCCATGCTCATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAGCCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606324 Chironomidae sp. water mite diet isolate 1159-BHL110116-GBD27550_13428-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGTATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTGATATTAGGGGCTCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTACTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606325 Chironomidae sp. water mite diet isolate 1164-BHL110116-GBD25027_9239-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGTAGAATTTGGACACCCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGACTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTATTACCCCCTTCATTAACCTTACTTTTATCAGGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606326 Chironomidae sp. water mite diet isolate 1171-BHL110116-GBD5247_17439-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTCGGCACTTCTTTAAGTATTTTAATTCGACTAGAATTAGGACACCCTGGATCATTTATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCATCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606327 Chironomidae sp. water mite diet isolate 1172-BHL110116-GBD28491_18193-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCACATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGTGGATACTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTGCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606328 Chironomidae sp. water mite diet isolate 1174-BHL110116-GBD7066_10187-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCTTGATCGGGTATAGTAGGCACTTCTTTAAGAATTTTAATTTGAGTTGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTAATATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606329 Chironomidae sp. water mite diet isolate 1176-BHL110116-GBD20500_6319-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTTGGCACTTCTTTTAGAATTTTAATTCGACTTGAATTAGGACACCCAGGCTCATTCATCGGAGACGATCAACTTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGATCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606330 Chironomidae sp. water mite diet isolate 1178-BHL110116-GBD17773_13309-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTATCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGGATAAATAATATAAGATTTTGATTATTACCCCCATCATTAACCTTGCGTTTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606331 Chironomidae sp. water mite diet isolate 1179-BHL110116-GBD17375_7137-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTATTTTCGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATTCTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTACAGTGATACCAATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCATCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606332 Chironomidae sp. water mite diet isolate 1183-BHL110116-GBD18040_5394-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATGGGGAATAGTAGGCACTTCTTTAAGAATTCTAATTCGACTAGAATTAGGACACCCAGTCTCATTAATCGGAGACGATCAAATTTATAATGAAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTTATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606333 Chironomidae sp. water mite diet isolate 1185-BHL110116-GBD19684_15903-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACGTCCAGGCACATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTCATAGTGATACCAATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCCTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606334 Chironomidae sp. water mite diet isolate 1186-BHL110116-GBD6710_22729-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTTGGCACTTCTTTAAGTATTTTAATTCGACTAGAATTAGGACACCCTGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCACTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606335 Chironomidae sp. water mite diet isolate 1187-BHL110116-GBD22965_7947-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTCTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGATCATTAATCGGAGAAGATCAAATTTATAATGTAATGGTTACAGCACATGCTTTTTTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606336 Chironomidae sp. water mite diet isolate 1192-BHL110116-GBD28540_17417-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACATGCAGGCTCATTAATCGGAGACGAGCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTGATATTAGGGGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606337 Chironomidae sp. water mite diet isolate 1193-BHL110116-GBD21204_27791-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTATTTAAGAATTTTAATTCGACTAGAATTAGGACACACAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTCCCGCGAAAAAATAATATAAGATTTTGATTACTTCCCCCTTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606338 Chironomidae sp. water mite diet isolate 1197-BHL110116-GBD7461_25179-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAACTTTAATTCGACTAGAATTCGGTCACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTTTTATCAAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606339 Chironomidae sp. water mite diet isolate 1201-BHL110116-GBD11841_11927-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACAACCAGGATCATTAATCGGAGACGATCAAATTTATAATGTTATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGTGCTCCTGATATAGCTATTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606340 Chironomidae sp. water mite diet isolate 1203-BHL110116-GBD13511_27098-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCATTTGTAATAATTTTTTTATTGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTAGTATCAAGAGCAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606341 Chironomidae sp. water mite diet isolate 1211-BHL110116-GBD20743_14963-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCTGGCTCATTAATCGGAGACTATCAAATTTATAATGTCATTGTCACAGATCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606342 Chironomidae sp. water mite diet isolate 1222-BHL110116-GBD15707_5187-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTGATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGTTCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGTAAATTGATTAGTACCTTTGATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAACTGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606343 Chironomidae sp. water mite diet isolate 1223-BHL110116-GBD15442_20636-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTAGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCAATAATAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTCCCGCGAATAAATAATATAAGATTTTGATTACTACCCCCTTCATTAACCTTACTTTTATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606344 Chironomidae sp. water mite diet isolate 1225-BHL110116-GBD23226_18061-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATGTTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAAGTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAGCCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606345 Chironomidae sp. water mite diet isolate 1239-BHL110116-GBD27657_14559-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGTAGAATTAGGACACCCAGGTTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606346 Chironomidae sp. water mite diet isolate 1243-BHL110116-GBD28155_16713-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGTGTCTCCTGATATAGCTTTTCCGCGAATAAACAATATAAGAGTTTGATTATTACCCCCTACATCAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606347 Chironomidae sp. water mite diet isolate 1244-BHL110116-GBD27616_14566-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAAGTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACATATTTTAATTGGAGGTTTTGGAAATTGATTAGTACCTTTGTTATTAGAGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606348 Chironomidae sp. water mite diet isolate 1248-BHL110116-GBD19599_10611-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGATGAGCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTACTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606349 Chironomidae sp. water mite diet isolate 1250-BHL110116-GBD15926_9578-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGGTCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTGATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAACATAAGATTTTGATTATTACCCCCATCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606350 Chironomidae sp. water mite diet isolate 1261-BHL110116-GBD26457_22347-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGGTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTTTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTGATATTAGGGGCCCCTGATATAGCATTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606351 Chironomidae sp. water mite diet isolate 1263-BHL110116-GBD28182_15280-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAGTTGGAGACGATCAAATTTATAATGTTATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606352 Chironomidae sp. water mite diet isolate 1264-BHL110116-GBD26845_9606-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCCTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATACTTTTTTTTATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTCCCTTTGATATTAGGAGCCCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606353 Chironomidae sp. water mite diet isolate 1267-BHL110116-GBD23362_7487-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATTCCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTGATATTAGGGACTCCTGATAAAGCTTTTCCGCGAATAAATAAAATAAGATTTTGATTATTACCCCCTTCAATAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606354 Chironomidae sp. water mite diet isolate 1270-BHL110116-GBD11790_11512-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCACATTCATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATTGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAAAAATATAAGATTTTGATTATTACCCCCTTCATTAACCGTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606355 Chironomidae sp. water mite diet isolate 1273-BHL110116-GBD27143_17912-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTTAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATAGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCGTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTAGTATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606356 Chironomidae sp. water mite diet isolate 1274-BHL110116-GBD19393_14746-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGTGACGATCAAATTTATAATGTAATTGTAACGGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTGATATTAGGGGCTCCAGATATGGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606357 Chironomidae sp. water mite diet isolate 1276-BHL110116-GBD23885_25968-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGGTCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAGTCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTCTAATTGGAGGCTTTGGAAATTGATCAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTGTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAAGAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606358 Chironomidae sp. water mite diet isolate 1282-BHL110116-GBD2270_16517-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACAACCAGGCTCATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCAATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATACTAGGAGCTCCTGGTATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606359 Chironomidae sp. water mite diet isolate 1284-BHL110116-GBD17349_20966-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATCTTAATCGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGAATATTACCCCCTTCATTAACCTGACGTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606360 Chironomidae sp. water mite diet isolate 1286-BHL110116-GBD25120_20754-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTCGGAGCTTGATCGGGAATAGTAGGCACTTCCTTAAGAATCTTAATTCGACTAGAATTAGGACATCCAGGCTCATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCTGATATAGCTTTCCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606361 Chironomidae sp. water mite diet isolate 1289-BHL110116-GBD23927_23744-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTATGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGTGACGATCAAATTTATAATGTAATTGTTATAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606362 Chironomidae sp. water mite diet isolate 1293-BHL110116-GBD17067_4542-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTACTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGATACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTGATGTTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGTTCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606363 Chironomidae sp. water mite diet isolate 1296-BHL110116-GBD20252_10307-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCATTTCTTTAAGAATTTTAATTCGACTAGAATTCGGACACCCAGGCTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTCCCGCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACCTTATTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606364 Chironomidae sp. water mite diet isolate 1298-BHL110116-GBD24279_19424-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTATGACACCCAGGCTCATTAATCGGAGACGATCAAATTTCTAATGTAATTGTTACAGCACATGCTTTTGTCATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATGAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606365 Chironomidae sp. water mite diet isolate 1301-BHL110116-GBD14751_2223-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGAGCGGGAATAGTAGGCACTGCGTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGACTAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAAATCAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606366 Chironomidae sp. water mite diet isolate 1302-BHL110116-GBD18652_8909-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATCTTTTATTTTTGGAGCTTGATCGGGACTAGTAGGCACTTCTTTAAGTCTTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAGATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606367 Chironomidae sp. water mite diet isolate 1304-BHL110116-GBD26739_11606-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATATTAATTCGAGTAGAATTAGGACACCCAGGCTCATTAATCGGAGATTATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTATTACCCCCATCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606368 Chironomidae sp. water mite diet isolate 1305-BHL110116-GBD26142_11050-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGATCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCTTTGATATTAGGTACTCCTGATATAGCTTTTCCGCGAACAAATAATATAAGATTTTGATTATTACCCCCCTCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606369 Chironomidae sp. water mite diet isolate 1323-BHL110116-GBD26511_17142-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGCGCTTGATCGGGAATAGTAGGCACTTCTTTCAGAATTTTAATTCGATTAGAATTGGGACACCCAGGCTTATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606370 Chironomidae sp. water mite diet isolate 1325-BHL110116-GBD7384_9774-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTTAGAATTTTAATTCGACTAGAATTATGACACCCAGGCTCATTATTCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCAATATTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTTGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAGCAATAGTAGAAAATGGAGATGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606371 Chironomidae sp. water mite diet isolate 1332-BHL110116-GBD19018_14493-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATATTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGATTTTTATTTGGACTAGAATTAGGACACCCAGGCTCATTAATAGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606372 Chironomidae sp. water mite diet isolate 1336-BHL110116-GBD27847_11402-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGAAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACAACCAGGATCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTTGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606373 Chironomidae sp. water mite diet isolate 1338-BHL110116-GBD6468_25138-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACAACAAGGCTCATTGATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTTTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTTGTGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606374 Chironomidae sp. water mite diet isolate 1343-BHL110116-GBD25820_6157-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGATTAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCATGCTCATTAATCGGAGACGATCAAATTTATAATGCAATTGTTAAAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATACAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGCAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606375 Chironomidae sp. water mite diet isolate 1347-BHL110116-GBD11453_14197-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCAGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAGTTGATTAGTACCTTTGATATTAGGGGCTCCTGAAATAGCTTTTCCGCGAATAAAAAATATAAGATTTTGAATATTACCCCCTTCATTAACCTTACCTTTAACAAGATCAATAGGAAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606376 Chironomidae sp. water mite diet isolate 1348-BHL110116-GBD17816_7981-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGAGGCTCCTGAGATAGCTTTTCCGCGAATAAATAATATAAGATTGTGATTAATACCCCCTTCAAGAACCTTACGTTGATCAAGATCAATAGTAGAAAATGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606377 Chironomidae sp. water mite diet isolate 1353-BHL110116-GBD12378_21447-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTTATACCCATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTCTGATATTAGGGGCTCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606378 Chironomidae sp. water mite diet isolate 1358-BHL110116-GBD9156_25876-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTTGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTGTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATGTTGATTATTACCCCCGTCATTAACCTTACGTTTATCAAGATCAATAGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606379 Chironomidae sp. water mite diet isolate 1362-BHL110116-GBD22153_21982-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATCTTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGACTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606380 Chironomidae sp. water mite diet isolate 1372-BHL110116-GBD8919_14772-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTTGACTAGAATTAGGACACCCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCATCTTTAACCTTACTTCTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606381 Chironomidae sp. water mite diet isolate 1375-BHL110116-GBD3271_20941-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGTATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGTAGAATTAGGACACGCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAAGCTTTGGAAATTGATTAGTTCCTTTGATATTAGGGGCTCCTGATATAACTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606382 Chironomidae sp. water mite diet isolate 1378-BHL110116-GBD21644_3298-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGCAGGCACTTCTTTAAGAATCTTAATTCGACTAAAATTAGGACACCCAGGCTCATTAATCGGACACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606383 Chironomidae sp. water mite diet isolate 1383-BHL110116-GBD27552_14004-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGTATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACCCCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606384 Chironomidae sp. water mite diet isolate 1384-BHL110116-GBD23755_25073-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCATTTCTTTAAGAATTTTAATTCGACTAAAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAATTTTTAAATGTAATTGTTGCAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCATCATTAACCTTACTTTTAACAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606385 Chironomidae sp. water mite diet isolate 1392-BHL110116-GBD22729_24398-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTATGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGATACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACCTTTATCAAGATCAATAGTAGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606386 Chironomidae sp. water mite diet isolate 1394-BHL110116-GBD24225_23623-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTAATATAGCATTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606387 Chironomidae sp. water mite diet isolate 1395-BHL110116-GBD10953_18515-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTCTTATTCGACTAGAATTAGGACACCCAGGATCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTGTTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGATCCTGATATAGCTTTTCTGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606388 Chironomidae sp. water mite diet isolate 1410-BHL110116-GBD14049_3557-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAGTCGGAGACGATCTAATTTATAATGTAAGTGTTACAGCACATGCTTTTGTAATAATTTTTTTTGTAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTACCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGCGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606389 Chironomidae sp. water mite diet isolate 1502-BHL110116-GBD16354_2960-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTCCTTTGAGAATTTTAATTCGACTAGAATGAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTCCCCCCTTCATTACCCTTACTTTTATCAAGATCAATAGTAGAAAATGGCGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606390 Chironomidae sp. water mite diet isolate 1604-BHL110116-GBD10548_10831-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCGGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAACTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACCTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606391 Chironomidae sp. water mite diet isolate 1657-BHL110116-GBD26763_23510-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606392 Chironomidae sp. water mite diet isolate 1659-BHL110116-GBD13800_26252-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTACTTTATTTTTGGAGCTTGATCCGGAATAGTGGGAACATCTTTAAGAATATTAATTCGAGCAGAATTAGGACATCCAGGAACATTGATTGGGGATGATCAAATTTACAATGTAATTGTAACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGTGGGTTTGGAAATTGGCTTTTACCTTTAATACTTGGGGCCCCTGATATAGCCTTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCATCTATTTCATTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KP043758, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606393 Chironomidae sp. water mite diet isolate 1766-BHL110116-GBD24259_24503-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATCATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606394 Chironomidae sp. water mite diet isolate 1785-BHL110116-GBD18039_2937-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTCTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606395 Chironomidae sp. water mite diet isolate 1815-BHL011116-GBD9072_15445-Ldc73 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606396 Chironomidae sp. water mite diet isolate 1818-BHL011116-GBD8841_17345-Ldc73 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606397 Chironomidae sp. water mite diet isolate 1820-BHL011116-GBD18689_2732-Ldc73 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTGATCGGAGGCTTTGGAAATTGACTATTACCACTTATACTTGGAGCCCCTGATATGGCCTTTCCTCGAATAAATAACATAAGATTCTGGTTACTACCTCCGTCTATTTCTTTGCTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606398 Chironomidae sp. water mite diet isolate 1839-BHL072216-GBD17078_6747-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606399 Chironomidae sp. water mite diet isolate 1856-BHL072216-GBD25495_22882-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606400 Chironomidae sp. water mite diet isolate 1864-BHL072216-GBD18869_7228-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGGCATCCTGGTACTTTAATTGGTGACGACCAAATTTATAATGTAGTTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGTGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTTCCTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606401 Chironomidae sp. water mite diet isolate 2065-BHL072216-GBD16838_8265-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTGCCACCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606402 Chironomidae sp. water mite diet isolate 2212-BHL072216-GBD8259_14833-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAGCTGAATTAGGGCATCCTGGAACTTTAATTGGTGACGACCAAATTTATAACGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR285214, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606403 Chironomidae sp. water mite diet isolate 2228-BHL072216-GBD17900_7140-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606404 Chironomidae sp. water mite diet isolate 2277-BHL072216-GBD13904_16840-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGGTCGGGGATAGTAGGGACATCCCTAAGAACACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACCGCCCATGCTTTTATTATAATTTTTTTTATAGTTATCCCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTGTCTAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606405 Chironomidae sp. water mite diet isolate 2333-BHL072216-GBD22349_23163-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGTCATCCTGGATCTTTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606406 Chironomidae sp. water mite diet isolate 2400-BHL072216-GBD3761_8605-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGCGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTATTACTGTACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGGGTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606407 Chironomidae sp. water mite diet isolate 2418-BHL072216-GBD15664_3003-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACCTTCTTCCTTTCAAGAAGTTTTCTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606408 Chironomidae sp. water mite diet isolate 2461-BHL072216-GBD27268_14146-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTAGTTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACCCTTCTTCTTTCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606409 Chironomidae sp. water mite diet isolate 2480-BHL072216-GBD16245_4967-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTCTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTATTCGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606410 Chironomidae sp. water mite diet isolate 2489-BHL072216-GBD6660_17537-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCGGGGATAGTAGGAACTTCTCTAAGAATCTTAATTCGAGCTGAATTGGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTT-CTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM991192, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606411 Chironomidae sp. water mite diet isolate 2499-BHL072216-GBD26505_13113-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTATATTTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCCGAATTAGGTCATGCTGGATCATTTATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTGCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCTCCTTCTCTAACCTTATTACTTTCAAGTACAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606412 Chironomidae sp. water mite diet isolate 2503-BHL072216-GBD29559_15777-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGAGCTTGATCGGGTATAGTAGGTACTTCTTTAAGAATCTTAATTCGAGCTGAATTCGGTCATGCTGGATCTTTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTGGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTGCCCCCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KM991192, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606413 Chironomidae sp. water mite diet isolate 2553-BHL072216-GBD7977_7189-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGAGCTCCTGATATGGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACTCTTCTTCTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606414 Chironomidae sp. water mite diet isolate 2563-BHL072216-GBD27795_14244-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCCGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCTCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACCTTATTATTATCTAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606415 Chironomidae sp. water mite diet isolate 2568-BHL072216-GBD19093_17117-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACCTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGGCATCCTGGAACTTTAATTGGTGACTACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTGATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606416 Chironomidae sp. water mite diet isolate 2572-BHL072216-GBD19289_19871-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTTTATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGAGTTTTAATTCGAGCTGAATTAGGACATCCTGGCACTTTAATTGGTGACGACCAAATTTATAATGTAGTTGTTACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTTCCATTAATATTAGGAGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTGCCCCCCTCATTAACTCTACTTCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606417 Chironomidae sp. water mite diet isolate 2578-BHL072216-GBD27208_11593-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCGGGGATAGTAGGCACTTCTTTAAGAATCTTAATTCGAGTTGAATTAGGTCATCCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCTCCTCCTCTTACCTTATTACTATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606418 Chironomidae sp. water mite diet isolate 2581-BHL072216-GBD6928_16055-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTTATTTTCGGAGCTTGATCTGGAATTGTCGGAACTTCTTTAAGTATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606419 Chironomidae sp. water mite diet isolate 2594-BHL072216-GBD7395_8079-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTCATTGGTGACGACCAAATTTATAATGTAGTCGTTACTGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGATTACTACCACCCTCATTAACTCTACTTCTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606420 Chironomidae sp. water mite diet isolate 2619-BHL072216-GBD27214_14460-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCAGAATTAGGACATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGAAATTGATTAGTTCCATTAATATTAGGGGCTCCTGATACGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTACTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606421 Chironomidae sp. water mite diet isolate 2653-BHL072216-GBD27393_22476-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCGGGGATAGTAGGAACTTCTCTAAGTATATTAATTCGAGCAGAATTAGGTCATGCTGGATCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACTATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606422 Chironomidae sp. water mite diet isolate 2660-BHL072216-GBD17248_12576-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCGGGGATAGTTGGTACTTCTTTAAGAATCTTAATTCGAGCTGAATTAGGACATCCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTGCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTTACCTTATTACTTTCAAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KM991192, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606423 Chironomidae sp. water mite diet isolate 2931-BHL032417-GBD10165_12974-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTGAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATATAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606424 Chironomidae sp. water mite diet isolate 2982-BHL032417-GBD20741_19843-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATCTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTGGGAAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTATACCCTCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606425 Chironomidae sp. water mite diet isolate 3151-BHL032417-GBD4744_9557-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATACTTCGTTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGATCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR287035, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606426 Chironomidae sp. water mite diet isolate 3482-BHL032417-GBD11353_28591-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTATTTTGTATTCGGAGCCTGATCAGGTATAGTAGGTACTTCCCTTAGTAATCTAGTACGAGCTGAATTAGGACACCCCGGGGCATTAATTGGAGACGATCAAATTTATAACGTAATGGTTACAGCTCATGCCTTTGTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTACCACTAATATTAGGTGCACCAGATATAGCTTTCCCTCGAATAAATAATATATGCTTTTGATTATTACCCCCATCTTTAACATTACTATTAGCTAACTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606427 Chironomidae sp. water mite diet isolate 3700-BHL032417-GBD10825_13034-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAATATACTTGTTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGATGATCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTGCTAGTTCAGTTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR287035, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606428 Chironomidae sp. water mite diet isolate 4050-BHL032417-GBD10099_17833-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTGTTTTCGGAGCCTGATCAGGTATAGTAGGTACTTCCCTTAGTATTCTAGTACGAGCTGAATTAGGACACCCCGGGACATTAATTGGAGACGATCAAATTTATAACGTAATGGTTACAGCTCATGCCTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAACTGATTAGTACCACTAATATTAGGTGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGCTTCTGATTATTACCCCCATCTCTAACATTACTATTAGCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606429 Chironomidae sp. water mite diet isolate 4078-BHL032417-GBD4536_23001-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGTGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCATGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606430 Chironomidae sp. water mite diet isolate 4079-BHL032417-GBD11851_13710-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCAAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606431 Chironomidae sp. water mite diet isolate 4090-BHL032417-GBD8887_9596-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGTATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGTGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGAGATACCTATTTTAATTGGAGGCTATGGAAAATGATTAGTACCTTTGATAATAGGGGCTCCTGATATAGCTTATCCGCGAATAAATAATATAAGATTGTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606432 Chironomidae sp. water mite diet isolate 4166-BHL032417-GBD25876_22580-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGTAGAATTAGGACACCCAGGCTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606433 Chironomidae sp. water mite diet isolate 4185-BHL032417-GBD5485_10666-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTCCCTTTTATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAAAAATAAAAGATTTTGATTATTAGCCCCTTCATCATCCTTACATTTATCAAGATCAATAGTAGAAAATGGAGCTGGAGCAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606434 Chironomidae sp. water mite diet isolate 4194-BHL032417-GBD21637_20294-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTTAGATTTTTAATTCGAGTAGAATTAGGACACCCAGGTTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCAATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606435 Chironomidae sp. water mite diet isolate 4198-BHL032417-GBD9684_2886-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGTATTTTAATTCGATTAGAATTAGGACACCCTGGCTCATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCGGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCATCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606436 Chironomidae sp. water mite diet isolate 4205-BHL032417-GBD27736_18883-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTGATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTTCTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606437 Chironomidae sp. water mite diet isolate 4225-BHL032417-GBD29071_17867-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTATGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGGGCTCCTGATATAGCTTTCCCGCGAATAAATAATATAAGATTTTGACTATTACCCCCTTCATTAACCTTATTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606438 Chironomidae sp. water mite diet isolate 4227-BHL032417-GBD17810_3945-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATCAGGACACCCATTCTCATTAATCGTAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTACCCTTACTTTTATCAAAATCAATAGTAGCAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606439 Chironomidae sp. water mite diet isolate 4230-BHL032417-GBD9928_8102-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGCACTTCTTTAAGAATTCTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCATCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606440 Chironomidae sp. water mite diet isolate 4232-BHL032417-GBD21074_23261-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGTATTTTAATTCCACTAGAATTAGGTCACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCATCAGTAACCTTACTATTAGCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606441 Chironomidae sp. water mite diet isolate 4235-BHL032417-GBD17396_4534-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGTCTCATTAATCGGAGACGTTCTAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTTTAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTCCTTTTATCAAGCTCACTAGTAGAAAATGGCGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606442 Chironomidae sp. water mite diet isolate 4237-BHL032417-GBD18590_4718-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTGTATTCGGAGCCTGATCAGGTATAGTAGGTACTTCCCTTAGTAATCTAGTACGAGCTGAATTAGGACACCCCGGGGCATTAATTGGAGACGATCAAATTTATAACGTAATGGTTACAGCTCATGCCTTTGTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTACCACTAATATTAGGTGCACCAGATATAGGTTTCCCTCGAATAAATAATATATGCTTTTGATTATTACCCCCATCTTTAACACTACTATTAGCTAGCTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606443 Chironomidae sp. water mite diet isolate 4239-BHL032417-GBD6605_15161-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTTGAATTAGGACAACCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATCTTGACTACTACCCCCTTCATTAACCCTATTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606444 Chironomidae sp. water mite diet isolate 4254-BHL032417-GBD21046_26358-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTTATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGATGATCAAATTTATAATGTTATTGTTACTGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606445 Chironomidae sp. water mite diet isolate 4255-BHL032417-GBD12627_23679-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTCTTATTCGACTAGAATTAGGACACCCAGGCTCATTCATTGGAGAAGAACAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606446 Chironomidae sp. water mite diet isolate 4262-BHL032417-GBD9556_11594-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTATGACACCCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTACTTGTTACTGCACATGCTTTTGTAATAATTTTTTTCTAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTATTACCCCCTTCATTAACCTTACTTTTATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606447 Chironomidae sp. water mite diet isolate 4264-BHL032417-GBD13149_11445-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCACTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTATTACCCCCTTCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606448 Chironomidae sp. water mite diet isolate 4269-BHL032417-GBD29106_16971-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGCACACCCAGGATCATTAATCGGAGACGATCAAATTTATAATGCACTTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCAATATTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606449 Chironomidae sp. water mite diet isolate 4283-BHL032417-GBD21427_5669-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGACTGGAATTAGGACACCCAGGCTCATTAATCTGAGACGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCACCATCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606450 Chironomidae sp. water mite diet isolate 4291-BHL032417-GBD15009_18598-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTATTCTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATACAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTACCCCCATCATTAACTTTATTATTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606451 Chironomidae sp. water mite diet isolate 4297-BHL032417-GBD18081_19797-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCATTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCACATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTTATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGACATAGCTTTTCCGCGAATAAATAATATAAGATTCTGATTATTACCCCCTTCATTAACCTTACTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606452 Chironomidae sp. water mite diet isolate 4299-BHL032417-GBD27491_19099-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCTTTAAGAATTTTAATTCGACTAGAATTCGGATACCCAGGTTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTCGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTATTATCAAGATCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606453 Chironomidae sp. water mite diet isolate 4321-BHL032417-GBD7587_23790-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTTATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTTATATTAGGAGCTCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCTTCACTAACCTTACTTTTATCAAGAAAAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606454 Chironomidae sp. water mite diet isolate 4331-BHL032417-GBD25778_11841-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTCGGCACTTCCTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGAACATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCCGATATAGCTTTTCCGCGAATAAATAACATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606455 Chironomidae sp. water mite diet isolate 4342-BHL032417-GBD12538_23155-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTGTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCATTTCCGCTAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTTTTATCAAGATCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606456 Chironomidae sp. water mite diet isolate 4350-BHL032417-GBD21912_10449-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTACCGCGAATAAATAATATAAGATTTTGAATATTACCACCATCAATAACCTTACTAATATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606457 Chironomidae sp. water mite diet isolate 4355-BHL032417-GBD6656_10990-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGAAGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTATTACCACCATCATTAACCTTACTTTTATCAAGAGCAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606458 Chironomidae sp. water mite diet isolate 4368-BHL032417-GBD25214_18127-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGCTTTGGTAATTGATTAGTACCTTTGATATTAGGGGCCCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTATTACCCCCTTCATTAACCTTACTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606459 Chironomidae sp. water mite diet isolate 4369-BHL032417-GBD14543_2684-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACAACCAGTCTCAATAATCGTAGACGATCTAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATTCCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606460 Chironomidae sp. water mite diet isolate 4370-BHL032417-GBD22282_22734-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTTATTCGACTAGAATTAGGACACCCAGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCCTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGTCTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606461 Chironomidae sp. water mite diet isolate 4371-BHL032417-GBD14258_4446-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATTCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGTTTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTGTTGCCCCCGTCTTTAACTTTATTATTATCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606462 Chironomidae sp. water mite diet isolate 4374-BHL032417-GBD4095_16173-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCTGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGATGCTTTGGAAATTGATTAGTACCTTTAATATTAGGTGCTCCTGATATAGATTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCCTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606463 Chironomidae sp. water mite diet isolate 4375-BHL032417-GBD4744_23195-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTCATTTTTTGGAGCTTGATCGGGATTAGTAGGCACTTCTTTAAGATTTTTATTTCGACTAGAATTAGGACACCCAGGCTCTTTAATCGGAGACGATCAATTTTATAATGTAATTGTTACAGCACATGCTTTTGTATTAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGAGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606464 Chironomidae sp. water mite diet isolate 4377-BHL032417-GBD28573_17285-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTCTTATTCGACTAGAATTAGGACTACCAGGATCATTAATCGGAGATGATCAAATTTATAATGTAATTGTTATAGCACATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606465 Chironomidae sp. water mite diet isolate 4379-BHL032417-GBD27774_15763-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGAACTTCTTTAAGAATTTTTATTCGAGTAGAATTAGGACAACCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGACTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTTTCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606466 Chironomidae sp. water mite diet isolate 4395-BHL032417-GBD4411_12160-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCTGGAATAGTAGGCACTTCTTTAAGTATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTACTACCCCCTTCATTAACCTTACCTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606467 Chironomidae sp. water mite diet isolate 4404-BHL032417-GBD6632_21689-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAAAATTAGGACACCCAGGATCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGGAATTGATTAGTACCTTTGATATTAGGGACTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCCTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606468 Chironomidae sp. water mite diet isolate 4405-BHL032417-GBD29246_17487-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTACGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGAATGTTGCCCCCTTCA	Using NCBI BLASTN in June 2018, this sequence was 98.9% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606469 Chironomidae sp. water mite diet isolate 4415-BHL032417-GBD27504_15800-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATATTAATTCGAGTAGAACTAGGACAACCAGGTTCATTAATCAGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606470 Chironomidae sp. water mite diet isolate 4434-BHL032417-GBD5874_8873-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATTTTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTCTAATTCGACTAGAATTAGGACACCCAGGCCCATCAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCAGATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTGTTATCAAGATCAATTGTGGAAAATGGTGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606471 Chironomidae sp. water mite diet isolate 4439-BHL032417-GBD15834_19218-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTTGGACAACCTGGCACATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCAATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGTTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606472 Chironomidae sp. water mite diet isolate 4458-BHL032417-GBD21229_16695-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTTTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGTCACCCAGGCTCATTAATCGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAATGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCACCATCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606473 Chironomidae sp. water mite diet isolate 4465-BHL032417-GBD10327_10948-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGTTGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATATATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606474 Chironomidae sp. water mite diet isolate 4474-BHL032417-GBD5905_24629-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTAGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGTACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTGTTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTCTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCATCATTAACCTTACTTTTATCAAGAGCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606475 Chironomidae sp. water mite diet isolate 4486-BHL032417-GBD24669_13748-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTATTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACGGCACACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGTGCTCCTGATATAGCATTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606476 Chironomidae sp. water mite diet isolate 4490-BHL032417-GBD11816_28193-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTAGAGCTTGACCGGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTACTCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCCTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTGTATCAAGAGCAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606477 Chironomidae sp. water mite diet isolate 4550-BHL032417-GBD17274_5319-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCATTAACCTTACTTTTATCAAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606478 Chironomidae sp. water mite diet isolate 4633-BHL032417-GBD12519_18231-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGATATAGCTTTCCCCCGTCTAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606479 Chironomidae sp. water mite diet isolate 4786-BHL032417-GBD20905_20374-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTGTATTCGGAGCCTGATCAGGTATAGTAGGTACTTCCCTTAGTAATCCAGTACGAGCTAAATTAGGACACCCCGGAGCATTAATTGGAGACGATCAAATTTATAACGTAATGGTTACAGCTCATGCCTTTGTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTACCACTAATATTAGGTGCACCAGATATAGCTTTCCCTCGAATAAATAATATATGCTTTTGATTATTACCCCCATCTTTAACATTACTATTAGCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606480 Chironomidae sp. water mite diet isolate 4894-BHL032417-GBD16804_4186-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGGATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGATATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTTCTTCCTCCCTCTCTATCTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ166684, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606481 Chironomidae sp. water mite diet isolate 5082-BHL032417-GBD15155_21535-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGATTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCACTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGATTTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGATTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606482 Chironomidae sp. water mite diet isolate 5113-BHL032417-GBD14453_27449-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGAAGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGCTGCCCCCATCATTAACTTTATTATTATCTAGAGCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606483 Chironomidae sp. water mite diet isolate 5122-BHL032417-GBD13602_26047-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACAACCAGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTAGAGGATTTGGGAATTGATTGGTCCCTCTAATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606484 Chironomidae sp. water mite diet isolate 5134-BHL032417-GBD10826_19789-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTCATTTTCGGTGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606485 Chironomidae sp. water mite diet isolate 5136-BHL032417-GBD19785_23655-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAGATTTATAACGTAATTGTTACTGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTGGTCCCTCTAATATTAGGAGCCCCAGACATAGCTTTCCCCCGAATAAATAATATAAGTTTTTGACTTTTACCCCCGTCATTAACTTTACCTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606486 Chironomidae sp. water mite diet isolate 5231-BHL032417-GBD16783_19741-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCGTGATCGGGAATAGTAGGAACTTCTCTTAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAAATTTAATTGGAGATGATCAAATTTATAATGTTATTGTAACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTGCCATTAATATTAGGAGCACCTGATATGGCATTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCTTCCTTAACATTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KR754220, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606487 Chironomidae sp. water mite diet isolate 5271-BHL032417-GBD14961_3025-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCTGAACTTTCATTGGTGATGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTACACCTATTTTAATTTGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTATCTTTACTTCTTTCTAATTCAATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606488 Chironomidae sp. water mite diet isolate 5296-BHL032417-GBD13789_2565-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTGTATTCGGAGCCTGATCAGGTATAGTAGGTACTTCCCTTAGTAATCTAGTACGAGCTGAATTAGGACACCCCGGTGCATTAATTGGAGACGATCAAATTTATAACGTAATGGTTACAGCTCATGCCTTTGTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTACCGCTAATATTAGGTGCACCAGATATAGCTTTCCCTCGAATAAATAATATATGCTTTTGATTATTACCCCCATCTTTAACATTACTATTAGCTAGTTCAATTGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606489 Chironomidae sp. water mite diet isolate 5302-BHL032417-GBD17853_28427-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGCGCCTGATCTGGGATATTCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCACATTTATAACATAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCTCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGTTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606490 Chironomidae sp. water mite diet isolate 5308-BHL032417-GBD14621_28717-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACAAGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGATTGTTGCCCCCATCATTTACCTTATTGTTATCTAGAGCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606491 Chironomidae sp. water mite diet isolate 5310-BHL032417-GBD19842_4870-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCCTGATCTGGGATAATCGGGACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACTACCCGGTACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCCTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAACTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606492 Chironomidae sp. water mite diet isolate 5318-BHL032417-GBD13686_15613-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATACTTCATTTTGGGGGCTTGATCCGGAATAGTAGGTACTTCCTTAAGTATGCTTATTCGAACAGAATTAGGACGACCAGGAACTTTTATTGGAGATGATCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KP040037, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606493 Chironomidae sp. water mite diet isolate 5324-BHL032417-GBD4571_6941-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGTATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCCATTTTAATTGGAGGATTTTGGAATTGATTTGTCCCTCTTATATTAGGAGCCCCCGACATAGCTTTCCCCCGTATAAATAATATAAGGTTTTGGCTTTTACCCCCGTCAATAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606494 Chironomidae sp. water mite diet isolate 5325-BHL032417-GBD29388_14585-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGAGCCTGATCTGGGATAATAGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGACGATCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTGGTCCCTCTAATATTAGGTGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCTTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606495 Chironomidae sp. water mite diet isolate 5326-BHL032417-GBD15886_6654-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGCTACATCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTGTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCAACATTAACTTTATTGTTATCGAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606496 Chironomidae sp. water mite diet isolate 5442-BHL032417-GBD3863_21086-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTGGGAACTTCTTTAAGATTTCTAATTCGAGCGGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAAATGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCACCATCATTAACTTTATTGTTATCTAGAACAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606497 Chironomidae sp. water mite diet isolate 5463-BHL032417-GBD13752_22132-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTATTAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTGTAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTAATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606498 Chironomidae sp. water mite diet isolate 5511-BHL032417-GBD27410_18793-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGTACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGTTCTATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606499 Chironomidae sp. water mite diet isolate 5525-BHL032417-GBD16530_4503-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCAGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACACGTAACCTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATGATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGCTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606500 Chironomidae sp. water mite diet isolate 5554-BHL032417-GBD18876_13127-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTAATACCACCATCATTAACCTTGCGTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606501 Chironomidae sp. water mite diet isolate 5556-BHL032417-GBD12273_5238-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGGGACGACCAAATTTATAACGTAATTGTTAAAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTGATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCCTTTACCCCCGTCATTAACTTTACTTCTTTCTAATTCAATTGTAGCAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606502 Chironomidae sp. water mite diet isolate 5559-BHL032417-GBD20968_4820-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTTTTGGAGATGATCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTACTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR287035, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606503 Chironomidae sp. water mite diet isolate 5583-BHL032417-GBD5917_6622-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTATTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606504 Chironomidae sp. water mite diet isolate 5675-BHL032417-GBD15002_10750-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGATACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTATCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606505 Chironomidae sp. water mite diet isolate 5694-BHL032417-GBD14377_5302-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCATGAACTTTTATTGGAGATGATCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGTGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCCTCTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR287035, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606506 Chironomidae sp. water mite diet isolate 5781-BHL032417-GBD29503_14735-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTATCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCAGATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAACACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606507 Chironomidae sp. water mite diet isolate 5855-BHL032417-GBD11627_24603-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTGTATTCGGAGCCTGATCAGGTATAGTAGGTACTTCCCTTAGTAATCTAGTACGAGCTAAATTAGGACACCCCGGGGCATTAATTGGAGACGATCAAATTTATAACGTAATGATTACAGCTCATGCCTTTGTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTACCACTAATATTAGGTGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGCTTTTGATTATTACCCCCATCTTTAACATTACTATTAGCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606508 Chironomidae sp. water mite diet isolate 5874-BHL032417-GBD21622_10826-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGATCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCATCTTTCTAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR287035, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606509 Chironomidae sp. water mite diet isolate 5883-BHL032417-GBD14279_8099-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCGTGATCAGGAATACTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTGATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCTCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGTGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606510 Chironomidae sp. water mite diet isolate 5894-BHL032417-GBD26223_12823-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCCATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGAGGACCCGGAACTTTCATTGGTGACGACCAAATTTCTAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCGATTTTAATTGGAGGATTGGGAAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAACTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTATACCCTCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606511 Chironomidae sp. water mite diet isolate 5992-BHL032417-GBD12064_3410-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAAAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATTAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606512 Chironomidae sp. water mite diet isolate 6191-BHL032417-GBD21644_12477-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTGGGAAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTATACCCGCGTCATTAACATTACTTCTTTCTAGTGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606513 Chironomidae sp. water mite diet isolate 6250-BHL032417-GBD16455_21942-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCACATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCAACTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACCTTTATCAAGACCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606514 Chironomidae sp. water mite diet isolate 6458-BHL032417-GBD18470_12375-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACAGCCAGGAACTTTTATTGGAGATGATCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATACAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTTCTACTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR287035, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606515 Chironomidae sp. water mite diet isolate 6613-BHL032417-GBD11257_2698-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTGTATTCGGAGCCTGATCAGGTATAGTAGGTACTTCCCTTAGTAATCTAGTACGAGCTGAATTAGGACACCCCGGGGCATTAATTGGAGACGATCAAATTTATAACGTAATGGTTACAGCTCATGCCTTTGTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTATCACTAATATTAGGTGCACCAGATATATCTTTCCCTCGAATAAATAATATATGCTTTTGACTATTACCCCCATCTTTAACATTACTATTAGCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606516 Chironomidae sp. water mite diet isolate 6704-BHL032417-GBD12053_3549-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGATTGACCGGGAATAGTAGACACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGTCTCCTGATATAGCTTTTCCGCGAATAAATAATATAATATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606517 Chironomidae sp. water mite diet isolate 7152-BHL032417-GBD22826_6613-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTGTATTCGGAGCCAGATCAGGTATAGTAGGTACTTCCCTTAGTATTCTAGTACGAGCTGAATTAGGACACCCCGGGATATTAATTGGAGACGATCAAATTTATAACGTAATCGTTACAGCTCATGCCTTTTTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTACCACTAATATTAGGTGCACCAGATATAGCTTTACCTCGAATAAATAATATAAGATTTTGATTATTACCACCATCTTTAACATTACTATTAGCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606518 Chironomidae sp. water mite diet isolate 7198-BHL032417-GBD25071_14512-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGATCAATTCTATAATGTAATTGTAACTGCACATGTTTTTATTATATTTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACCCTTCTTCTTTCTAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR287035, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606519 Chironomidae sp. water mite diet isolate 7620-BHL040517-GBD10501_5550-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTATTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606520 Chironomidae sp. water mite diet isolate 7637-BHL040517-GBD8073_12988-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTCTATTTTTGGGGCCTGATCGGGGATAGTAGGCACATCCTTAAGAATACTAATTCGTGCTGAGTTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAAATGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTCTGATTACTCCCACCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606521 Chironomidae sp. water mite diet isolate 7646-BHL040517-GBD5245_18399-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACTTCCCTAAGAATACTAATTCGTGCTGAATTAGGTCCCCCAGGAACATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTATACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAAAAATATAAGTTTCTGATTACTCTCTCCTTCTCTTACTCTATTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606522 Chironomidae sp. water mite diet isolate 7651-BHL040517-GBD18097_9913-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCATGCTGGATTAGGTCACCCAGGAACATTGATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCAGAAATTGACTTTTACCTTTAATATTAGGAGCCCATGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606523 Chironomidae sp. water mite diet isolate 7671-BHL040517-GBD2625_13176-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606524 Chironomidae sp. water mite diet isolate 7709-BHL040517-GBD22410_21485-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAAATGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KM993958, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606525 Chironomidae sp. water mite diet isolate 7771-BHL040517-GBD4628_17393-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGTGCCTGATCGGGAATAGTAGGAACTTCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTGTACCTTTAATATTAGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAATTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606526 Chironomidae sp. water mite diet isolate 7776-BHL040517-GBD28294_19310-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGAGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTTGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTATCTCTTTTATTGTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR278209, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606527 Chironomidae sp. water mite diet isolate 7805-BHL040517-GBD4439_10205-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGGGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGATTATTGCCACCTTCTCTTACCCTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606528 Chironomidae sp. water mite diet isolate 7809-BHL040517-GBD26660_17179-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGAACTTCATTAAGAATACTAATTCATGCTGAATTAGGTCACCCAGGAACATTCATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTACTCCCTCCTTCTCTTACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606529 Chironomidae sp. water mite diet isolate 7822-BHL040517-GBD27248_9993-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATACTAATTCGAGCTGAATTAGGTCATCCAGGAACATTAATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR278209, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606530 Chironomidae sp. water mite diet isolate 7852-BHL040517-GBD24632_25377-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCCTGATCAGGTATAGTAGGTACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTAGTGACGACCAAATTTATAATGTAATTGTTACAGCCAATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTTGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCATTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KM993958, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606531 Chironomidae sp. water mite diet isolate 7861-BHL040517-GBD20616_22570-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACTTCCCTAAGAATACTAATTCGAGCTGAACTAGGTCACCCAGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTAACCCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR278209, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606532 Chironomidae sp. water mite diet isolate 7903-BHL040517-GBD20393_21483-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATATTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCACCTTCTCTATCACTTTTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR278209, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606533 Chironomidae sp. water mite diet isolate 7927-BHL040517-GBD28096_18421-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGTATAGTAGGTACATCCCTATGAATACTAATTCGAGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATCCCAATTTTAATTGGAGGGTTCGGAAATCGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTATCTCTTTTACTTTCTGGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606534 Chironomidae sp. water mite diet isolate 7932-BHL040517-GBD13529_2705-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGAGCTGAATTAGGCCACCCAGGAACATTAATTGGGGACGACCAAATTTATAATGTAATTGTTACATCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTCACCTTTAATATTAGGAGCCCCTGGTATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606535 Chironomidae sp. water mite diet isolate 7945-BHL040517-GBD9360_24584-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCAGAAATTGACTTGTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCCCCTTCTCTTACTCTTTTGCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606536 Chironomidae sp. water mite diet isolate 7949-BHL040517-GBD14228_3659-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAAAATACTAATTCGAGCTGAATTAGGTCACCCATTAACATTAATTGGTGACGTCCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTACAATTTTTTTTATAGTTATCCCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAATTCAATTGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606537 Chironomidae sp. water mite diet isolate 7986-BHL040517-GBD8411_24083-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGCTTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATCGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTTCTTCCCCCCTCATTAACTCTTCTTCTTTCTAGATCAATTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606538 Chironomidae sp. water mite diet isolate 8007-BHL040517-GBD9335_16961-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGTATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATCCCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGAGATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTGCACTATTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606539 Chironomidae sp. water mite diet isolate 8027-BHL040517-GBD6493_4857-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGAGGCCTGATCTGGTATAGTAGGTACTTCCCTAAGAATGCTAATTCGTGCTGAATTAGGTCACCCAGGAACATTTATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAATTCAATTGTAGAAGATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606540 Chironomidae sp. water mite diet isolate 8030-BHL040517-GBD5065_10166-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCTTAAGAATACTAATTCGTGTTGAATTAGGTCACCCAGGAACATTAATTGGTGACGAACAAATTTATAATGTAATTGTTACATCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGATTACTACCTCCTTCTCTTTCTCTTTTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606541 Chironomidae sp. water mite diet isolate 8042-BHL040517-GBD18503_2797-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGGGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTATAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGAGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATGGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAATTCAATTGTTGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606542 Chironomidae sp. water mite diet isolate 8057-BHL040517-GBD17125_5854-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGGGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTTCTTCTCTTTCCCTTTTACCTTCTAGTTCAAATGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606543 Chironomidae sp. water mite diet isolate 8063-BHL040517-GBD12845_26177-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCATTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTCATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTTTACCTATAATATTAGGAGCCCCTGATATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCCCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606544 Chironomidae sp. water mite diet isolate 8092-BHL040517-GBD18034_28163-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGTTCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGGGCTGAATTAGGTCCACCCGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCCCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606545 Chironomidae sp. water mite diet isolate 8093-BHL040517-GBD16859_5610-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGAGCTGAATTAGGACACCCAGGAACATTAATTGGAGACGACCAACTTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTGTGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606546 Chironomidae sp. water mite diet isolate 8119-BHL040517-GBD6396_17559-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCATGCTGAATTAGGTCACCCAGGAACTTTAATTGGTAACGTCAAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTTACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAATTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606547 Chironomidae sp. water mite diet isolate 8131-BHL040517-GBD28195_16250-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCAGAATTAGGTCACCCATTAACATTAATAGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATGTGAATTGGAGGATTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606548 Chironomidae sp. water mite diet isolate 8136-BHL040517-GBD14658_10335-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGGATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCCCTTTCTCTTTTACTTTCAAATAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606549 Chironomidae sp. water mite diet isolate 8141-BHL040517-GBD17957_25923-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGTTAGTAGGGACATCCCTAAGAATACTAATTCGTGTTGAATTAGGTCACCCAGGAACATTAATTGATGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTGTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGATTACTCCCTCCTTCTCTAACTCTATTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606550 Chironomidae sp. water mite diet isolate 8171-BHL040517-GBD15777_27872-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGTACATCCCTAAGAATACTAATTCGTGCTGCATTAGGTCACCCAGGAACATTAATTGGTGACGACCACATTTATAATGTACTTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTCTACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTGCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606551 Chironomidae sp. water mite diet isolate 8226-BHL040517-GBD13142_24697-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGCCCTGATCGGGGATAGTTGGGATATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTGCGCGTTTACTGTCTAGTGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606552 Chironomidae sp. water mite diet isolate 8229-BHL040517-GBD20048_16208-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGTTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCATATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTTTTACCTCTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTACCTCCTTCTCTTACACTTTTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR278209, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606553 Chironomidae sp. water mite diet isolate 8238-BHL040517-GBD10336_2451-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGTACATCCCTAAGAATACTAATTCGTGCTGAATTAGTTCACCCAGGAACATTAATTGGTGACGACCAAGTTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCAGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCTTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTATCTCTATTACTGTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606554 Chironomidae sp. water mite diet isolate 8243-BHL040517-GBD19028_14652-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCCAATTTATAATGTAATTGTTATGGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606555 Chironomidae sp. water mite diet isolate 8245-BHL040517-GBD27413_16190-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGGGCTTGATCGGGGATAGTAGGGACTTCTCTAAGTATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGACCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGAGTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606556 Chironomidae sp. water mite diet isolate 8265-BHL040517-GBD12530_28079-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCTGGGATAGTAGGGACTTCTCTAAGAATACTAATTCGTGCTGAATTAGGTCAACCAGGGACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAACCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTGTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTGTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606557 Chironomidae sp. water mite diet isolate 8290-BHL040517-GBD5187_15478-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGTACATCCCTAAGAATACTAATTCGTGTTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTGATACCAATTTTAATTGGAGGGTTCGGAAATTGACTAGTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCCCCTTCTCTTTCCCTATTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606558 Chironomidae sp. water mite diet isolate 8293-BHL040517-GBD24156_7040-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCGGGGATAGTAGGGACATCTCTAAGAATACTAATTCGTGCTGAACTAGGTCAACCAGGAACATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGGATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606559 Chironomidae sp. water mite diet isolate 8304-BHL040517-GBD23966_22470-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTACTCTTTCTCATTTACTTGCTAGTTCAATTGTAGAAAATGGCGCTGAAAC	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606560 Chironomidae sp. water mite diet isolate 8319-BHL040517-GBD19617_22642-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGTTACATCCCTAAGAATACTAATTCGTGCGGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGCTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606561 Chironomidae sp. water mite diet isolate 8327-BHL040517-GBD26749_19006-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGTTACATCCATAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGAGACGAACAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATCCCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTATCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTATTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606562 Chironomidae sp. water mite diet isolate 8331-BHL040517-GBD25223_23080-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGTGACATCCTTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTATAGTTATACCGATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTGCTCTAACACTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606563 Chironomidae sp. water mite diet isolate 8347-BHL040517-GBD23360_5677-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTATGACACCCAGGAACATTATTTGGTGAAGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTATCTGATTACTCCCTCCTTCTCTTACCCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606564 Chironomidae sp. water mite diet isolate 8348-BHL040517-GBD13589_5067-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGTTAGTAGGGACATCCCTAAGAATACTAATTCGAGCTAAATTAGGTCACCCAGTAACATTAATTGGTGACGTCCATATTTATAATGTAATTGTTACAGCCCATGCCTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGCTATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTGGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606565 Chironomidae sp. water mite diet isolate 8358-BHL040517-GBD16179_2552-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATGCGAGCTGAATCAGGTCACCCAGGAACATTAATTGGTGACGACTCAATTTATATTGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606566 Chironomidae sp. water mite diet isolate 8361-BHL040517-GBD10222_14447-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGGGCTTGATCGGGGATAGTAGGGACATCCCTTAGAATACTAATTCATGCTGAATTAGGTCACCCATGAACATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTCTAATTGGAGGATTCGGAAATTGACTTTTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606567 Chironomidae sp. water mite diet isolate 8362-BHL040517-GBD20705_5306-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCCTGATCAGGGATAGTAGGGACATCCCTAAGAATATTAATTCGAGCTGAACTAGGACACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTTTGCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KM993958, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606568 Chironomidae sp. water mite diet isolate 8413-BHL101416-GBD13193_28968-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606569 Chironomidae sp. water mite diet isolate 8458-BHL101416-GBD3431_8890-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGACATCCTGGAAATTTAATTGGAGATGATCAAATTTATAATGTTATTGTAACAGCCCATGCTTTCATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTGCCATTAATATTAGGAGCACCTGATATGGCATTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCTTCCTTAACATTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR754220, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606570 Chironomidae sp. water mite diet isolate 8459-BHL101416-GBD18536_4737-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACATCCCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTCAATATTAGGAGCACCTGTTATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606571 Chironomidae sp. water mite diet isolate 8680-BHL101416-GBD24557_17787-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTGTATTCGGAGCCTGATCAGGTATAGTAGGTACTTCCCTTAGTAATCTAGTACGAGCTGAATTAGGACACCCCGGGGCATTAATTGGAGACGATCAAATTTATAACTTAATGGTTACAGCTCATGCCTTTGTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTACCACTAATATTAGGTGCACCAGATATAGCTTTCCCTCGAATAAATAATATATGCTTTTGATTATTACCCCCATCTTTAACATTACTATTAGCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606572 Chironomidae sp. water mite diet isolate 8752-BHL101416-GBD16465_18601-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCGTGATCGGGAATAGTAGGAACTTCTTTTAGAATATTAATTCGAGTTGAATTAGGACATCCTGGAAGATTAATTGGAGATGATCAAATTTATAATGCTATTGTAACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTGCCATTAATATTAGGAGCACCTGATATGGCATTTCCTCGAATAAATAATATAAGATTTTGACTATTACCCCCTTCCTTAACATTACTTCTATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR754220, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606573 Chironomidae sp. water mite diet isolate 8776-BHL101416-GBD23308_26878-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTTGGCCATCCAGGAACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGGCTTGTACCTCTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTGCTACCTCCATCTCTAACTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ166684, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606574 Chironomidae sp. water mite diet isolate 8803-BHL101416-GBD2491_17109-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTATAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTACATTAACCTGACGTTTATCAAGATCAATAGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606575 Chironomidae sp. water mite diet isolate 8854-BHL101416-GBD6110_19403-Lq60 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTGTAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606576 Chironomidae sp. water mite diet isolate 8869-BHL101416-GBD7256_8713-Lq60 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCACTAAGAATGCTTGTTCGAGCAGAATTAGGACGACCTGGAACCTTTATTGGAGACGATCAAATTTATAATGTAATCGTTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTCCCTTTAATGCTAGGGGCCCCAGATATGGCCTTCCCTCGGATAAATAATATAAGTTTCTGACTTTTACCCCCTTCGCTTACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KM993512, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606577 Chironomidae sp. water mite diet isolate 8966-BHL032417-GBD24308_11360-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATACTGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCATCAATAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606578 Chironomidae sp. water mite diet isolate 9603-BHL032417-GBD4875_9242-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCACTAAGAATGCTTGTTCGAGCAGAATTAGGACGACCTGGAACCTTTATTGGAGACGATCAAATTTATAATGTAATCGTTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTCCCTTTAATGCTATGGGCCCCAGATATGGCCTTCCCTCGGATAAATAATATAAGTTTTTGACTTTTACCTCCTTCGCTTACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KM993512, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606579 Chironomidae sp. water mite diet isolate 9640-BHL032417-GBD23597_9796-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTGTGATTGTTGCCCCCATCATTAACTCTATTGTTATCTAGATCAACTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606580 Chironomidae sp. water mite diet isolate 10239-BHL040517-GBD16818_15461-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTTGGAGCTTGGTCTGGTATAGTAGGAACTTCACTAAGAATGCTTGTTCGAGCAGAATTAGGACGACCTGGAACCTTTATTGGAGACGATCAAATTTATAATGTAATCGTTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTCCCTTTAATGCTAGGAGCCCCAGATATGGCCTTTCCTCAGATAAATAATATAAGTTTTTGACTTTTACCTCCTTCGCTTACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KM993512, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606581 Chironomidae sp. water mite diet isolate 10325-BHL040517-GBD29090_13162-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGACTTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGCTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAAGTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAAAAATATAAGATTTTGATTATTACCCCCTACATTAACCTGACTTTTATCGAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606582 Chironomidae sp. water mite diet isolate 10448-BHL040517-GBD6612_19874-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTTGAATTAGGACACCCAGGCTCATTTATCGGAGAAGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTGATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTATTACCCCCTTCATTAACCTTACTTCTATCGAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606583 Chironomidae sp. water mite diet isolate 10516-BHL040517-GBD21635_8263-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTCAAGAATTTTAATTCGACTAGAATTAGGACACCCTGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAAGGATACCCATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCATCATTAACCTTACTTTTATCGAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606584 Chironomidae sp. water mite diet isolate 10587-BHL040517-GBD12441_16828-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACGCCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATGCCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTCCCGCGAATAAATAATATAAGATTTTGACTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606585 Chironomidae sp. water mite diet isolate 10718-BHL101516-GBD3684_9927-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606586 Chironomidae sp. water mite diet isolate 10777-BHL101516-GBD25197_21702-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGTTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTAACCGCACATGCTTTTATTATAATTTTTTTATAGTTATACCGATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGGGCCCCTGATATAGCCTTCCCGCGAATAAATAATATAAGATTTTGACTTCGCCCACCGTCTCTTTCTCTTCTCCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ208847, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606587 Chironomidae sp. water mite diet isolate 10914-BHL101516-GBD23010_3753-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606588 Chironomidae sp. water mite diet isolate 10946-BHL101516-GBD18241_28737-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGAACAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606589 Chironomidae sp. water mite diet isolate 10949-BHL101516-GBD23447_14534-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATCTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACTTTAAATGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTATAGTAATACCTATTTTGATCGGAGGCTTTGGAAATTGACTATTACCACTTATACTTGGAGCCCCTGATATGGCCTTTCCTCGAATAAATAACATAAGATGCTGGTTACTACCTCCGTCTATTACTTTGCTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606590 Chironomidae sp. water mite diet isolate 11002-BHL110116-GBD10511_11214-Lq74 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGATCAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606591 Chironomidae sp. water mite diet isolate 11005-BHL110116-GBD20369_13506-Lq74 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTATAGTAATACCTATTTTGATCGGAGGCTTTGGAAATTGACTATTACCACTTATACTTGGAGCCCCTGGTATGGCCTTTCCTCGAATAAATAACATAAGATTCTGGTTACTACCTCCGTCTATTTCTTTGCTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606592 Chironomidae sp. water mite diet isolate 11006-BHL110116-GBD21751_17194-Lq74 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606593 Chironomidae sp. water mite diet isolate 11008-BHL110116-GBD15956_16824-Lq74 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606594 Chironomidae sp. water mite diet isolate 11015-BHL110116-GBD8688_8591-Lq75 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTCTGATTATTACCCCCGTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606595 Chironomidae sp. water mite diet isolate 11017-BHL110116-GBD18081_6548-Lq75 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACTTTCATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTGATTGGAGGCTTTGGAAATTGACTAGTACCACTAATACTTGGAGCCCCTGATATGGCTTTTCCTCGAATAAATAACATAAGATTCTGGTTACTACCCCCGTCTATTTCTTTGCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606596 Chironomidae sp. water mite diet isolate 11019-BHL110116-GBD23733_17195-Lq75 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTGTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606597 Chironomidae sp. water mite diet isolate 11021-BHL110116-GBD26364_14472-Lq75 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTTGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACTTTAATTGGTGATGATCAAATTTATAATATTATTGTCACTGCTCATGCATTTATTATAATTTTTTTATAGTAATACCTATTTTGATCGGAGGCTTTGGAAATTGACTATTACCACTTATACTTGGAGCCCCTGATATGGCATTTCCTCGAATAAATAACATAAGGTTCTGGTTACTACCTCCGTCTATATCTTGGCTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606598 Chironomidae sp. water mite diet isolate 11022-BHL110116-GBD18398_15065-Lq75 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGTGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTGATATTAGGAGCTCCAGATATAGCATTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606599 Chironomidae sp. water mite diet isolate 11025-BHL110116-GBD13658_20243-Lq76 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTAGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGAACAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATCTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATAAAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606600 Chironomidae sp. water mite diet isolate 11029-BHL110116-GBD13852_14602-Lq76 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTATAGTAATGCCTATTTTGATTGGAGGCTTTGGAAATTGACTATTACCACTTATACTTGGAGCCCCTGATATGGCCTTTCCTCGAATAAATAACATAAGATTCTGGTTACTACCTCCGTCTATTTCTTTGCTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606601 Chironomidae sp. water mite diet isolate 11172-BHL110116-GBD22148_4144-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606602 Chironomidae sp. water mite diet isolate 11216-BHL110116-GBD9556_13759-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606603 Chironomidae sp. water mite diet isolate 11293-BHL110116-GBD25098_20598-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATCTTTTATTTTTGGAGCTTTATCGGGTATAGTATGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCTGAGACCATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATCATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGTGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTGCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606604 Chironomidae sp. water mite diet isolate 11402-BHL101516-GBD7401_21031-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGAGATACCTATTTTAATTGGAGGTTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGACAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606605 Chironomidae sp. water mite diet isolate 11411-BHL101516-GBD26908_21095-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGTCACCCAGGCTCATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCAGCATTAACCTTACTATTATCAAGATGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606606 Chironomidae sp. water mite diet isolate 11420-BHL101516-GBD11183_13792-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATTTTCGGGGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTATAGTAATACCTATTTTGATCGGAGGCTTTGGAAATTGACTATTACCACTTATACTTGGAGCCCCTGATATGGCCTTTCCTCGAATAAATAACATAAGATTCTGGTTACTACCTCCGTCTATTTCTTTGCTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606607 Chironomidae sp. water mite diet isolate 11449-BHL101516-GBD23142_4307-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAACTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGAGCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTATTACCCCCATCATTAACCTGACTATTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606608 Chironomidae sp. water mite diet isolate 11451-BHL101516-GBD15059_10691-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGAGGCTCCTGATATAGCTTTTCCGCCAATAAATAAAATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAACAATAGGAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606609 Chironomidae sp. water mite diet isolate 11472-BHL101516-GBD13108_28962-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATATTAATTGGAGGAATTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATGTGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606610 Chironomidae sp. water mite diet isolate 11475-BHL101516-GBD13345_14678-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAAAATTAGGACGCCCAGGCTCATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTGATATTAGGGGCTCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606611 Chironomidae sp. water mite diet isolate 11495-BHL101516-GBD18291_2184-Lq80 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTCCCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606612 Chironomidae sp. water mite diet isolate 11500-BHL101516-GBD24252_9272-Lq80 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGACCAGAATTAGGACACGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATGATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606613 Chironomidae sp. water mite diet isolate 11502-BHL101516-GBD28466_10890-Lq80 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATTTTCGGGGCTTGATCCGGAATAGTGGGGATTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGTAACTTTAATTGGAGATGATCAAATTTATAATGTTATTGTCACTGTTCATGCATTTATTATAATTTTTTTATTGTAATACCTATTTTGTTCGGAAGCTTTGGAAATTCACTATTACCACTTATACTTGGAGCCCCTGATATGGCCTTTCCTCGAATAAATAACATAAGATTCTGGTTACTACCTCCGTCTATTTCTTTGCTTCTATCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606614 Chironomidae sp. water mite diet isolate 11506-BHL101516-GBD17359_19173-Lq80 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGCTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAAGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGACCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606615 Chironomidae sp. water mite diet isolate 11530-BHL101516-GBD12626_16666-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTTGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606616 Chironomidae sp. water mite diet isolate 11684-BHL101516-GBD21644_14632-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGTATTTTTATTCGACTAGAATTAGGTCACCCAGGCTCATTAATCGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCACCTGATATAGCTTTTCCGCGGATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606617 Chironomidae sp. water mite diet isolate 11750-BHL101516-GBD19828_5427-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATCTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTCTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606618 Chironomidae sp. water mite diet isolate 12052-BHL040517-GBD13193_28968-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606619 Chironomidae sp. water mite diet isolate 12097-BHL040517-GBD3431_8890-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGACATCCTGGAAATTTAATTGGAGATGATCAAATTTATAATGTTATTGTAACAGCCCATGCTTTCATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTGCCATTAATATTAGGAGCACCTGATATGGCATTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCTTCCTTAACATTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR754220, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606620 Chironomidae sp. water mite diet isolate 12098-BHL040517-GBD18536_4737-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACATCCCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTCAATATTAGGAGCACCTGTTATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606621 Chironomidae sp. water mite diet isolate 12319-BHL040517-GBD24557_17787-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTGTATTCGGAGCCTGATCAGGTATAGTAGGTACTTCCCTTAGTAATCTAGTACGAGCTGAATTAGGACACCCCGGGGCATTAATTGGAGACGATCAAATTTATAACTTAATGGTTACAGCTCATGCCTTTGTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTACCACTAATATTAGGTGCACCAGATATAGCTTTCCCTCGAATAAATAATATATGCTTTTGATTATTACCCCCATCTTTAACATTACTATTAGCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606622 Chironomidae sp. water mite diet isolate 12391-BHL040517-GBD16465_18601-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCGTGATCGGGAATAGTAGGAACTTCTTTTAGAATATTAATTCGAGTTGAATTAGGACATCCTGGAAGATTAATTGGAGATGATCAAATTTATAATGCTATTGTAACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTGCCATTAATATTAGGAGCACCTGATATGGCATTTCCTCGAATAAATAATATAAGATTTTGACTATTACCCCCTTCCTTAACATTACTTCTATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR754220, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606623 Chironomidae sp. water mite diet isolate 12415-BHL040517-GBD23308_26878-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTTGGCCATCCAGGAACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGGCTTGTACCTCTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTGCTACCTCCATCTCTAACTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ166684, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606624 Chironomidae sp. water mite diet isolate 12442-BHL040517-GBD2491_17109-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTATAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTACATTAACCTGACGTTTATCAAGATCAATAGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606625 Chironomidae sp. water mite diet isolate 12523-BHL040517-GBD18838_4809-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGATCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAATAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606626 Chironomidae sp. water mite diet isolate 12536-BHL040517-GBD13225_20940-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606627 Chironomidae sp. water mite diet isolate 12559-BHL040517-GBD28563_17839-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCTTGATCGGGACTAGTAGGCACTTCTTTAAGAATTTTAATTCGACTCGAATTAGGACACACAGGCTCATTAATCGGAGACGATCAAATTTACAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATGGATTAGTACCTTTGATATTAGTGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCCAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606628 Chironomidae sp. water mite diet isolate 12607-BHL040517-GBD29495_17504-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCTTGATCGGGACTAGTAGGCACTTCTTTAAAACTTTTAATTCGACTAGAATTAGGACACCCAGGCTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCTGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606629 Chironomidae sp. water mite diet isolate 12628-BHL040517-GBD22084_26729-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGTATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTGATATTAGAGACTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606630 Chironomidae sp. water mite diet isolate 12634-BHL040517-GBD7356_9038-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTATGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTGTATTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCATCACTAACCTTACTTTTATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606631 Chironomidae sp. water mite diet isolate 12635-BHL040517-GBD9051_4571-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTTATTGTTACAGCACATGCTTATATAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTGTGATATTTGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606632 Chironomidae sp. water mite diet isolate 12651-BHL040517-GBD23247_4247-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCCTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCTCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTATCTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606633 Chironomidae sp. water mite diet isolate 12671-BHL040517-GBD27103_16236-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAACTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGGGCTCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTATTTCCCCCTTCATTAACCTTACTATTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606634 Chironomidae sp. water mite diet isolate 12681-BHL040517-GBD17315_26845-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGATCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTATTACTCTTCTTCTTTCTAATTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR287035, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606635 Chironomidae sp. water mite diet isolate 12713-BHL040517-GBD23796_14046-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCCTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTCATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGAGTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606636 Chironomidae sp. water mite diet isolate 12719-BHL040517-GBD21474_24693-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCATGCTCATTAATCTGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCGTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCAGTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606637 Chironomidae sp. water mite diet isolate 12740-BHL040517-GBD26230_10472-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGATTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAGATTGATTAGTACCTTTGATATTGGGGGCTCCTGATATAGCTTTTCCGCGAATAAAAAATAAAAGAATTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606638 Chironomidae sp. water mite diet isolate 12746-BHL040517-GBD13258_5111-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGAAGGCGGTTCTTTAAGAATTTGAATTCGACTAGAAGTAGGACACCCAGTCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606639 Chironomidae sp. water mite diet isolate 12750-BHL040517-GBD7007_20288-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATCAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATTATGTAATTGTTACAGCACATGCCTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTTGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACCTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606640 Chironomidae sp. water mite diet isolate 12765-BHL040517-GBD2318_18236-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGCAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGTCACCCTGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCATTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACGTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606641 Chironomidae sp. water mite diet isolate 12776-BHL040517-GBD17097_6725-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTCTTTATTTTGTATTCGGAGCCTGATCAGGTATAGTAGGTACTTCCCTAAGTAATCTAGTACGAGCTGAATTAGGACACCCCGGGGCATTAATTGGAGACGATCAAATTTGTAACGTAATGGTTACAGCACATGCCTTTGTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTACCACTAATATTAGGTGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGCTTTTGATTATTACCCCCATCTTTAACATTACTATTAGCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606642 Chironomidae sp. water mite diet isolate 12840-BHL040517-GBD22237_26886-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGACACCTATTTTAATTGGAGGCGTTGGAAATTGATTATTACCTTTGATATTAAGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAGCCTTACTTTTATCAAGATCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606643 Chironomidae sp. water mite diet isolate 12863-BHL040517-GBD16703_18007-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAAAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGTCTCCTGATATAACTTTTCCGCGAATAAATAATATAAGAGTTTGATTATTACCCCCATCATTAACCTTGCTTTTAGCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606644 Chironomidae sp. water mite diet isolate 12864-BHL040517-GBD9337_6032-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTATGACACCCAGGCTCATTAATCGGAAGAGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCAATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTATATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606645 Chironomidae sp. water mite diet isolate 12873-BHL040517-GBD23807_23110-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGACTTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTAGTAATAATTTTTTTATAGTGATACCTATCTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCATCATTAACTGTACTTTTAGCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606646 Chironomidae sp. water mite diet isolate 12884-BHL040517-GBD23419_23732-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGGGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATGTTAATTCGAGTAGAATTAGGACACCCAGGCTCATTAATCGGAGAAGATCAGATTTATAATGTAATTGTTACAGCACTTGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606647 Chironomidae sp. water mite diet isolate 12912-BHL040517-GBD3552_9692-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGTACTAGTTGGATCGTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATAATAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGAATGTTGCCCCCATCTTTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606648 Chironomidae sp. water mite diet isolate 12936-BHL040517-GBD25618_10738-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606649 Chironomidae sp. water mite diet isolate 12941-BHL040517-GBD12942_11927-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTTAGAATTCTAATTCGAGTAGAATTATGACATCCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTTATTGTTACTGCACATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606650 Chironomidae sp. water mite diet isolate 12962-BHL040517-GBD23045_5844-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCTAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATCTTAATTGGAGTATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGTACCTGATATGGCTTTCACACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATGATCTAGATCAAGTGTGGAAAATGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606651 Chironomidae sp. water mite diet isolate 12976-BHL040517-GBD11978_28297-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCGGAATTAGGACATGCAGGATCATTAATTGGAGACGATCAAATTTCTAATGTAATTGGTACAGATCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATATTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606652 Chironomidae sp. water mite diet isolate 12982-BHL040517-GBD12030_22853-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGTATAGTTGGAACTTCTTTAAGAATTCTAGTTCGAGCAGAGTTAGGACATGCAGGCTCAATAATTGGAGACGATCAAATTTATAATGTAATTGCTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGAACAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606653 Chironomidae sp. water mite diet isolate 13027-BHL040517-GBD29245_18396-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTCCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAACTCGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAACAATATAAGTTTTTGATTGTTGCCCCCATCAGTAAC	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606654 Chironomidae sp. water mite diet isolate 13028-BHL040517-GBD8083_25604-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCCGGAATAGTTGTAACTTCTTTTAGAATTCTAATTCGAGCCGCATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCCTGCTTTTGTAATAATTTTTTTATATTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606655 Chironomidae sp. water mite diet isolate 13031-BHL040517-GBD13844_2551-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCTAATTTATAATGTAATTGTTACAGTTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTTGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCATGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTGTTATTATCTAAATCAATTGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606656 Chironomidae sp. water mite diet isolate 13044-BHL040517-GBD4989_20860-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGTAACTTCTTTAAGAATTCTAATTCGATCAGCATTAGGACATGCAGTCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTGGGAGCACATGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606657 Chironomidae sp. water mite diet isolate 13049-BHL040517-GBD23036_11408-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTGCCACCTTCTCTTACCTGATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606658 Chironomidae sp. water mite diet isolate 13058-BHL040517-GBD28016_11458-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAGCTTGTTTAAGAATTCTAATTCGAGTAGAATTAGGACATGCAGGCTCATTAATAGGAAAAGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTAATATCTAGATCAATTGTGGAAAATGGAGCCGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606659 Chironomidae sp. water mite diet isolate 13063-BHL040517-GBD25973_5886-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTATCAAGAAGAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606660 Chironomidae sp. water mite diet isolate 13064-BHL040517-GBD13452_28411-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTACTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTATTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCATATTTATAATGTATTTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTGATTAATATCTAGAGCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606661 Chironomidae sp. water mite diet isolate 13067-BHL040517-GBD27406_19079-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTATTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGGTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCATGAATAAATAAAATAAGTTTTTGATTGTTGCCCCCAACATTAACTTTATTATTATCTAGATCAATTGCGGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606662 Chironomidae sp. water mite diet isolate 13078-BHL040517-GBD19216_5445-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTTGGACATGCCGGCTCATTTATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATATCATTCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTCTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606663 Chironomidae sp. water mite diet isolate 13082-BHL040517-GBD15796_19429-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATATTAATTCGAGCAGAACTAGGACATCCAGGCTCATTTATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606664 Chironomidae sp. water mite diet isolate 13090-BHL040517-GBD5893_17205-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAGCTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCTCGAATAAATAATATAATTTTTTTATTGTTGCCCCCATCATTAACTTTATCATTATCTAGGTTAATTGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606665 Chironomidae sp. water mite diet isolate 13094-BHL040517-GBD22582_10253-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAGGAATTCTAATTCGAGCAGATTTAGGACATGCAGGCTCATTAATTGGAGACGATCAATTTTATAATGTAATTGTTACAGCTCATGCTTTTTTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGAATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGACTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606666 Chironomidae sp. water mite diet isolate 13106-BHL040517-GBD19246_19624-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGGCATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCGCGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATGAATACTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606667 Chironomidae sp. water mite diet isolate 13142-BHL040517-GBD15281_6011-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATCCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATGATTTTTTTATAGTTATACCAATCTTAATTGGAGGATATTGAAACTGACGAGTTCCTTTAATATTAGGAGCACCTGATATGGTTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAACTGGAGCTGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606668 Chironomidae sp. water mite diet isolate 13144-BHL040517-GBD26347_10911-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGCTCAGAATTAGGACATGCAGGCTCATTAATTTGAGACGAGCAAATTTATAATTTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGGTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606669 Chironomidae sp. water mite diet isolate 13157-BHL040517-GBD26448_18579-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGATCATTTATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGGTCCTCTAATATTAGGAGCACCTGATATGGCTTTCCCATGAATAAATAATATAAGTTTTTGATTGTGGCCCCCATCATTAACTTTATTATTATCTAGAACAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606670 Chironomidae sp. water mite diet isolate 13158-BHL040517-GBD28332_17572-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTACTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCCTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCACATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTTTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606671 Chironomidae sp. water mite diet isolate 13196-BHL040517-GBD10334_5132-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTACGAATATTAATTCGAGCTGAATTAGGACATCCTGTTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGCTACTGCACATTCTTTCATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCGTGCCATTAATACTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATGACTTTCAAGAAGTATTGTAGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR287302, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606672 Chironomidae sp. water mite diet isolate 13203-BHL040517-GBD25408_22607-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATATTAATTCGAGCTGAATTAGGACAACCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTATTGCCATTAATACTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR280729, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606673 Chironomidae sp. water mite diet isolate 13246-BHL040517-GBD21251_24317-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACAGCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTCGTGCCTTTAATACTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTATCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606674 Chironomidae sp. water mite diet isolate 13247-BHL040517-GBD4089_14960-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGTATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTCTTGGAGATGATCAAATTTATAACGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTATAGTTATACCAATTTTAAATGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAAGAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606675 Chironomidae sp. water mite diet isolate 13268-BHL040517-GBD14358_3350-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGATGGAACTTCCTTAAGAATATTAATGCGAGCTGAAGTAGGACATCCTGGTACTTTTATTGAAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGCGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606676 Chironomidae sp. water mite diet isolate 13272-BHL040517-GBD24088_10742-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACAACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTTCCATTAATACTAAGAGCCCCAGATATAGCTTTTCCTCCAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAAAATTATTACTTTCAAGAAGTATTATACAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606677 Chironomidae sp. water mite diet isolate 13275-BHL040517-GBD25528_23780-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTTATTCGAGCTGAATTAGGACATCCCGGTACTTTTATTGGAGATGATCAAATTTATAATGTTATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTTTTGCCATTAATACTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606678 Chironomidae sp. water mite diet isolate 13295-BHL040517-GBD20623_15956-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606679 Chironomidae sp. water mite diet isolate 13307-BHL040517-GBD23392_26008-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGTATATTAATTCGGGCTGAACTAGGACATCCTGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606680 Chironomidae sp. water mite diet isolate 13311-BHL040517-GBD23338_13904-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTGCCACCTTCTCTTACCTTATTACTATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606681 Chironomidae sp. water mite diet isolate 13314-BHL040517-GBD14278_6080-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTCGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAACTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAACATAAGTTTTTGATTATTACCCCCATCTCTAACCTTATTTCTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606682 Chironomidae sp. water mite diet isolate 13315-BHL040517-GBD7618_7767-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGAAGCTTGATCAGGAATAGTTGGAACTTCCTTAAGAATTTTAATTCGAGCTGAATTAGGACATCCTGGCACTTTTATTGGAGATGATCATATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGAATTGGGAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATAAAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606683 Chironomidae sp. water mite diet isolate 13325-BHL040517-GBD17995_2521-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTTGGAGCATGAACAGGAATAGTTGGAACTTCCTTAAGAATACTAATGCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCCCGAATAAATAATATAAGTTTTTGATTATTATCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606684 Chironomidae sp. water mite diet isolate 13332-BHL040517-GBD23336_22611-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCTGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606685 Chironomidae sp. water mite diet isolate 13333-BHL040517-GBD3815_11910-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGTTGAATTAGCTCATCCTGGTACTTTTATAGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTATCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606686 Chironomidae sp. water mite diet isolate 13336-BHL040517-GBD16766_23228-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGATCATTAATCGGTGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCATGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCACCATCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606687 Chironomidae sp. water mite diet isolate 13338-BHL040517-GBD5466_16140-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGATTCTTGCCATTAATACTAGGAGCCCCAGATATAGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTATTACCCCCATCTCTAACACTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606688 Chironomidae sp. water mite diet isolate 13339-BHL040517-GBD25215_5161-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCATTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGATACTTTTATTGTAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTTGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAAAAATATAAGTTTTTGAGTATGACCCCCATCTCTAACATTATTACTATCAAGAAGTATTGTAGAAAATCGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606689 Chironomidae sp. water mite diet isolate 13350-BHL040517-GBD24008_26047-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATCTTTTATTTTTGGAGCCTGCTCAGGACTAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATACTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTGTTAGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606690 Chironomidae sp. water mite diet isolate 13356-BHL040517-GBD12938_18668-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCGGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAGTTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCTATTAATACTAGGAGCCCCAGATATAGCCTTTCCTCGAATAAATAATATAAGTTTTTGTTTATTACCCCCACCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606691 Chironomidae sp. water mite diet isolate 13357-BHL040517-GBD16624_2597-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTGTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGCGACTATCAAATTTATAATGTAATTGTTACAGAACATGCTTTTATAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTCCCCCCTTCATTAACCTTACTTTTATCAAGATCACTAGTAGAAAATGGTGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606692 Chironomidae sp. water mite diet isolate 13363-BHL040517-GBD27569_17093-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCATTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAACTGACTATTGCCATTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTTTAACATTATTACTTTCAAGTAGTATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606693 Chironomidae sp. water mite diet isolate 13365-BHL040517-GBD25629_6357-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAGTTTTAATTGGAGGATTTGGTAATTGATTCTTGCCTTTAATACTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606694 Chironomidae sp. water mite diet isolate 13369-BHL040517-GBD24331_7565-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGCTCAGGCATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTATGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATGTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTCTCCTCGAATAAATAATATAAGTTTTTGATTAGGACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606695 Chironomidae sp. water mite diet isolate 13373-BHL040517-GBD3780_21192-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTCGGACATCCTGGTTCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATCGGAGGATTTGGTAATTGATTATTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTATCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606696 Chironomidae sp. water mite diet isolate 13379-BHL040517-GBD25025_13134-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGTCATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTTATTGTTACTGCACATGCTTTCATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTCTTGTCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606697 Chironomidae sp. water mite diet isolate 13382-BHL040517-GBD9696_7638-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGTACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTATAGTGATACCAATTTTAATTGGAGGATTTGGAAATTGACTCTTTCCATTAATACTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCACTAACATTATTACTATCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606698 Chironomidae sp. water mite diet isolate 13383-BHL040517-GBD28842_13761-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGTCATCCCGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTATAGTTATACCAATTTTATTAGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACAGGATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606699 Chironomidae sp. water mite diet isolate 13385-BHL040517-GBD8891_24073-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCCTTAAGTATACTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTCTTGCCTTTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCACTAACATTATTACTTTCAAAAACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606700 Chironomidae sp. water mite diet isolate 13386-BHL040517-GBD3720_21890-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTTCTTAAGAATATTAATTCGAGTTGAATTAGGACATCCTGGTACTTTTCTTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGGCTCATGCCTTTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCACTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606701 Chironomidae sp. water mite diet isolate 13397-BHL040517-GBD23464_24298-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTTTATTTTACTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTCTTGCCATTAATACTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTATGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAGAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR287302, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606702 Chironomidae sp. water mite diet isolate 13398-BHL040517-GBD16376_24153-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTTATTCGAGCTGAATTATGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTGATTGTTACTGCACATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTTCTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR287302, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606703 Chironomidae sp. water mite diet isolate 13401-BHL040517-GBD6431_8111-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGTCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGTTATTGATTAGTACCCCCAGCTCTAACAGTATTGCTGTCAAGAAGTATTGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606704 Chironomidae sp. water mite diet isolate 13418-BHL040517-GBD18245_2262-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAACTGAATTGGGTCATCCTGGTACTTTTATTGGAGATGATCAAATTTATAAAGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTACCATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606705 Chironomidae sp. water mite diet isolate 13420-BHL040517-GBD21976_19651-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGTGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGATTATTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCATCTCTAACATTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606706 Chironomidae sp. water mite diet isolate 13424-BHL040517-GBD23959_23890-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGGACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATGCTGGTTCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCACTAATACTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTATTACCCCCATCTCTAACAGTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR295408, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606707 Chironomidae sp. water mite diet isolate 13427-BHL040517-GBD10007_26870-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGATGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGACCCAGATATAGCCTTTCCTCGATTAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAGGTAGTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606708 Chironomidae sp. water mite diet isolate 13431-BHL040517-GBD15466_4873-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATCTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCAGTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGTCTCTTGCCATTAATACTATGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR287302, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606709 Chironomidae sp. water mite diet isolate 13433-BHL040517-GBD29137_12263-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGTAGAATTAGGACACCCAGGATCATTAATCGGAGACGACCAATTTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTGACTATTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606710 Chironomidae sp. water mite diet isolate 13441-BHL040517-GBD26653_10871-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTCTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTTGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAATTTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606711 Chironomidae sp. water mite diet isolate 13442-BHL040517-GBD24436_7202-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCCGGAATAGTTGGAACTTCCTTAAGAATATTTATTCGAGCTGAATTAGGACATACTGGTACTTTTATTGGTGATGATCAGATTTATAATGTTATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTGCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606712 Chironomidae sp. water mite diet isolate 13446-BHL040517-GBD11567_16010-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTTGTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATAATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGTTTTTGGAAATTGACTCTTTCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606713 Chironomidae sp. water mite diet isolate 13447-BHL040517-GBD11153_13342-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTGCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGAAGATCAACTTTATAATATAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAGTTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR295408, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606714 Chironomidae sp. water mite diet isolate 13449-BHL040517-GBD26562_15187-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTTAGAATATTAATTCGAGTTGAATTATGACATCCTGATACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCTTTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCGTGCCATTAATACTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR295408, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606715 Chironomidae sp. water mite diet isolate 13455-BHL040517-GBD19851_25835-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTCGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCTGGCTCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTATGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606716 Chironomidae sp. water mite diet isolate 13460-BHL040517-GBD22636_4450-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCCTTATATTTTATTTTTGTAGTCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGATGATTTGGTAATTGACTCTTGCCATTAATACTAGGTGCCCCAGATACAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCAGCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606717 Chironomidae sp. water mite diet isolate 13462-BHL040517-GBD28160_21133-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATGTTATTTTTGGAGCCTGATCAGGAATAGTTGGTACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCACATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCCATTTTAATTGGAGGATTTGGTAATTGACTATTGCCATTAATACTAGGTGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606718 Chironomidae sp. water mite diet isolate 13465-BHL040517-GBD26811_16304-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTCTTTTTGGAGCCTGAGCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCATGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATATTAATTGGAGGATTTGGTAATTGACTCTTTCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCTCATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606719 Chironomidae sp. water mite diet isolate 13466-BHL040517-GBD13996_17208-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGACCTAAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAATTTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGTAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTGTCAAGAAGTATTGGAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606720 Chironomidae sp. water mite diet isolate 13469-BHL040517-GBD24581_14456-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTTAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTTATCGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606721 Chironomidae sp. water mite diet isolate 13483-BHL040517-GBD7139_20740-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTGTTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTACTACTTTCAAGAACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606722 Chironomidae sp. water mite diet isolate 13485-BHL040517-GBD4912_9664-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCATTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGTATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTCTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCCTCTCTAACATTATTACTTTCAAGAAGTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606723 Chironomidae sp. water mite diet isolate 13490-BHL040517-GBD11452_15574-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTTTGAGTATTAATTCGAGCTGAATTCGGATATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGTCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTGTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606724 Chironomidae sp. water mite diet isolate 13493-BHL040517-GBD9206_7681-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTTGGAGCCTGATCCGGAATAGTTGGAACTTCCTTAAGAATCTTAATTCGAGTTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGCAATTGTTACTGCTCATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACTCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606725 Chironomidae sp. water mite diet isolate 13494-BHL040517-GBD16628_27772-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCCTGCTCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGTTACTTTTCTTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATCGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCAGTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606726 Chironomidae sp. water mite diet isolate 13503-BHL040517-GBD18063_26526-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTGCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCATTAAGAATATTAAGTCGAGCTGAAGTAGGACATACTGGTACTTTTATTGGAGATGATCAAATTTATAATGAAATTGTGACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606727 Chironomidae sp. water mite diet isolate 13509-BHL040517-GBD22375_20869-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTCGGAGCCTGACCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCCGATTCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606728 Chironomidae sp. water mite diet isolate 13513-BHL040517-GBD27790_11331-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTTTATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAATTTCCTTAAGAATTTTAATTCGAGCTGAATTAGGACATCCTGGTTCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGATTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACGTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606729 Chironomidae sp. water mite diet isolate 13514-BHL040517-GBD9804_12053-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATACTTTATTTTTGGAGCCTGATCCGGAATAGTTGGAACTTCCTTAGGAATATTTATTCGAGCTGAATTAGGCCATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCAACAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR287302, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606730 Chironomidae sp. water mite diet isolate 13519-BHL040517-GBD16733_27826-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGACACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCATGCTCGTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATACTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606731 Chironomidae sp. water mite diet isolate 13522-BHL040517-GBD7714_14733-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCAGAATTAGGACATCCTGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGATTATTGCCCCCATCACTAACATTATTACTATCAAGAAGTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606732 Chironomidae sp. water mite diet isolate 13530-BHL040517-GBD22950_5727-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTAAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAGTTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTTTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCCCGAATAAATAATATAAGTTTTTGATCATTACCCCCATCTCTAACACTATTACTTTCAAGAAGTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606733 Chironomidae sp. water mite diet isolate 13537-BHL040517-GBD27299_17490-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGTCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGATTCGTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTCGATTATTACCCCCTTCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606734 Chironomidae sp. water mite diet isolate 13556-BHL040517-GBD29160_15390-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTGTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGACTTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATAGGAGATGATCAAATTTATAATGTAATCGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCACTCGAGTTGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606735 Chironomidae sp. water mite diet isolate 13631-BHL040517-GBD21145_24502-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGATCTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTGCCCCCGTCATTAACTTTATTATTATCTAGATCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606736 Chironomidae sp. water mite diet isolate 13799-BHL040517-GBD24057_25408-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.7% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606737 Chironomidae sp. water mite diet isolate 13835-BHL040517-GBD5063_6742-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTGATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGGCATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606738 Chironomidae sp. water mite diet isolate 13839-BHL040517-GBD16435_15111-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGATTACTCCCCCCTTCTCTTCCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606739 Chironomidae sp. water mite diet isolate 13892-BHL040517-GBD19238_7114-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCTGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCGTTAATATTAGGTGCCCCCGACATAGCATTCCCTCGAGTAAATAATATAAGTTTCTGATTACTTCCCCCGTCATTAACCTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606740 Chironomidae sp. water mite diet isolate 13985-BHL040517-GBD13703_9179-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAAGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCTCCATCATTAACATTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606741 Chironomidae sp. water mite diet isolate 14001-BHL040517-GBD23323_17640-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATTCTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGATGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAATTTCTGATTACTTCCTCCTTCTCTTACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606742 Chironomidae sp. water mite diet isolate 14061-BHL040517-GBD7317_23728-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAGTTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATCGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGAGGATCCTGATATAGCTTTTCCGCGAATAAATAATATAATATTTTGAATATTACCCCCTTCATGAACCTGACTTTTATCAAGAACAATAGTACAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606743 Chironomidae sp. water mite diet isolate 14185-BHL040517-GBD23501_9975-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTTAGAATTTTAATTCGACTAGAATTATGACACCCAGGCTCATTATTCGGAGACGATCAACTTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606744 Chironomidae sp. water mite diet isolate 14215-BHL040517-GBD28257_16106-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACCTTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACGTTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATCCCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606745 Chironomidae sp. water mite diet isolate 14267-BHL040517-GBD17284_25145-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGCAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTCCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR636712, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606746 Chironomidae sp. water mite diet isolate 14272-BHL040517-GBD18715_4988-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCCTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTGCCACCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606747 Chironomidae sp. water mite diet isolate 14385-BHL040517-GBD6656_7705-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACATCCAGGTACATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTCTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCACCATCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606748 Chironomidae sp. water mite diet isolate 14391-BHL040517-GBD27397_14598-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATTTTTATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTTATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606749 Chironomidae sp. water mite diet isolate 14400-BHL040517-GBD25510_13875-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAAGTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGGAATTGATTATTACCTTTGATATTAGTGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606750 Chironomidae sp. water mite diet isolate 14408-BHL040517-GBD5550_22866-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTTGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCAGTAACTCTTCGTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606751 Chironomidae sp. water mite diet isolate 14600-BHL040517-GBD8476_14873-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACTTTATATTTTATTTTCGGGGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTGATCGGAGGCTTTGGAAATTGACTATTACCACTTATACTTGGAGCCCCTGATATGGCCTTTCCTCGAATAAATAACATAAGATTCTGGTTACTACCTCCGTCTATTTCTTTGCTTCTTTCTAGAGCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606752 Chironomidae sp. water mite diet isolate 14688-BHL040517-GBD12002_7578-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAATAATTCTAATTCGAGCAGAATTAGGACATGCAGGTTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCACCATCATTAACTTTATTATTATCTAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606753 Chironomidae sp. water mite diet isolate 15287-BHL040517-GBD17606_15151-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTAATTGGTGACGACCAAATTTATAACGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGTCTCCTGATATGACTTTCCCTCGAATAAATAATATAAGTTTTTTATTTCTTCCCCCCTCATTAACTCTTCTTCTTGCTAGAACAATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606754 Chironominae sp. water mite diet isolate 1011-BHL100916-GBD6223_17655-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAGATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTAGAGGATTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCCTTCACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606755 Chironominae sp. water mite diet isolate 1254-BHL110116-GBD13143_28285-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGAGGCTTTGGAGATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KM988908, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606756 Chironominae sp. water mite diet isolate 1311-BHL110116-GBD27211_10261-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACATCATTTAGTATATTAATTCGAGCAGAACTAGGTCACCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTAACCCTTCTTCTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM988908, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606757 Chironominae sp. water mite diet isolate 1329-BHL110116-GBD13904_28286-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KM994686, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606758 Chironominae sp. water mite diet isolate 1403-BHL110116-GBD14908_20162-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCT-TACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.0% identical to accession ID KR166401, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606759 Chironominae sp. water mite diet isolate 1409-BHL110116-GBD24857_13316-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGGACATCTTTTAGTATATTAATTCGAGCAAAATTAGGTCACCCTGGATCTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTATCCCTTCTTCTATCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM921023, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606760 Chironominae sp. water mite diet isolate 1415-BHL110116-GBD18633_6686-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACATCTTTTAGTATTTTAATTCGAGCAGAACTTGGTCACCCTGGATCTTTTATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTACTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCGTCTTTAACTCTACTTCTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR754526, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606761 Chironominae sp. water mite diet isolate 1465-BHL110116-GBD19342_7290-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTAGTCACCCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR642580, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606762 Chironominae sp. water mite diet isolate 1508-BHL110116-GBD12036_22649-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCATCTCTAATCT-TACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR159655, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606763 Chironominae sp. water mite diet isolate 1522-BHL110116-GBD7734_7328-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACCTCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTTCCACGAATAAATAATATAAGATTTTGATTACTACCCCCTTCTTTAACACTACTACTATCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988908, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606764 Chironominae sp. water mite diet isolate 1525-BHL110116-GBD21145_18301-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCT-TACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID KR166401, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606765 Chironominae sp. water mite diet isolate 1536-BHL110116-GBD21457_5010-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCATTTAGTATATCAATTCGAGCAGAACTTGGTCACCCCGGATCTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCGTCATTAACTCTACTACTATCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR159655, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606766 Chironominae sp. water mite diet isolate 1545-BHL110116-GBD26181_15544-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCCCTTAGTATATTAATTCGAGCAGAACTTGGTCACCCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTACTTTCAAGCACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR286005, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606767 Chironominae sp. water mite diet isolate 1552-BHL110116-GBD14250_18801-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR159655, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606768 Chironominae sp. water mite diet isolate 1605-BHL110116-GBD16822_2743-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAGTTCGAGCAGAACTTGGTCACCCCGTAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACAGCGCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAAATGGTGGATTTGGAAATTGATTATTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTTCTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCACTTGTCGAAAATGGCGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR757074, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606769 Chironominae sp. water mite diet isolate 1609-BHL110116-GBD11854_6642-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCTTTTAGTATATTAATTCGAGCAGAACTTGGTCACCCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCACGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTCCCTCGAATAAATAATATGAGATTTTGATTACTTCCCCCGTCATTAACTCTACTATTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR286005, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606770 Chironominae sp. water mite diet isolate 1615-BHL110116-GBD21599_21204-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCACTTAGTATATTAATTCGAGTAGAATTTGGACACCCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCCCTACTTCTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR642580, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606771 Chironominae sp. water mite diet isolate 1622-BHL110116-GBD10021_2701-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCATTTAGTATATTAGTTCGAGCAAAACTTGGTCACCCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTACCCCCTTCTTTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988908, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606772 Chironominae sp. water mite diet isolate 1786-BHL110116-GBD19066_4437-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACTTTATATTTCATTTCTGGAGCCTGATCCGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAATTCCTCTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606773 Chironominae sp. water mite diet isolate 1798-BHL101516-GBD4617_8063-Ldc86 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606774 Chironominae sp. water mite diet isolate 1809-BHL101516-GBD13567_2272-Ldc86 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACGTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAGATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTCACTCTTCTTCTTTCTAGTTCTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606775 Chironominae sp. water mite diet isolate 1828-BHL022317-GBD18504_17927-Ldc88 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTTCTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606776 Chironominae sp. water mite diet isolate 1847-BHL072216-GBD20390_17181-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGTACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTACTACTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606777 Chironominae sp. water mite diet isolate 1885-BHL022317-GBD22473_15364-Ldc90 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCATCCCATACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606778 Chironominae sp. water mite diet isolate 1904-BHL022317-GBD25443_22618-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTTACAGCCCACGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTTCCTCTTATACTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTGCCCCCATCCCTTACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606779 Chironominae sp. water mite diet isolate 1916-BHL022317-GBD18183_27565-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCCCACGCTTTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTAATACTTGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTTCCTCTTTCAAGATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID JF286707, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606780 Chironominae sp. water mite diet isolate 1935-BHL022317-GBD10107_25370-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGAGACTTTTATTGGAGATGATCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTAATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCCACTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID JF286707, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606781 Chironominae sp. water mite diet isolate 1940-BHL022317-GBD22679_22477-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGTGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTAATACTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCATCCCTTACCCTTCTTCTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606782 Chironominae sp. water mite diet isolate 1957-BHL022317-GBD9141_21474-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATTTGGACGACCTGGTACTTTTATTGGAGATGACCACATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGAATTATTCCTTTAATGTTAGGAGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACGTCTTCCCCCTTCATCAACTCTTTTACTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606783 Chironominae sp. water mite diet isolate 1971-BHL022317-GBD8000_20388-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTATGACGACCCGGGACTTTTATTGGAGATGATCAAATTTATAATGTCATTGTTACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCATCCCTTACCCTTCTACTTTCAAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID JF286707, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606784 Chironominae sp. water mite diet isolate 2014-BHL022317-GBD15368_25006-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCTTTAAGTATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTCACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGTTTTGGAAATTGATTAGTTCCTCTAATACTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTAACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606785 Chironominae sp. water mite diet isolate 2033-BHL022317-GBD26316_22657-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGGACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGTCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTAATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCATCCCTAACCCTACTTCTGTCAAGATCAATTGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606786 Chironominae sp. water mite diet isolate 2034-BHL022317-GBD12791_4730-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTAGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGTACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606787 Chironominae sp. water mite diet isolate 2041-BHL022317-GBD24476_22312-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATTGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCCCTTACCCTTCTTCTTTCAAGATGAATTGTAGAAAATGGAGCTGGGACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.4% identical to accession ID KR287333, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606788 Chironominae sp. water mite diet isolate 2101-BHL072216-GBD24918_11501-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACGCCCAGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606789 Chironominae sp. water mite diet isolate 2104-BHL072216-GBD22556_9921-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTATATTTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606790 Chironominae sp. water mite diet isolate 2106-BHL072216-GBD5687_19938-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTTATTTTCGGAGCTTGATCTGGAATAGTCGGAACTTCTTTAAGTATATTAATCCGTGCAGAATTAGGACACCCGGGAACTTTAATCGGAGATGGTCAAATTTATAATGTTATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606791 Chironominae sp. water mite diet isolate 2112-BHL072216-GBD19921_22729-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTAATACCTATTCTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCCTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606792 Chironominae sp. water mite diet isolate 2117-BHL072216-GBD12979_23464-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGCTTTGGGAATTGATTAGTTCCCCTAATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606793 Chironominae sp. water mite diet isolate 2124-BHL072216-GBD27872_12894-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACCTTATACTTTATTTTCGGAGCTTGATCTGGAATAGTCGGAACTTCTTTAAGTATATTAATCCGTGCAGAATTAGGACACCCGGGAACTTTAATCGGAGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606794 Chironominae sp. water mite diet isolate 2129-BHL072216-GBD11359_7508-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KM960768, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606795 Chironominae sp. water mite diet isolate 2137-BHL072216-GBD19067_18722-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACGCCCAGGTACTTTTATTGGTGATGGTCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTTATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGACCTGTACCTCTAATACTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR289362, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606796 Chironominae sp. water mite diet isolate 2148-BHL072216-GBD3115_9469-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606797 Chironominae sp. water mite diet isolate 2149-BHL072216-GBD2326_13055-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAGCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606798 Chironominae sp. water mite diet isolate 2150-BHL072216-GBD26887_8723-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTCGGAACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACTACCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606799 Chironominae sp. water mite diet isolate 2152-BHL072216-GBD5872_21677-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KT118816, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606800 Chironominae sp. water mite diet isolate 2154-BHL072216-GBD23898_8706-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGACGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTTCCCCCTTCTTTATCACTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606801 Chironominae sp. water mite diet isolate 2156-BHL072216-GBD8290_6726-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACGCCCAGGTACTTTTATTGGTGATGATCAAATTTGTAATGTAATTGTAACTGCCCACGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606802 Chironominae sp. water mite diet isolate 2158-BHL072216-GBD19165_15008-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTTTATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTGCCCCCTTCTTTATCTCTACTTCTATCTAGTTCTATTGTAGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606803 Chironominae sp. water mite diet isolate 2161-BHL072216-GBD7712_21043-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCCCTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR286005, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606804 Chironominae sp. water mite diet isolate 2163-BHL072216-GBD5661_23203-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATTTTCGGAGCTTGATCTGGAATAGTCGGAACTTCTTTAAGTATATTAATCCGTGCAGAATTAGGACACCCGGTAACTTTAATCGGAGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTTTACCACCCTCTTTAACTCTTTTACTTTCAAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.4% identical to accession ID KR285347, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606805 Chironominae sp. water mite diet isolate 2166-BHL072216-GBD10011_22456-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAAC---TCTTCTTT-TGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606806 Chironominae sp. water mite diet isolate 2168-BHL072216-GBD5893_12949-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCCCTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTGCCACCTTCTCTTACCT-TATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR286005, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606807 Chironominae sp. water mite diet isolate 2170-BHL072216-GBD20569_4432-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACGCCCAGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTTATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCA---GTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR289362, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606808 Chironominae sp. water mite diet isolate 2175-BHL072216-GBD22438_6965-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR746550, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606809 Chironominae sp. water mite diet isolate 2176-BHL072216-GBD11445_25591-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACGCCCAGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTTATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCACCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR289362, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606810 Chironominae sp. water mite diet isolate 2177-BHL072216-GBD10887_12592-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACACTATATTTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606811 Chironominae sp. water mite diet isolate 2187-BHL072216-GBD27832_11534-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTTGGAGCATGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTACTACTATCAAGAACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606812 Chironominae sp. water mite diet isolate 2194-BHL072216-GBD8995_13938-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTACTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACGCCCAGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KT115418, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606813 Chironominae sp. water mite diet isolate 2197-BHL072216-GBD7976_8933-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACATCTTTAAGTATACTTATTCGTGCAGAATTAGGTCATCCAGGCACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCCCATGCTTTTATCATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTACTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.4% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606814 Chironominae sp. water mite diet isolate 2199-BHL072216-GBD9590_5849-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAGGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCCTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606815 Chironominae sp. water mite diet isolate 2203-BHL072216-GBD25561_22364-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAATAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606816 Chironominae sp. water mite diet isolate 2205-BHL072216-GBD28662_17561-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTTTACCACCCTCTTTAACTCGTTTACTTTCAAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR285347, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606817 Chironominae sp. water mite diet isolate 2211-BHL072216-GBD27571_13870-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACATTATATTTTATTTTTGGAGTTTGGACCGGGATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606818 Chironominae sp. water mite diet isolate 2214-BHL072216-GBD16773_20586-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGAGGCTTTGGGAATTGATTAGTTCCCCTAATTTTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606819 Chironominae sp. water mite diet isolate 2217-BHL072216-GBD27714_9968-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTCGGAACTTCTTTAAGCATGCTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCCCTAATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAATAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGAACAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KR290859, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606820 Chironominae sp. water mite diet isolate 2234-BHL072216-GBD29402_14025-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTACTCTAATATTAGGAGCACCAGATATAGCATTTCCCCGAATAAATAATATAAGATTCTGATTACTTCCCCCTGCTTTAGCTCTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606821 Chironominae sp. water mite diet isolate 2243-BHL072216-GBD12623_5103-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606822 Chironominae sp. water mite diet isolate 2244-BHL072216-GBD5722_8948-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR641103, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606823 Chironominae sp. water mite diet isolate 2246-BHL072216-GBD25559_19487-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTACTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTATTTCCTCTAATATTAGGAGCGCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTGCTTTAACTCTTCTTCTTTCTAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606824 Chironominae sp. water mite diet isolate 2249-BHL072216-GBD24631_8226-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGATCATTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACCCTTCTTCTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606825 Chironominae sp. water mite diet isolate 2251-BHL072216-GBD7152_22667-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACT	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606826 Chironominae sp. water mite diet isolate 2254-BHL072216-GBD20936_3005-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCCGAATTAGGACGCCCAGGTACTTTTATCGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTTATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTTTACCACCCTCTTTAACTCTTTTACTTTCAAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR289362, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606827 Chironominae sp. water mite diet isolate 2255-BHL072216-GBD28351_13687-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAGCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGTTTTTGATTATTGCCACCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606828 Chironominae sp. water mite diet isolate 2257-BHL072216-GBD8810_8382-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTCATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCACCGGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTTTACCACCCTCTTTAACTCTTTTACTTTCAAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR289362, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606829 Chironominae sp. water mite diet isolate 2259-BHL072216-GBD25379_24546-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCATCCTGGATCTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCGTCTTTAACTCTTCTTCTATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606830 Chironominae sp. water mite diet isolate 2261-BHL072216-GBD24414_15299-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCCCTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCA---GTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR286005, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606831 Chironominae sp. water mite diet isolate 2267-BHL072216-GBD18479_14960-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACGCCCAGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTTATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR289362, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606832 Chironominae sp. water mite diet isolate 2273-BHL072216-GBD26332_7273-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACAACCAGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTTATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCCCCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTATTACCACCATCTCTAACACTATTACTTTCAAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR285347, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606833 Chironominae sp. water mite diet isolate 2290-BHL072216-GBD14400_4945-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTATACTTTATTTTCGGAGCTTGATCTGGAATAGTCGGAGCTTCTTTAAGTATATTAATCCGAGCAGAATTAGGACACCCGGGAACTTTAATCGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR641103, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606834 Chironominae sp. water mite diet isolate 2291-BHL072216-GBD24430_19059-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTCATAGTTATGCCTATTTTAATTGGGGGCTTTGGGAATTGATTAGTTCCCCTAATATTAGGAGCACCAGATACGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACCCTCTTACTATCTAGAACAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KT106016, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606835 Chironominae sp. water mite diet isolate 2293-BHL072216-GBD20746_25602-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTTGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCATTAACTCTTCTACTTTCAAGTTCTAGAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606836 Chironominae sp. water mite diet isolate 2299-BHL072216-GBD23180_7388-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAGATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCCCCATCTCTAACCCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606837 Chironominae sp. water mite diet isolate 2300-BHL072216-GBD3524_20601-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCCCTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTTTACCACCCTCTTTAACTCTTTTACTTTCAAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR285347, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606838 Chironominae sp. water mite diet isolate 2304-BHL072216-GBD21456_24877-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGTACTTCTTTAAGAATTCTAATTCGAGCAGATTTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATGCTGATTACTTCCCCCTTCTTTAGCACGACTTCTGTCTAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606839 Chironominae sp. water mite diet isolate 2305-BHL072216-GBD22000_22061-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGTAGAATTAGGACATCCTGGCACTTTTATTGGTGACGACCAAATTTATAATGTTATCGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACCCTTCTTCTATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606840 Chironominae sp. water mite diet isolate 2309-BHL072216-GBD28412_18107-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTCTTATAGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCCACTTTCTAGTGCTACTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606841 Chironominae sp. water mite diet isolate 2311-BHL072216-GBD19671_5980-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM991068, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606842 Chironominae sp. water mite diet isolate 2326-BHL072216-GBD24076_19024-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAACATAAGATTCTGATTACTTCCCCCTTCGTTATCACATCTTCAATCTAGTGCTATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606843 Chironominae sp. water mite diet isolate 2334-BHL072216-GBD15556_2903-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606844 Chironominae sp. water mite diet isolate 2335-BHL072216-GBD18603_12867-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCAGAATTAGGACATCCCGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTACTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606845 Chironominae sp. water mite diet isolate 2347-BHL072216-GBD16270_15665-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR641103, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606846 Chironominae sp. water mite diet isolate 2348-BHL072216-GBD9876_5992-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACACCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCATCTTTAACTCTTCTTCTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606847 Chironominae sp. water mite diet isolate 2351-BHL072216-GBD26163_8569-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACCTCTTTAAGAATATTAATCCGAGCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGGTATGGCTTTCCCGCGAATAAATAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606848 Chironominae sp. water mite diet isolate 2353-BHL072216-GBD22627_24255-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTACCATAAGTTTCTTCATAGTTATGCCTATTTTAATTGTGGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KR166401, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606849 Chironominae sp. water mite diet isolate 2365-BHL072216-GBD28985_18183-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGTCATCCTGGTACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTGATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCGTCTTTATCTCTACTACTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606850 Chironominae sp. water mite diet isolate 2366-BHL072216-GBD11463_20244-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACACTTTATTCTATTTTTGGAGCTTGATCTGGTATAGTAGGAACATCTTTAAGTATACTTATTCGTGCAGAATTAGGTCATCCAGGCACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606851 Chironominae sp. water mite diet isolate 2369-BHL072216-GBD21531_8089-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATACTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTACAACTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606852 Chironominae sp. water mite diet isolate 2371-BHL072216-GBD12498_10491-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTATAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATCACTTCCACCTTCTTTAACTCTTCTTCTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606853 Chironominae sp. water mite diet isolate 2382-BHL072216-GBD14974_20034-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGATCTTCTTTAAGAATTCTAATTCTAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACGGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCTTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTGCTTCCCCCTTCTTTATCTCTGCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606854 Chironominae sp. water mite diet isolate 2389-BHL072216-GBD23905_4919-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGACCATTATATTTTATTTTTGGAGCCTGCTCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGTAGAATTAGGTCATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTGTATCTCAGCTACTTTCTAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606855 Chironominae sp. water mite diet isolate 2392-BHL072216-GBD27087_19448-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCCGGTATAGTCGGAACTTCTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTCTTCATAGTTATGCCTATTTTAATTGGAGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAATAATATAAGCTTTTGACTTCTTCCCCCTTCTCTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR279055, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606856 Chironominae sp. water mite diet isolate 2398-BHL072216-GBD20913_17190-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCCCTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTACCCCCATCTCTTACTTTATTTCTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR286005, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606857 Chironominae sp. water mite diet isolate 2405-BHL072216-GBD23750_19732-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCATTATCGCTACTTCTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606858 Chironominae sp. water mite diet isolate 2414-BHL072216-GBD18439_25655-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTTGGAACTTCTTTAAGAATTCTTATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCATCTTTATCTCTACTACTATCTAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606859 Chironominae sp. water mite diet isolate 2416-BHL072216-GBD7317_25802-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTCGGAACTTCTTTAAGTATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCTAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606860 Chironominae sp. water mite diet isolate 2423-BHL072216-GBD26144_10094-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTCATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606861 Chironominae sp. water mite diet isolate 2431-BHL072216-GBD20990_11278-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTTAGAATTCTAATTCGAGCAAAATTAGGACATCTTGGAACTTTTATTGGTGACGACCAAATTTATGATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGAATAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCGTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606862 Chironominae sp. water mite diet isolate 2435-BHL072216-GBD20295_6130-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGCAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGTTTTTGACTTTTACCACCCTCTTTAACTCTTTTACTCTCAAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606863 Chironominae sp. water mite diet isolate 2457-BHL072216-GBD13463_9122-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTCTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATGGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606864 Chironominae sp. water mite diet isolate 2466-BHL072216-GBD29450_13412-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACATTGTATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAGCTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTACTTGATCTCATCTGCTTTCTAGTTCTATTGTAGAAAATGGCGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606865 Chironominae sp. water mite diet isolate 2479-BHL072216-GBD11925_20055-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTGTATTTTATTTTTGGAGCCTGCTCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCGGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCGTAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCGTCTTCTTTCTAGTTCTAGAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606866 Chironominae sp. water mite diet isolate 2481-BHL072216-GBD15526_13886-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACACCCTGGATCTTTTATTGGTGACGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATAGTAGAAAATGGAGCTGGAACGGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606867 Chironominae sp. water mite diet isolate 2482-BHL072216-GBD4338_9361-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTCGGACATCCTGGTTCTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTGATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTGTGATTACTTCCCCCGTCATTAACTCTACTACTATCTAGTTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606868 Chironominae sp. water mite diet isolate 2486-BHL072216-GBD8890_11472-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAACTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAACATGAGATTCTGATTGCTTCCCCCATCTATTTCTTTACTTCTTTCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606869 Chironominae sp. water mite diet isolate 2488-BHL072216-GBD24081_10154-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTCGGAACGTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606870 Chironominae sp. water mite diet isolate 2493-BHL072216-GBD28667_13235-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTCGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATTTTAATTCGAGCCGAATTAGGACACCCAGGTTCTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTATTATAATTTTTTTTATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCACCAGATATAGCATTCCCACGAATAAATAATATAAGTTTTTGACTATTACCACCCTCTTTAACTCTATTACTATCAAGATCAATAGCTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR285347, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606871 Chironominae sp. water mite diet isolate 2500-BHL072216-GBD8755_15708-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACGCCCAGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTTATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCTCCTGATATAGCTTTCCCTCGAATAGATGATATAAGTTTTTGATTATTGCCACCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR289362, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606872 Chironominae sp. water mite diet isolate 2504-BHL072216-GBD2949_20713-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACGTTATATCTTATTTTTGGAGCCTGATCAGGATTAGTTGTAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATACTATAAGATTCTGATTACTTCCCCCTTCTTTAGCTCTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606873 Chironominae sp. water mite diet isolate 2506-BHL072216-GBD27114_23290-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTAGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGAAGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGTGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTATTACCTCCTTCTCT-TACCTGATTACTTTCAAGTACAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606874 Chironominae sp. water mite diet isolate 2507-BHL072216-GBD4649_14853-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGGCATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTTATTGTAGCAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606875 Chironominae sp. water mite diet isolate 2509-BHL072216-GBD27032_20630-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACATCTTTAAGTATACTTATTCGTGCAGAATTAGGTCATCCAGGCACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTTATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGATTTTGACTTTTACCACCCTCTTTAACTCTTTCACTTTCAAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR285347, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606876 Chironominae sp. water mite diet isolate 2510-BHL072216-GBD16407_11323-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATTCTTATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCCTCTTTAACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606877 Chironominae sp. water mite diet isolate 2515-BHL072216-GBD11194_3291-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGAATTCTAATTCGAGCAGAATTAGGTCAACCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTGTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606878 Chironominae sp. water mite diet isolate 2518-BHL072216-GBD10666_2332-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR286005, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606879 Chironominae sp. water mite diet isolate 2523-BHL072216-GBD22606_26395-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAATAATTCTAATTCGAGCAGAATGAGGACATCCTGGAACTTTTATTGGTGACTACCAATTTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606880 Chironominae sp. water mite diet isolate 2528-BHL072216-GBD15547_6618-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGCTCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTTGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTGCCTCGAATAAATAATATAAGATACTGATTACGTCCCCCTTCTTTATCTCTTCTTCTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606881 Chironominae sp. water mite diet isolate 2532-BHL072216-GBD21332_13997-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATCTTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGAGTACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTCTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATGTGGCTTTTCCACGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606882 Chironominae sp. water mite diet isolate 2533-BHL072216-GBD22797_14120-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACATCTTTAAGAATACTTATCCGAGCAGAATTAGGTCATCCAGGTACTTTTATTGGAGACGACCAAATTTATAGTGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTGTCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606883 Chironominae sp. water mite diet isolate 2534-BHL072216-GBD5723_16910-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCACTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAAC---TCTTCTTT-TGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606884 Chironominae sp. water mite diet isolate 2536-BHL072216-GBD17383_14879-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGGCATCCTGGAACTTTAATTGGTGACGACCAAATTCATAATGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGATCTCCTGATATAGCTTTCCCTCGAAGAAATAATATAAGTTTTTGAATATGGCCGCCTTCTCTTAC-CTTATTACTGTCAAGTGCATTTGTTGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID KT110221, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606885 Chironominae sp. water mite diet isolate 2541-BHL072216-GBD5036_12708-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGTACCTCCCTTAGTATCCTTATTCGTACAGAATTAGGTCACCCAGGAGCTTTTATTGGTGATGATCAAATTTATAATGTAGTTGTAACTGCTCACGCTTTTATTATAATTTTTTTTATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTTTACCACCCTCTTTAACTCTTTTACTTTCAAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR285347, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606886 Chironominae sp. water mite diet isolate 2547-BHL072216-GBD11006_17372-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTTTATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACATCTTTAAGTATACTTATTCGTGCAGAATTAGGTCATCCAGGCACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCCCATGCTTTTATCATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606887 Chironominae sp. water mite diet isolate 2551-BHL072216-GBD17871_29003-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATGTTGAGTATTGCCACCTTCTCT-TACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606888 Chironominae sp. water mite diet isolate 2557-BHL072216-GBD23525_25241-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACTTTATATTTCATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGTATTCTTATTCGAGCAGAGTTAGGTCATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTCTAACTCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606889 Chironominae sp. water mite diet isolate 2560-BHL072216-GBD23669_21949-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTCGGTCAGGCTGGTACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCGTCATTATCTCTACTACTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606890 Chironominae sp. water mite diet isolate 2562-BHL072216-GBD11760_6312-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGCACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCTGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTCTCTAGATCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606891 Chironominae sp. water mite diet isolate 2567-BHL072216-GBD20497_21321-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGCGCATGATCCGGAATAGTAAGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTAATTGGTGACGACCAATTTTATAATGTAGTCGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGTGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606892 Chironominae sp. water mite diet isolate 2569-BHL072216-GBD9742_19685-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATACTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATTAATAATATGAGATTTTGATTACTTTCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606893 Chironominae sp. water mite diet isolate 2573-BHL072216-GBD11626_17356-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCCCTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTCTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGAAATTGGTTATTACCACTGATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606894 Chironominae sp. water mite diet isolate 2574-BHL072216-GBD19276_18463-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTCGGACATCCTGGATCTTTAATTGGTGACGACCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTCCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCGTCATTGACTCTACTACTATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606895 Chironominae sp. water mite diet isolate 2584-BHL072216-GBD5355_12045-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACAACCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTACTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTCCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTACTTCTTTCTAGTGCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606896 Chironominae sp. water mite diet isolate 2599-BHL072216-GBD22744_25111-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGTAGCCTGATCAGTAATAGTTGGAACTTCTTTAATAATTCTAATTCGAGCTGAATTATGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGACTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606897 Chironominae sp. water mite diet isolate 2600-BHL072216-GBD13412_25606-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACGCCCAGGTACTTTTATCGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGACTTGTATCTCTAATACTAGGAGCACCAGATATAGCTTTCCCACGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR289362, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606898 Chironominae sp. water mite diet isolate 2607-BHL072216-GBD16273_18178-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGTACTTCTTTATGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTCATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACACATTTTAATTGGAGGATTTGGAAATTGAATAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTGCTTCTTGCTAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606899 Chironominae sp. water mite diet isolate 2609-BHL072216-GBD15444_13457-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACATCGTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTCATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGTGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606900 Chironominae sp. water mite diet isolate 2610-BHL072216-GBD20779_21987-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTCTATTTTTGGTGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATCCGAGCAGAATTAGGACATCCTGGTACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTGCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606901 Chironominae sp. water mite diet isolate 2614-BHL072216-GBD4433_7462-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTATATTTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATATTAATCCGAACGAAATCAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGCAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGGAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606902 Chironominae sp. water mite diet isolate 2615-BHL072216-GBD10983_24365-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCGTTAAGAATTCTAATTCGAGCAGAATTATGACATCCTGGAACTTTTATTGGAGACGACCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCGTTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606903 Chironominae sp. water mite diet isolate 2620-BHL072216-GBD14577_27813-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAAAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTACATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTACTACTTTCTAGTAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606904 Chironominae sp. water mite diet isolate 2622-BHL072216-GBD19983_2154-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGTATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAACATAAGATTCTGATTACTTCCCCCATCTATAACTCTACTTCTTTCTAGATCAGTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606905 Chironominae sp. water mite diet isolate 2628-BHL072216-GBD7922_13776-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACAACCTGGTACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTCACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAATTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606906 Chironominae sp. water mite diet isolate 2633-BHL072216-GBD20513_19939-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTTATTCGAGCAGAACTTGGGCACCCTGGCACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGTTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGAATACTTCCCCCTTCTTTAACTCTTCTTCTGGCTAGCACAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606907 Chironominae sp. water mite diet isolate 2646-BHL072216-GBD18299_6701-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAACTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KT115418, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606908 Chironominae sp. water mite diet isolate 2652-BHL072216-GBD10327_10225-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAAGTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGTCCATATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATAACCACTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATGTAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606909 Chironominae sp. water mite diet isolate 2657-BHL072216-GBD20989_22429-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGAATTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCGGCTTTAACTCTACATCGATCTAGTTCTAGTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606910 Chironominae sp. water mite diet isolate 2659-BHL072216-GBD7286_26261-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGCATTCTAATTCGAGCAGAATTAGGTCATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAAGATAGGATTCTGATTACTTCCCCCTTCTTTATCTCTGCTACTTTCTAGTACGAGAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606911 Chironominae sp. water mite diet isolate 2662-BHL072216-GBD9185_7493-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATCATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606912 Chironominae sp. water mite diet isolate 2665-BHL072216-GBD26414_21053-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTGAGCATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCGTCGTCTATCTAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606913 Chironominae sp. water mite diet isolate 2672-BHL072216-GBD17794_28190-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGTAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAGTTTTTTTCATAGTTATACCCATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTACTTTGTCTCATCTTCTTTCTAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606914 Chironominae sp. water mite diet isolate 2674-BHL072216-GBD27966_10901-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATACTTTATTTTTGGGGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAAAATTAGGACATCCTGGAACTTTTATTGGAGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTAATACTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCCTCTTTAACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606915 Chironominae sp. water mite diet isolate 2675-BHL072216-GBD23984_13195-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTTAGAATTCTAATTCGAGCCGAATTAGGACATACTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCACATTCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTCGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606916 Chironominae sp. water mite diet isolate 2679-BHL072216-GBD26055_22127-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCATCCTGGTACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCATTAACTCTACTACGACCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606917 Chironominae sp. water mite diet isolate 2681-BHL072216-GBD16935_20136-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTTAGAATTCTAATTCGAGCAGAATTATGACATCCTGGAACTTTTCTTGGTGACGATCAAATTTATAATATTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTACTACTTTCTAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606918 Chironominae sp. water mite diet isolate 2682-BHL072216-GBD23864_21556-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCATGAGCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCAAGCTGAATTAGGACATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACCCTACTACTTTCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606919 Chironominae sp. water mite diet isolate 2684-BHL072216-GBD4661_9300-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTGCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCCTCTTTATCTCTTCTTCTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606920 Chironominae sp. water mite diet isolate 2685-BHL072216-GBD25021_8590-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACGCCCAGGTACTTTTATTGGTGATGATCAAATTTATATTCTAATTGTAACTGCTCACGCATTTATTATATTTTTTTTATGGTTCTGACTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR289362, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606921 Chironominae sp. water mite diet isolate 2687-BHL072216-GBD25539_6303-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGTCTAGTTGGTACTTCTTTAAGAATTCTAATTCGAGCAGCATTAGGACATCCTGGAACTTTTATTGGTGACGACCATATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCACTACATCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606922 Chironominae sp. water mite diet isolate 2695-BHL072216-GBD8183_18812-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGACGTCCAGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACCTTATTACTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606923 Chironominae sp. water mite diet isolate 2707-BHL032417-GBD11597_12510-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCAACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTATTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606924 Chironominae sp. water mite diet isolate 2714-BHL032417-GBD4990_9416-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTGGATCTTGAACAGGTATAGTAGGTACTTTTTTAAGACTATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCCATTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606925 Chironominae sp. water mite diet isolate 2762-BHL032417-GBD15998_6260-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTGGGGCTTGATCAGGGATAGTAGGAACTTCTTTAAGAATATTAATCCGGACGGAATTAGGGCATCCTGGAAAATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTCTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCTTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606926 Chironominae sp. water mite diet isolate 2770-BHL032417-GBD22347_8606-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAAAGGAATTAGGACATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGAATATTACCACCATCACTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606927 Chironominae sp. water mite diet isolate 2785-BHL032417-GBD9145_23935-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTATGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGTATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTAGGAAATTGGTTATTACCACTAATATTAGGAGCCCCCGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTTATTTCTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606928 Chironominae sp. water mite diet isolate 2823-BHL032417-GBD20495_25150-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTAGTTGTGATGACCAAATTTATAATGTAATTTTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATAGTAGGAGCCCCTGATATGGCTTTTCCACTAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606929 Chironominae sp. water mite diet isolate 2825-BHL032417-GBD22948_16528-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTGGAGCTTGATCAGGTATAGGAGGAAATTTTTTAGAATTTTAATCCGAACGGGATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTTTAATGTAATCGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTTGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606930 Chironominae sp. water mite diet isolate 2828-BHL032417-GBD9876_13401-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTTTTTTTTGGAGCTTGATTAGGTTTTGTAGGAACTTTTTTAAGAATTTTAATCCGAACGGAATTTGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAGTTGGTTATTACCACTAATACTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCATCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606931 Chironominae sp. water mite diet isolate 2840-BHL032417-GBD20459_10848-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGCTATTACCACTAATATTAGGAGCCCCAGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTACCACCATCTCTTACTTCATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606932 Chironominae sp. water mite diet isolate 2850-BHL032417-GBD25376_9416-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACAGAATTCGGTCATCCTGGAACATTTATTGGTGATCACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTAACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606933 Chironominae sp. water mite diet isolate 2852-BHL032417-GBD12202_24739-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTGGAGCTTGTTCAGGAATAGTAGGAACTTCTTTAAGATTTTTAATCCGAAGGGAATTAGGTCACCTTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGGTATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606934 Chironominae sp. water mite diet isolate 2868-BHL032417-GBD16972_9581-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTTTTTTGGAGCTTGATCAGGTATAGTCGGAACTTCTTTAAGTATATTAATTCGAACAGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAACATAAGATTTTGATTACTACCACCATCTCTTACCCTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606935 Chironominae sp. water mite diet isolate 2874-BHL032417-GBD28681_16143-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCATTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCATCAATAACTTTATTATTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606936 Chironominae sp. water mite diet isolate 2875-BHL032417-GBD5352_9911-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGACTTTTTTAATATTTTTAAACCGAACGGATTTAGGTCATCCTGGAACATTTATTGGTGATGACAAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606937 Chironominae sp. water mite diet isolate 2876-BHL032417-GBD15673_18259-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAATATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATCGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606938 Chironominae sp. water mite diet isolate 2878-BHL032417-GBD8071_20128-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGAATCTTCTTCAAGTATATTAATCCGAACGGTATTAGGTCATACTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTTGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606939 Chironominae sp. water mite diet isolate 2893-BHL032417-GBD15473_19333-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGGGCTTTATCAGGTATTGTAGGAACTTCTTTTAGAATTTTTATTCGAAAGAGATTTGGTCATCCTGGAACATTTATTGGTGATGAACAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606940 Chironominae sp. water mite diet isolate 2897-BHL032417-GBD24555_7796-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCGGAATTAGGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTATTACCACCATCTCTAACTTTATTACTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606941 Chironominae sp. water mite diet isolate 2911-BHL032417-GBD21711_26817-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTTTTTTTTTTTTTTTGGAGCTTGGTCGGGTATAGTGGGAACTTTTTTAAGAATATTAATCCGAACGGAATTGGGTTATCCTGGAACATTTATTGGTGATGACCAAATTTATAATTTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606942 Chironominae sp. water mite diet isolate 2917-BHL032417-GBD23223_25001-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTGGAGCATGATCAGGTATAGTAGGAATTTCTTTTAGAATATTTATCCGAACGGTATTAGGTCATCCTTGAACATTTATTGGAGATTACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606943 Chironominae sp. water mite diet isolate 2923-BHL032417-GBD7888_26150-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGAAGCTTGATCCGGTATAGTAGGAACTTCTTTAAGAATATTTATTCGAACGGAATTAGGTCAACCTGGAACATTTATTGGCGATGACCAAATTTATAATGTTGTTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606944 Chironominae sp. water mite diet isolate 2925-BHL032417-GBD21621_24187-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTGTATTTTTTTTTTTGGAGCTTGATCAGTTATAGTAGTAACTTCTTTAAGAATATTAATCCTAACGGAATTAGGTCATCCTGGAACATTTTTTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGTCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATGACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606945 Chironominae sp. water mite diet isolate 2937-BHL032417-GBD25043_5592-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAATTGATTATTACCTCTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606946 Chironominae sp. water mite diet isolate 2951-BHL032417-GBD24587_11455-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATCTTTTTTTTGGAGCTTGATCCGGTATAGTAGGAACTTCTTTAAGAATTTTAATCCGAACGGGATTAGGTCATACTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTTGAGGATCTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACGTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606947 Chironominae sp. water mite diet isolate 2960-BHL032417-GBD8676_7455-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTGTAGCTTGATCCGGTATAGTATGAACTTTTTTTAGAATATTTATCCGAACGGAATTAGGTCATCCTGGAATATTTATTAGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCTCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606948 Chironominae sp. water mite diet isolate 2974-BHL032417-GBD12069_10655-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTAGTCCCACTAATATTAGGAGCACCTGATACAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTACTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606949 Chironominae sp. water mite diet isolate 2980-BHL032417-GBD10056_21009-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGACCGGAATTCGGTCACCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTAGTACCTTTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606950 Chironominae sp. water mite diet isolate 2995-BHL032417-GBD24618_6880-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606951 Chironominae sp. water mite diet isolate 2997-BHL032417-GBD22019_10777-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCCTTGTCAGGTATAGGAGGAACTTCTTTTAGAATATTAATTCGGACGGGATTAGGGCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGATTAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606952 Chironominae sp. water mite diet isolate 2999-BHL032417-GBD16767_23465-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTACGAATATTAATTCGAACTGAATTGGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTGCCACTAATATTAGGAGCCCCAGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606953 Chironominae sp. water mite diet isolate 3009-BHL032417-GBD15081_16722-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGGCATCCTGGGACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCTCTAATTTTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAACATAAGATTTTGATTATTACCACCATCTCTAACCTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606954 Chironominae sp. water mite diet isolate 3010-BHL032417-GBD26577_12755-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTTGGCTCTTGATCAGGTATAGTAGGAACTTCTTTAATATTATTTATCCGAACGGTATTAGGTCATACTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606955 Chironominae sp. water mite diet isolate 3020-BHL032417-GBD22821_8500-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTCTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATGACCACCATCTCTTACTTTATTACAAGCAAGAAGAAGAGTAGAAGATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606956 Chironominae sp. water mite diet isolate 3021-BHL032417-GBD21613_27098-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTTTTTTGGAGCTTGATCGGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACACTTATTGGAGATGACCAAATTTATAATGTAATTATTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACCTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606957 Chironominae sp. water mite diet isolate 3033-BHL032417-GBD24064_23465-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATGCCTATTTTAATTGGAGGATTTGGAAACTGGTTATTACCACTAATATTAGTAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTGTATTACTGGCAAGAAGAAGAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606958 Chironominae sp. water mite diet isolate 3036-BHL032417-GBD11192_10324-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGTGCCTGATCAGGTATAGTAGGAACTTCTTTAAGATTATTAATTCGAGCTGAACTAGGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCAGATATGGCTTTTCCACGAATAAATAATGTAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606959 Chironominae sp. water mite diet isolate 3038-BHL032417-GBD12755_26369-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCAAACGGAATTAGGTCATCCTGGTACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCTTTAATATTAGGAGCCCCAGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606960 Chironominae sp. water mite diet isolate 3042-BHL032417-GBD13364_8350-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACAGAATTTGGTCGTCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTAATACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTACCACCATCACTTACTCTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606961 Chironominae sp. water mite diet isolate 3053-BHL032417-GBD27114_9971-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTTAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTTATGATCAAATTTATAATGTAATTGTTACTGCTCTTGCTTTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCAGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACATTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606962 Chironominae sp. water mite diet isolate 3055-BHL032417-GBD26400_22250-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATACTTTTTTTTGGAGCTTGATCCGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTACTTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTTATTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606963 Chironominae sp. water mite diet isolate 3062-BHL032417-GBD9268_22172-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCGGAATTAGGTCATCCTGGATCATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCATTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTCACCTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606964 Chironominae sp. water mite diet isolate 3069-BHL032417-GBD20711_28053-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTATTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCATTAATATTAGGAGCCCCAGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGACTATTACCACCATCTCTAACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606965 Chironominae sp. water mite diet isolate 3074-BHL032417-GBD7008_23082-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATAGGTTAGTACCTCTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGACTATTACCACCATCTCTGACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606966 Chironominae sp. water mite diet isolate 3082-BHL032417-GBD8555_17621-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCGGAATTTGGTCATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTATTATAATTTTTTTTATAGTAATGCCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606967 Chironominae sp. water mite diet isolate 3100-BHL032417-GBD22929_16528-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTTGTAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGTAAAATTTATTGGTGATGACCATATTTTTAATGTAATCGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTTGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACGTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606968 Chironominae sp. water mite diet isolate 3104-BHL032417-GBD15618_2486-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTTGGAGCATGATCAGGGATAGTAGGAACTTCTTTAAGAATAATAATCCGAACGGAATTAGGTCATCCTGGAAAATTTATTGGTGATGACCAATTTTATAATGTAATTGTTACTGCTCATGCTTTTATTTTAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATACAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGCATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606969 Chironominae sp. water mite diet isolate 3109-BHL032417-GBD6484_20600-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAACAGAATTAGGTCATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATGATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606970 Chironominae sp. water mite diet isolate 3111-BHL032417-GBD7961_14648-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGCATAGTAGGAACTTCTTTAAGAATTTTAATTCGAACGGAATTAGGTCATCCTGGAACATTAATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCATTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAGACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606971 Chironominae sp. water mite diet isolate 3115-BHL032417-GBD28359_16299-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCACTATATTTTTTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGACAACCTGGAACATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAAATGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATGTAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606972 Chironominae sp. water mite diet isolate 3123-BHL032417-GBD28860_14514-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAACGGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCTCTAATATTAGGAGCACCTGATATAGCATTTCCACGAATAAATAATATAAGATTTTGATTACTTCCACCATCTCTAACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606973 Chironominae sp. water mite diet isolate 3127-BHL032417-GBD24968_22663-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTATTCCGAACGGAATTAGGACTTCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTAATTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTTACTTTATTACTTTCAAGAAGAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606974 Chironominae sp. water mite diet isolate 3136-BHL032417-GBD25384_19110-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTTTTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGGTATGGCTTCTCCACAAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606975 Chironominae sp. water mite diet isolate 3142-BHL032417-GBD10205_3248-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTTGGAACTTCTTTTAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATAGGTGATGACCAAATTTATAATGTCCTTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTATGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606976 Chironominae sp. water mite diet isolate 3143-BHL032417-GBD22463_16191-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGATCAGGTATAGTAGGAACTTCCTTAAGTATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGTTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606977 Chironominae sp. water mite diet isolate 3146-BHL032417-GBD21424_9146-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAACGGAATTAGGTCATCCTGAAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATGACCACCAGCTTCTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606978 Chironominae sp. water mite diet isolate 3148-BHL032417-GBD19583_4714-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTGTTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGACTATTACCACCATCTCTTACTCTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606979 Chironominae sp. water mite diet isolate 3150-BHL032417-GBD29555_17266-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACGGGAGGACTTGCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606980 Chironominae sp. water mite diet isolate 3153-BHL032417-GBD12735_27429-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCCGGTATAGTAGAAACTTCTTTAAGAATTTTTATTCGAACGAGATTAGGGCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTTTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606981 Chironominae sp. water mite diet isolate 3156-BHL032417-GBD20187_23713-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGACCTTCTTTAAGAATATTAATCCGAACGGAATTTGGTCCTTCTGGATCATTTATTGGTGATGACCAATTTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606982 Chironominae sp. water mite diet isolate 3163-BHL032417-GBD26036_21899-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTTTTTTTGGAGCTTGATCGGTTATAGTAGGATCTTCTTTAAGATTTTTATTCCGACCGGAATTGGTTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606983 Chironominae sp. water mite diet isolate 3168-BHL032417-GBD9128_6028-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATATTAATCCGAGCGGAATTTGGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTACCACCATCTCTAACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606984 Chironominae sp. water mite diet isolate 3171-BHL032417-GBD22931_13679-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCATTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGTTTTGGAAAGTGATTATTACCCCTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606985 Chironominae sp. water mite diet isolate 3181-BHL032417-GBD8058_25770-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCAGTATATTTTTTTTTTGGAGCTTGCTCAGGTATAGTAGGAACTTCTTTTAGAATATTAATCCGAATGGAATTATGTCAACCTGGAACATTTATTGGTTATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606986 Chironominae sp. water mite diet isolate 3182-BHL032417-GBD4120_12831-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGACATCCTGGATCATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTTCCACTAATATTAGGAGCCCCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTACTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606987 Chironominae sp. water mite diet isolate 3196-BHL032417-GBD25530_21733-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGGGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATGTTAATCCGAGCGGAATTAGGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTAGTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATCATTACCCCCATCTCTTACTTTATTAGTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606988 Chironominae sp. water mite diet isolate 3202-BHL032417-GBD25754_19489-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGATCAAATCTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGTTTTGGAAATTGGTTATTTCCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTCTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606989 Chironominae sp. water mite diet isolate 3205-BHL032417-GBD4093_22297-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCGTTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606990 Chironominae sp. water mite diet isolate 3210-BHL032417-GBD18565_20925-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATACTTATTCGAGCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCTCTAATATTAGGAGCACCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTACTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606991 Chironominae sp. water mite diet isolate 3232-BHL032417-GBD5131_10337-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATCTGGAAATTGATTATTACCACTAATATTAGGAGCTCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCGGACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606992 Chironominae sp. water mite diet isolate 3233-BHL032417-GBD21737_15219-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAATGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTGTTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCAGATATGGCTTTTCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606993 Chironominae sp. water mite diet isolate 3238-BHL032417-GBD19094_23359-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTTTTTTGGAGCTTGACCAGGAATAGTAGGAACTTCTTTTAGAATATTAATTCGAATTGAATTAGGTCATCCTGGAACATTTATTGGTAATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATAATAATTTTTTTTATAGTAATACCTATATTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACCTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606994 Chironominae sp. water mite diet isolate 3239-BHL032417-GBD6965_7820-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGCACTTCTTTAAGAATATTAATTCGACCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAACTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCATTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTTACCTTATTTCTATCATGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606995 Chironominae sp. water mite diet isolate 3241-BHL032417-GBD27374_12241-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGAGCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATTGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCACCAACTCCTACATTATTACAATCAAGAAGAATAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW606996 Chironominae sp. water mite diet isolate 3253-BHL032417-GBD11116_26710-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606997 Chironominae sp. water mite diet isolate 3256-BHL032417-GBD23096_24921-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGGGCTTGATCGGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAACGGAATTAGTCCAACCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606998 Chironominae sp. water mite diet isolate 3269-BHL032417-GBD22707_18510-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAACGGAATTAGGTCATCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGGTTATTACCATTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW606999 Chironominae sp. water mite diet isolate 3275-BHL032417-GBD26910_11223-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTACCACCATCTCTTACTCTATTACTTTCTAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607000 Chironominae sp. water mite diet isolate 3277-BHL032417-GBD2499_12661-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGCATAGTAGGAACTTCTTTATGTATATTAATCCGAACGGAATTAGGTCATACTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATACGGCTTTTCCACGAATAAACAATATAAGATTTTGATTATTACCACCAACTCTTACTTTATCACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607001 Chironominae sp. water mite diet isolate 3280-BHL032417-GBD18159_28757-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCACTATATTTTCTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTTAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATGAATAATATAAGATTTTGATTATTACCACCATCTCTTACCTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607002 Chironominae sp. water mite diet isolate 3285-BHL032417-GBD24458_13030-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGGGCTTTGTCCGGGATAGTTGGAAATTTTTTTAGAATATTAATTCGAATGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607003 Chironominae sp. water mite diet isolate 3289-BHL032417-GBD12658_11232-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGAAATTAGGTCATCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGGTTATTACCTCTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACGACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607004 Chironominae sp. water mite diet isolate 3291-BHL032417-GBD26615_7768-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGACCGGAATTAGGACATCCTGGAACATTTATTGGTGACGACCGAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTAACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607005 Chironominae sp. water mite diet isolate 3292-BHL032417-GBD9181_7394-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAACTAGGTCATCCTGGATCATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTAGCACTAATACTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGTTTATTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607006 Chironominae sp. water mite diet isolate 3293-BHL032417-GBD27447_22697-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATACTAATTCGAACGGAATTAGGTCAACCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGTTTATTACCACTAATATTAGGAGCTCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACCTTACTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607007 Chironominae sp. water mite diet isolate 3296-BHL032417-GBD24538_7351-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATACTAATTCGAATGGAATTAGGTCACCCTGGAACTTTTATTGGTGATGACCAAATCTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCTCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607008 Chironominae sp. water mite diet isolate 3301-BHL032417-GBD5850_23593-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCCGGTATATTAGGAACTTCTTTAAGAATATTAATTCGGACGGAATTAGGTCAACCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCCTCTCTTACCTTATTTCTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607009 Chironominae sp. water mite diet isolate 3305-BHL032417-GBD7807_4387-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTTTATTTTTTTTTGGAGCTTGATCAGGAATAGTCGGAACTTCTTTAAGAATATTAATCCGAACTGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCATTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTACCACCATCTCTTACTCTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607010 Chironominae sp. water mite diet isolate 3306-BHL032417-GBD26336_15615-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGCACTTCTTTAAGTATATTAATTCGAGCGGAATTAGGTCATCCTGGTCCATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCACTAATATTAGGAGCCCCTGATATGGCATTTCCACGAATAAATAATATAAGATTTTGAATATTACCACCATCACTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607011 Chironominae sp. water mite diet isolate 3309-BHL032417-GBD11918_15951-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTTTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAAGATTTGGAAATTGGTTATTACCACTAATATTAGGATCCCCTGATATGGCTTTTCCACCAATAAAAAAAATAAGAATTTTATTATTACCACCATCTCCTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607012 Chironominae sp. water mite diet isolate 3313-BHL032417-GBD28821_18220-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTCCCTCTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTAGTACCACCATCTCTAACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607013 Chironominae sp. water mite diet isolate 3314-BHL032417-GBD25423_25334-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAACTGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTACCACCATCTCTAACTCTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607014 Chironominae sp. water mite diet isolate 3315-BHL032417-GBD6461_13868-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATTAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCTCTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607015 Chironominae sp. water mite diet isolate 3318-BHL032417-GBD3085_14879-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTGGAGCTTGATCGGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGCACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGATGATTTGGAAATTGGTTATTACCTCTAATATTAGGAGCCCCTGGTATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607016 Chironominae sp. water mite diet isolate 3325-BHL032417-GBD5309_15250-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGGGCTTGATCAGGAATAGTGGAACTTCTTTAAGAATATTTATTCGAACGGAATTAGGTCAACCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTTCTCTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607017 Chironominae sp. water mite diet isolate 3329-BHL032417-GBD27969_20832-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAACGGAATTCGGTCATCCTGGGTCATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACAAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTGCTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607018 Chironominae sp. water mite diet isolate 3333-BHL032417-GBD17526_8319-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTGATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTAGTACCACTAATATTAGGAGCCCCAGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTAATTTCAAGAAAAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607019 Chironominae sp. water mite diet isolate 3335-BHL032417-GBD18218_12054-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCCTGGTCAGGGATAGTTGGAACTTCCTTTAGGATATTTATTCGAACGGAATTAGGGCATCCTGGAAAATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607020 Chironominae sp. water mite diet isolate 3338-BHL032417-GBD21364_18031-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTTTTTTTGGAGCTTGGTCAGGAATAGTCGGAACTTCCTTAAGTATATTAATTCGAACGGAATTAGGTCATCCTGGAACATGTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTTTTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607021 Chironominae sp. water mite diet isolate 3343-BHL032417-GBD27824_11567-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAACAGAATTAGGGCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGCTATTTCCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAACATAAGATTTTGATTATTACCCCCATCTCTTACCTTACTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607022 Chironominae sp. water mite diet isolate 3344-BHL032417-GBD17241_25682-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAACAGAATTAGGTCATCCTGGATCTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTATTGCTCATGCTTTTATAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGAGTTGGAAATTGATTAGTACCACTAATATTAGGAGCCCCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607023 Chironominae sp. water mite diet isolate 3347-BHL032417-GBD11277_19041-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTTGGAACTTCTTTAAGTATATTTATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGACGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTAATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGGTTGTTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607024 Chironominae sp. water mite diet isolate 3352-BHL032417-GBD22270_15854-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAACAGAATTAGGTCATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGAAGGATTTGGAAATTGATTATTACCGCTAATATTAGGAGCCCATGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607025 Chironominae sp. water mite diet isolate 3366-BHL032417-GBD17802_11190-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCGGAATTAGGTCATCCTGGATCATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGCAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCATTAATATTAGGAGCCCCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTTACTTTATTACTATCAAGAAGACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607026 Chironominae sp. water mite diet isolate 3367-BHL032417-GBD3928_15850-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGATTGTTAATTCGAGCGGAATTTGGACA TCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTA ATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCATTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATA AATAATATAAGATTTTGACTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAA	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607027 Chironominae sp. water mite diet isolate 3368-BHL032417-GBD12948_18129-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAACAGAATTAGGACA TCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTT ATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTTCCACTAATATTAGGAGCACCAGATATGGCATTTCCACGAAT AAATAATATAAGATTTTGATTATTACCCCCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAAC AGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607028 Chironominae sp. water mite diet isolate 3372-BHL032417-GBD18359_16804-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAGAATATTAATCCGAACGGAATTATGTCAT CCTGGAACATTTATTGGTAATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAA TACCAATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATA AATAATATAAGATTCTGAGTACTACCACCATCTCTTACCTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAAC AGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607029 Chironominae sp. water mite diet isolate 3378-BHL032417-GBD22216_17243-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCCGGTATAGTTGGAACTTCTTTAAGTATATTTATTCGAACTGAATTAGGTCAT CCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAA TACCTATTTTAATTGGAAGATTTGGAAATTGGTTATTACCTTTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAA ATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTTCTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAG G	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607030 Chironominae sp. water mite diet isolate 3380-BHL032417-GBD10013_22058-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTTATCCGGGATAGTAGGAACTTCATTAAGAATATTTATCCTAACGGAATTAGGTAA TCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTA ATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAGTATTATGAGCCCCTGATATGGCTTTTCCACGAATA AATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACA GG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607031 Chironominae sp. water mite diet isolate 3382-BHL032417-GBD9542_8685-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATATTAATCCGAACGGAATTAGGTCA TCCTGGTACATTTATTGGTTATGACCAAATTTATAATGTAATTGTTACTGCTCATGCGTTTATTATAATTTTTTTTATAGTA ATACCTATTTTAATAGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAAT AAATAATATAAGATTTTGAATATTACCACCATCACTGACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAA CAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607032 Chironominae sp. water mite diet isolate 3388-BHL032417-GBD24955_19856-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTTATTCGAACTGAATTAGGTCA ACCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTA ATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCTCGAATA AATAATATAAGATTTTGATTATTTCCACCATCTCTTACTTTATTACTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACA GG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607033 Chironominae sp. water mite diet isolate 3394-BHL032417-GBD22463_14516-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCGGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGACA TCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTA ATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATAAGGCTTTTCCACGAAA AAAAAATATAAGATTTTGATTATTACCACCATCTCATACTTTATTACATTCAATAAGAATAGTAGAAAATGGAGCTGGAA CAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607034 Chironominae sp. water mite diet isolate 3395-BHL032417-GBD22236_14663-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCCGGTATAGTGGGAACTTCTTTAAGAATATTAATTCGAGCGGAATTAGGTCA TCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGAACATGCTTTTATTATAATTTTTTTAATAGTA ATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATA AATAATATAAGATTTTGATTTTTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACA GG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607035 Chironominae sp. water mite diet isolate 3398-BHL032417-GBD10966_22233-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTTTTTAATAATATTAATCCGAACGGAATTAGGT CATCGTGGTATATTTATTGGTGATGACCAATTTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAG TAATACCTATTTTAATTGGAGGTTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAA TAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGA ACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607036 Chironominae sp. water mite diet isolate 3399-BHL032417-GBD6317_9654-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCTCTAATATTAGGAGACCCTGATATGGCTTTTCCACGAATAAATAATATAAGATGTTGATTATTACCACCATCTCTAACTTTAGTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607037 Chironominae sp. water mite diet isolate 3401-BHL032417-GBD24317_13752-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCAAACGAAATTAGGCCATCCTGGAACACTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATACTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607038 Chironominae sp. water mite diet isolate 3412-BHL032417-GBD10954_17941-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGAATAATAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGGCACCCTGGAACATGTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCCGATATGGCTTTTCCACGAATAAATAACATAAGATTTTGATTATTACCACCATCTCTTACCTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607039 Chironominae sp. water mite diet isolate 3417-BHL032417-GBD19286_11176-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGAATAGTGGGAACTTCTTTAGGAATTTTAATCGGAACGGAATTAGGTAATCCTGGAACATTTATTGGTGAGGACGAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAATAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607040 Chironominae sp. water mite diet isolate 3418-BHL032417-GBD25084_9740-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTGGGAACTTCTTTTAGAATTTTAATCCGAACGGAATTAGGTCATGCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCAGATATGGCATTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607041 Chironominae sp. water mite diet isolate 3422-BHL032417-GBD23214_5795-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAACGGAATTCGGTCATACTGGTTCTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTCATTACTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607042 Chironominae sp. water mite diet isolate 3423-BHL032417-GBD15608_24330-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATTATAGGAACTTTTTTTAGCATATTTATTCGGACGGGATTAGGGCATTCTGGAACATTTATTGGTAATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607043 Chironominae sp. water mite diet isolate 3427-BHL032417-GBD24742_21090-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGCTCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAATGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTTGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATATTGATTAGTACCACCATCGCTTACTGTATTACTTGCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607044 Chironominae sp. water mite diet isolate 3429-BHL032417-GBD8821_17031-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATTAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTGGGTCAACCAGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTAATATAATTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGGTTATTTCCACTAATATTAGGAGTCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607045 Chironominae sp. water mite diet isolate 3435-BHL032417-GBD9432_11013-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATCCGAACGGAATTCGGTCATCCTGGAACATTAATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTAGTACCTCTAATATTAGGAGCCCCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTTACTTTATTACGATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607046 Chironominae sp. water mite diet isolate 3437-BHL032417-GBD27758_8735-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCTCTAATATTAGGAGCCCCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTACTACCACCATCTTTTACTTTATTACTATCAAGAAGACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607047 Chironominae sp. water mite diet isolate 3438-BHL032417-GBD5622_14293-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATACTGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGACCCTGATATGGCTTTTCCTCGAACAAATAATATAATATTTTGATTAAAACCACCATCTCTTACTTTATTACGTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607048 Chironominae sp. water mite diet isolate 3442-BHL032417-GBD6312_19223-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGATATAGCATTTCCACGAATAAATAATATAAGATTTTGATTACTACCACCATCTCTTACTCTACTTCTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607049 Chironominae sp. water mite diet isolate 3449-BHL032417-GBD9733_12444-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCTCTAATATTAGGAGCCCCTGACATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTTCCACCATCTCTTACTTTATTTCTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607050 Chironominae sp. water mite diet isolate 3451-BHL032417-GBD25893_18751-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCACTTATATTAGGAGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607051 Chironominae sp. water mite diet isolate 3453-BHL032417-GBD11716_15590-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTTTTTTTTGGAGCTTGATCCGGTATAGTAGGAACTTCCTTAAGAATATTAATCCGAACGGAATTAGGTCGTCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCATTAATATTAGGAGTCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCGTCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607052 Chironominae sp. water mite diet isolate 3454-BHL032417-GBD12213_9883-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAACAGAATTAGGTCATCCTGGTACATTTATTGGTGATGATCAAATTTATATTGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTAGTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607053 Chironominae sp. water mite diet isolate 3458-BHL032417-GBD2738_13984-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGCACGGAATTAGGTCATCCTGGTACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTTACTTTATTACTATCAAGCAGACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607054 Chironominae sp. water mite diet isolate 3459-BHL032417-GBD11550_8207-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATAATAATTCGAACAGAATTAGGTTGTCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGTAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607055 Chironominae sp. water mite diet isolate 3460-BHL032417-GBD24385_6684-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCTTTAAGAATATTAATTAAAGCGGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGCTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607056 Chironominae sp. water mite diet isolate 3461-BHL032417-GBD16263_28512-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATACTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCTCTAATATTAGGAGATCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTTCCCCCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607057 Chironominae sp. water mite diet isolate 3464-BHL032417-GBD16787_7761-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGTGCTTGATCAGGTATAGTGGGAACTTCTTTAAGAATATTAATCCGAACTGAATTAGGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTCTCCACGAATAAATAATATAAGATTTTGACTACTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607058 Chironominae sp. water mite diet isolate 3466-BHL032417-GBD8252_7807-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGGTCCGGGATAGTTGGAACTTCTTTAAGTATATTTATTCGAACGGAATTAGGGCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATGCCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGAATATTACCACCATCTCTTACTTTATTCCTTGCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607059 Chironominae sp. water mite diet isolate 3471-BHL032417-GBD27201_15471-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGTTTGATCTGGAATAGTAGGAACTGCTTTTAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGAGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCAGCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607060 Chironominae sp. water mite diet isolate 3472-BHL032417-GBD22853_23430-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGATCATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTTATGCTTTTTTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTAACTTTATTACTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607061 Chironominae sp. water mite diet isolate 3473-BHL032417-GBD10116_10043-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGTTTGATCAGGTATAGTAGGAACCTCTTTAAGAATATTAATTCGAACGGAATTAGGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAGTTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAACTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACCTTATTAATTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607062 Chironominae sp. water mite diet isolate 3475-BHL032417-GBD4609_14750-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTTATTGTAATTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGATATGGCATTTCCACGAATAAATAATATAAGATTTTGATTACTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607063 Chironominae sp. water mite diet isolate 3476-BHL032417-GBD3124_11079-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTTATTCGAACGGAATTAGGTCGTCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGACATGGCTTTTCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCTCTTACTTTATTACTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607064 Chironominae sp. water mite diet isolate 3674-BHL032417-GBD17035_28824-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTAATTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACTGAATTAGGTCATCCTGGAACATTTATTGGTGATTACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTTGTGGATTTGGAAATTGATTAGTACCACTAATATTAGGTGCACCAGATATAGCTTTCCCTCGAATAAATAATATATGCTTTTGATTATTACCCCCATCTTTAACATTACTATTAGCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607065 Chironominae sp. water mite diet isolate 3725-BHL032417-GBD12974_8378-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTCTTTAATTGGAGACGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGCAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607066 Chironominae sp. water mite diet isolate 3960-BHL032417-GBD28354_12329-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCTTTAAGAATACTTATTCGAGCTGAACTTGGACGACCTGGTACTTTTATTGGTGATGAACAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607067 Chironominae sp. water mite diet isolate 3992-BHL032417-GBD27600_8962-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACAACCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGACATAGCATTCCCTCGAATAAATAATATAAGTTTCTGATTACTTCCCCCTTCTTTGACTCTTCTACTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607068 Chironominae sp. water mite diet isolate 4021-BHL032417-GBD21164_27373-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAATTATACCCATTTTAATCGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTGGAATAAATAATATAAGATTCTGATTACGTCCCCCTTCTTTAACACAGCATCATTCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607069 Chironominae sp. water mite diet isolate 4027-BHL032417-GBD4717_10864-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGGACTTCTTTAAGAATTCTTATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCTTTAACTCTTCTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607070 Chironominae sp. water mite diet isolate 4110-BHL032417-GBD3578_13325-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAATATGCTAATTCAAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAGCAAATTTACAAAGTAATTATCACAGCACACGCTTTTATTATAATTTTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATATGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607071 Chironominae sp. water mite diet isolate 4125-BHL032417-GBD15582_13624-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCAAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAGCATATTTATAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAAC---CTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607072 Chironominae sp. water mite diet isolate 4127-BHL032417-GBD10550_8845-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATTCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGTACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTGCTACTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607073 Chironominae sp. water mite diet isolate 4159-BHL032417-GBD4977_12520-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTATCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTTCTTCCCCCTTCATTAACCCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607074 Chironominae sp. water mite diet isolate 4180-BHL032417-GBD16106_10292-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCATTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCAAGCAGAATTTGGACGACCTGGTACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCATTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACCCTATTACTTTCAAGTGCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607075 Chironominae sp. water mite diet isolate 4197-BHL032417-GBD25825_7842-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCAAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAACAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCCGATAAGGCTTTCCCCCGAAAAAAAAAAAAAAGTTTTTGACTTCCTCCCCCTTCATTAACCCCTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607076 Chironominae sp. water mite diet isolate 4208-BHL032417-GBD16868_7108-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAGTTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGACCCAGATATGGCTTTCCCTCTAATAAATAATATAAGTTTTTGACTTCTGCCCCCTTCATGAACCCTTTTACGTTCAAGGTCTACTGTAGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607077 Chironominae sp. water mite diet isolate 4215-BHL032417-GBD18586_21246-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGTCGACCTGGTACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCTTACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCATTAACCCTATTACTATCAAGTTCTGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607078 Chironominae sp. water mite diet isolate 4275-BHL032417-GBD26371_7057-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGTTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGAACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607079 Chironominae sp. water mite diet isolate 4287-BHL032417-GBD5406_19084-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGAATAGTAGGAACTTCTTTAAGTATGCTAATTCAAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAGCAAATTTATAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAACTGACTTATTCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACCCTTTTACTTTCAAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607080 Chironominae sp. water mite diet isolate 4288-BHL032417-GBD27022_13473-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAGGTATGTTAATTCAAGCAGAACTTGGACAACCTGGTACCTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACCCTTTTACTTTCAAGTACAATAATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607081 Chironominae sp. water mite diet isolate 4298-BHL032417-GBD6884_13782-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCAAGCAGACCTTGGACGACCTGGTACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGACCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCGGTTACAATCAAGTGCTATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607082 Chironominae sp. water mite diet isolate 4300-BHL032417-GBD20505_18664-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCAAGCAGAACTTGGACAACCTGGTACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACACGCTTTTGTTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGGTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTCGACTTCTTCCCCCGTCATTAACCCTATTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607083 Chironominae sp. water mite diet isolate 4302-BHL032417-GBD18084_4729-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGCAGAACTAGGACGACCTGGAACTTTTATTGGAGATGAGCAAATTTACAACGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCACTAACCCTTTTTCTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607084 Chironominae sp. water mite diet isolate 4315-BHL032417-GBD17928_20495-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATTTGGACAACCTGGTACATTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCATCATTAACCCTATTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607085 Chironominae sp. water mite diet isolate 4334-BHL032417-GBD11040_6259-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGCACTTCTTTAAGAATGTTAATTCAAGTAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAGCAAATTTATAATGTAATTGTCACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCGCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTTTTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607086 Chironominae sp. water mite diet isolate 4340-BHL032417-GBD17287_2956-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAAAACTTGGACGACTTGGTACTTTTATTGGAGATGACCAATTTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGGAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607087 Chironominae sp. water mite diet isolate 4408-BHL032417-GBD14448_24859-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATATGGTATAGTAGGCACTTCTTTAAGTATGTTAATTCAAGCAGAACTTGGACTACCAGGTTCTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTTTTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607088 Chironominae sp. water mite diet isolate 4424-BHL032417-GBD7075_15845-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTCGGACGACCTGGTACTTTTATTGGATATGAGCAAATTTATAATGTAATTGTCACAGCACACGCATTTATTATAATTTTTTTTATAGCTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAAC---CTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607089 Chironominae sp. water mite diet isolate 4428-BHL032417-GBD5945_7448-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATATTATCTTTGGAGCTTGATCTGGAATAGTAGGAACTTCTTTAAGTATGCTAATTCAAGCAGAACTTGGACGACCTGGAACTTTCATTGGAGATGAGCAAATTTATAATGTAGTTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGGATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607090 Chironominae sp. water mite diet isolate 4445-BHL032417-GBD26889_14372-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTCGGACACCAAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTACAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCGTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607091 Chironominae sp. water mite diet isolate 4447-BHL032417-GBD13251_23466-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTCGGAGCTTGATCTGGTATAGTAGGTACTTCTCTAAGTATGCTAATTCGAGCAGAACTTGGACGACCAGGTACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACAAGCATTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACCCTTTTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607092 Chironominae sp. water mite diet isolate 4464-BHL032417-GBD18052_13551-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCAAGCAGAACTTGGACAACCTGGTACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTATGCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACCCTATTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607093 Chironominae sp. water mite diet isolate 4467-BHL032417-GBD18623_25282-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCATACCTTGGACAACCTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCACCTGATACGGCTGTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607094 Chironominae sp. water mite diet isolate 4947-BHL032417-GBD22414_12025-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACTCTATTACGTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607095 Chironominae sp. water mite diet isolate 5480-BHL032417-GBD9155_19127-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACATAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTATCTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KT115751, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607096 Chironominae sp. water mite diet isolate 5655-BHL032417-GBD16833_14270-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATACTTTATTTTTGGGGCTTGATCCGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCCTTAATGTTAGGAGCCCCTGACATAGCCTTCTCGCGAATAAATAATATAAGATTTTGGCTTCTTCCCCCGTCTCTTACTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR641103, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607097 Chironominae sp. water mite diet isolate 5738-BHL032417-GBD16382_27275-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGTTCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGTCCTGGTACTTTTATTGGAGATGACCAAATTTACAACGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607098 Chironominae sp. water mite diet isolate 5775-BHL032417-GBD8540_9311-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTCATTTTTTGGGGCTTGATCAGGAATAGTAGGCACTTCCTTAAGTATACTTATTCGAGCAGAGTTAGGACGGCCAGGAACTTTCATTGGAGATGACCAAATTTATAACGTAATTGTAACCGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCGATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAACATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACT-TTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KR751654, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607099 Chironominae sp. water mite diet isolate 5802-BHL032417-GBD6910_22098-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGATATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAACGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATGGTTATGCCAATTTTAACTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTCTCAAGTTCTATTATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607100 Chironominae sp. water mite diet isolate 5833-BHL032417-GBD4571_14085-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTGTGGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTCTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607101 Chironominae sp. water mite diet isolate 5834-BHL032417-GBD19864_22251-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGTAGAACTTGGACGACCTGGTACTATTATTGGAGATGACCAAATTTACAACGTAATTGTCACAGTACACGCTTTTATTATAATTTTTTTTATGGTTATGCCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607102 Chironominae sp. water mite diet isolate 5848-BHL032417-GBD15997_8272-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGTTTTGGAAAGTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCACGTTATTTAACTCTACATCATTCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607103 Chironominae sp. water mite diet isolate 5854-BHL032417-GBD17335_27304-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTTCTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGTATAAATAACATAAGATTCTGATTACTTCCCCCTTCTTTAACCCTTCTTCTATCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607104 Chironominae sp. water mite diet isolate 5858-BHL032417-GBD12282_10508-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAACTTTTTTTATAGTTATACCGATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGGGCCCCTGATATAGCCTTCCCGCGAATAAATAATATAAGATTTTGACTTCTCCCACCGTCTCTTTCTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KR751654, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607105 Chironominae sp. water mite diet isolate 5868-BHL032417-GBD25142_23523-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTCTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAACGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATGGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTGGGAGACCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607106 Chironominae sp. water mite diet isolate 5908-BHL032417-GBD7963_7989-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAAGTTCCCTTAGAATATTAATTCGATCAGAATTAGGACGTCCTGGAATTTTTATTGGAGATGACCAAATCTACAACGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATGGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTTTTACTTTCAAGTTCTATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607107 Chironominae sp. water mite diet isolate 5935-BHL032417-GBD22564_11384-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAATTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATATCCATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTTATATTAGGAGCACCAGATATAGCATTCCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGTTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607108 Chironominae sp. water mite diet isolate 5963-BHL032417-GBD7932_26114-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTCATTTTTGGGGCTTGGTCAGGAATAGTAGGCACTTCCTTAAGTATACTTATTCGAGCAGAGTTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTAACCGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCGATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGGGCCCCTGATATAGCCTTCCCGCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR751654, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607109 Chironominae sp. water mite diet isolate 5969-BHL032417-GBD7348_11993-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATGGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACGCTACTACTAGCTAGCTCTATAGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607110 Chironominae sp. water mite diet isolate 5974-BHL032417-GBD12229_15185-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGTATGCTAATTCGAGCAAAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAACGTAGTTGTCACAGCACACGCTTTTATTATAATTTTTTTTATGGTTATGCCAATTTTAATTGGGGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607111 Chironominae sp. water mite diet isolate 5982-BHL032417-GBD27396_18782-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGGATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCTTTAATATTAGGTGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTAACCTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607112 Chironominae sp. water mite diet isolate 5985-BHL032417-GBD27176_12447-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGTTCAGAATTAGGACATCCTGGTACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAGATAATATAAGATTCTGATTACTTCCTCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607113 Chironominae sp. water mite diet isolate 5996-BHL032417-GBD6498_11096-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTCTTTAAGAATTCTAATTCGTACAGAATTAGGACATCCCGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATGTTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607114 Chironominae sp. water mite diet isolate 5998-BHL032417-GBD21397_9716-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGAGCCTGATCTGGAATAGTTGGAACTTCTTTTAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATAATAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCGTTCTTTATCTCTTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607115 Chironominae sp. water mite diet isolate 5999-BHL032417-GBD17512_8959-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607116 Chironominae sp. water mite diet isolate 6002-BHL032417-GBD5692_20037-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATTCTGGAACTTTGATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATATGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACACTTCTTATTTCTAGTTCTATTGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607117 Chironominae sp. water mite diet isolate 6012-BHL032417-GBD3965_8780-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGGATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCACAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATATCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCCTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTCATCTCCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607118 Chironominae sp. water mite diet isolate 6036-BHL032417-GBD9076_16381-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGTATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTGTATTGTTATTGTAACAGTTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGACATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTCCTATTGTAGAAAATGGTGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607119 Chironominae sp. water mite diet isolate 6039-BHL032417-GBD24375_14271-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAACACAATTAGGACATCCTGGAACTTTTATTGGTGAAGACCAAATTTATAATGTTAATGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGACTTGTTCCTCTTATATTTGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATTGTAAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607120 Chironominae sp. water mite diet isolate 6047-BHL032417-GBD22018_11590-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGATCCTGATCATGAATAGTTGGAACTTCTTTATGAATTCTAATTCGAGCAGAATTCGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTACTATCGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607121 Chironominae sp. water mite diet isolate 6053-BHL032417-GBD26140_16917-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTTGGTACTTCTTTAAGAATTCTAATTCGAGCAGAACTCGGTCATCCTGGTTCTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCGTCATTAACTCTACTACTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607122 Chironominae sp. water mite diet isolate 6055-BHL032417-GBD17800_6359-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACTTTATATTTTATTTTTGGAGCCTGATCTGCAATACTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAACTAGGACATCCTGGAACCTTTATTGGGGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAATTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAACTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607123 Chironominae sp. water mite diet isolate 6058-BHL032417-GBD15023_7725-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCCTGATCCGGAATAGTTGGAACCTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTAACTGCTCATGGTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGATGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607124 Chironominae sp. water mite diet isolate 6062-BHL032417-GBD4125_8095-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTTATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCCCTAATATTAGGAGCACCAGACATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTCTAACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607125 Chironominae sp. water mite diet isolate 6075-BHL032417-GBD13940_12458-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTCGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGATGTTCAAATTTATAATGTTATTGTAACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTTTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607126 Chironominae sp. water mite diet isolate 6083-BHL032417-GBD2934_11885-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAACAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCATCTTTATCTCTACTTCTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607127 Chironominae sp. water mite diet isolate 6087-BHL032417-GBD23686_15815-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAATATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTATCTAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607128 Chironominae sp. water mite diet isolate 6108-BHL032417-GBD25850_23336-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATACTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTTTTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAATTTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTACTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607129 Chironominae sp. water mite diet isolate 6109-BHL032417-GBD7319_22441-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTAGAGCCTGATCAGGTATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTATTACCACCATCTCT-TACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607130 Chironominae sp. water mite diet isolate 6111-BHL032417-GBD22505_21024-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATACTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCAGATATAGCATTCCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607131 Chironominae sp. water mite diet isolate 6113-BHL032417-GBD26187_9898-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCGTTTCCACGAATAAATAATATAAGATTCTGATTACTGCCCCCTTCATTAACTCTACTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607132 Chironominae sp. water mite diet isolate 6123-BHL032417-GBD19318_5244-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCTTCTTTAACTCTTCTTCTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607133 Chironominae sp. water mite diet isolate 6124-BHL032417-GBD28371_15133-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTCGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTACTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607134 Chironominae sp. water mite diet isolate 6126-BHL032417-GBD27442_13437-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCTTCTTTAACTCTTCTACTTTCTAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607135 Chironominae sp. water mite diet isolate 6128-BHL032417-GBD25406_9884-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACATCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACATCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTATTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCCACTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607136 Chironominae sp. water mite diet isolate 6129-BHL032417-GBD26455_19635-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACCTTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTTACGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATAGAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTACTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607137 Chironominae sp. water mite diet isolate 6134-BHL032417-GBD9446_22774-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTCCCTCGAATAAATAATATAAGATCCTGATTACTTCCCCCTTCTTTAACACTACTACTATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607138 Chironominae sp. water mite diet isolate 6141-BHL032417-GBD24355_20627-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCGCTCTTACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607139 Chironominae sp. water mite diet isolate 6143-BHL032417-GBD26916_7670-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAGTTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAACCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTTTTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607140 Chironominae sp. water mite diet isolate 6144-BHL032417-GBD20346_10703-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATCCTGGATCTTTTATTGGTGACGACCAAATTTATTATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTCTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAACATAAGATTCTGATTACTTCCCCCTTCTTTAACACTACTACTATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607141 Chironominae sp. water mite diet isolate 6147-BHL032417-GBD20227_12665-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATCCTGGTACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCCTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTGTATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTACTTCTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607142 Chironominae sp. water mite diet isolate 6151-BHL032417-GBD21058_27713-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTTTATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTACCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607143 Chironominae sp. water mite diet isolate 6158-BHL032417-GBD25633_13008-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGGATAGTTGGAACTTCTTTAAGTATTCTTATTCGAGCAGAATTAGGGCATCCTGGCACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTGTCTAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607144 Chironominae sp. water mite diet isolate 6160-BHL032417-GBD12185_13219-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGTTCTTTTATCGGTGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTACTATTATCTAGCTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607145 Chironominae sp. water mite diet isolate 6162-BHL032417-GBD26527_9592-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTCTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAGTTGATTAGTTCCTCTTATATTAGGAGCACCAGAAACAGCATTTCCTCGAATAAATAAAATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTACTTCAATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607146 Chironominae sp. water mite diet isolate 6163-BHL032417-GBD12454_11785-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTCTAATTCGAGCAGCATTAGGACACCCTGGAACTTTTATCGGTGACGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTACTACTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607147 Chironominae sp. water mite diet isolate 6170-BHL032417-GBD15447_25402-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGCTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGTTATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCATTAACTCTACTACTTTCTAGTGCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607148 Chironominae sp. water mite diet isolate 6171-BHL032417-GBD24542_17498-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGTATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCATCAGATAAAGCATTTCCACGAAAAAATAATAAAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607149 Chironominae sp. water mite diet isolate 6173-BHL032417-GBD16176_18335-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCTGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGTACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAACATAAGATTCTGATTACTTCCCCCTTCTTTAACACTACTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607150 Chironominae sp. water mite diet isolate 6174-BHL032417-GBD10095_16028-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGAATTTGGAAATTGATTAGTTCCTCTTATATTAGAAGCACCAGATATAGCTATTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCTTCTTTAACTCTTCTACTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607151 Chironominae sp. water mite diet isolate 6178-BHL032417-GBD3848_20999-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGCATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTCCCCCGAATAAATAATATAAGCTTCTGATTACTTCCCCCTTCTTTAACTCTCCTTCTTTCTAGTTCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607152 Chironominae sp. water mite diet isolate 6180-BHL032417-GBD27579_12285-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGAGTCTGATTACTTCCCCCTACTTTATCTCAGCTTCTTGCTAGTACTATTTTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607153 Chironominae sp. water mite diet isolate 6181-BHL032417-GBD22212_16338-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGTCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTACTTCCTCTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACCCTTCTTCTATCTAGTTCTTTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607154 Chironominae sp. water mite diet isolate 6184-BHL032417-GBD20582_14489-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACTTTATGTTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTTAGAATTCTAATTCGAGTAGAATTATGACATCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607155 Chironominae sp. water mite diet isolate 6185-BHL032417-GBD22470_16340-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACAACCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCTTCTTTAACTCTTCTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607156 Chironominae sp. water mite diet isolate 6187-BHL032417-GBD6511_15981-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTTTATTTTATTTTCGGGGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACAACCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607157 Chironominae sp. water mite diet isolate 6192-BHL032417-GBD27339_12028-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTGGGAACTTCTTTAAGAATTCTTATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTCTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTAGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTTTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607158 Chironominae sp. water mite diet isolate 6195-BHL032417-GBD6809_11134-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGATGATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACACTACTTCTATCTAGTTCTGTTGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607159 Chironominae sp. water mite diet isolate 6203-BHL032417-GBD3978_10464-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATTCTAATTCGAGCAGAATTAGGACAACCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTTTTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCTAGTACTATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607160 Chironominae sp. water mite diet isolate 6205-BHL032417-GBD18480_23341-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGAACAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAATTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTATTACCCCC------ATCACTAATTCTAT-TAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607161 Chironominae sp. water mite diet isolate 6206-BHL032417-GBD9275_11287-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACAACCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGAATTTGGAAACTGATTATTGCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607162 Chironominae sp. water mite diet isolate 6208-BHL032417-GBD25890_22192-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGATCAAACTTATAATGTTATTGTTACCGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCATTAACTCGGCTACTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607163 Chironominae sp. water mite diet isolate 6209-BHL032417-GBD7406_13879-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATGGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607164 Chironominae sp. water mite diet isolate 6210-BHL032417-GBD9025_22655-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGATCAACCTTATAATGTTATTGTAACAGCTCATGCTTTTCTTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACCCTACTTCTTTCTAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607165 Chironominae sp. water mite diet isolate 6211-BHL032417-GBD27606_20877-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTGTTTAGGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGATGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAACTAATATAAGATTCTGATTACTTCCCCCTTCTTTATCGCTTCTTCTTTCTAGTTCTATTTTAGAAAATCGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607166 Chironominae sp. water mite diet isolate 6219-BHL032417-GBD6895_24324-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGTCATGCTGGTTCTTTTATTGGTGACGATCAAATTTATAATGTAATTGTAACCGCTCATGCTTTTATTATAATTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCGTCATTAACTCTACTACTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607167 Chironominae sp. water mite diet isolate 6221-BHL032417-GBD24139_6681-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGTCATCCTGGTACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACATCTCATGCTTTTATAATAATTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGCTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607168 Chironominae sp. water mite diet isolate 6222-BHL032417-GBD12291_25451-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATACTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTCATAGTTATACTCATTTTAATTGGAGGATTTGGAAATTGATTAATTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAAAAATAAAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607169 Chironominae sp. water mite diet isolate 6225-BHL032417-GBD27605_22494-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGCACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGAAACTTTTATTGGTGACGACCAAATTTATAATTTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTAATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTGATATTAGGAGCACCAGCTATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTCCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607170 Chironominae sp. water mite diet isolate 6232-BHL032417-GBD25154_23946-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTACTTTATTTTTTATTTTTGGAGCCTGATCAGGAATAGTTGGACCTTCTTTAAGATTTCTAATTCGAGCAGATTTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607171 Chironominae sp. water mite diet isolate 6234-BHL032417-GBD19472_5989-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATACTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCATGGAACTTTCATTGGTGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAAGTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTCTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607172 Chironominae sp. water mite diet isolate 6236-BHL032417-GBD4339_14569-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTTATTCGAGCAGAATTAGGACATCCTGGAACTTTTATAGGTGACGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGATATAGCATTTCCTCAAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCAATTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607173 Chironominae sp. water mite diet isolate 6239-BHL032417-GBD25361_23970-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGATCTTTTATTGGTGACGATCAAATTTATAATGTTATTGTTACAGCTCATGCCTTTATTATAATTTTTTTATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTCCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTTTACTACTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607174 Chironominae sp. water mite diet isolate 6240-BHL032417-GBD13734_27747-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGATCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCCTCTTTATCTCTTCTTCTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607175 Chironominae sp. water mite diet isolate 6244-BHL032417-GBD20787_11344-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATGTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACAACCCGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCATCTGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607176 Chironominae sp. water mite diet isolate 6245-BHL032417-GBD24304_4437-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTATAAGAATTCTAATTCGAGCAGAATTAGGTCATACTGGATCTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTACTACTTTCTAGTTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607177 Chironominae sp. water mite diet isolate 6249-BHL032417-GBD8959_4147-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGGTCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGTCCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607178 Chironominae sp. water mite diet isolate 6252-BHL032417-GBD25586_9000-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTATTTCCTTTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTACTCCCCCCCTCTTTAACTCTTCTTCTATCTAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607179 Chironominae sp. water mite diet isolate 6254-BHL032417-GBD25043_7080-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGATCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATACTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGATTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCAAGTAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607180 Chironominae sp. water mite diet isolate 6256-BHL032417-GBD16638_23742-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTTGGTACTTCTTTAAGAATTCTAATTCGAGCAGAATTCGGACATCCTGGATCTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCCTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTACTACAATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607181 Chironominae sp. water mite diet isolate 6257-BHL032417-GBD17374_26305-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGGGCCTGATCCGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGACTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCCTCTTTATCTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607182 Chironominae sp. water mite diet isolate 6263-BHL032417-GBD12326_2567-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTCGGACATCCTGGAACTTTTATTGGTGACGACCAATTTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCCCCAGATAAAGCATTCCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAATTCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607183 Chironominae sp. water mite diet isolate 6265-BHL032417-GBD25713_12430-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGTATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATTCCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATAAAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTATCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607184 Chironominae sp. water mite diet isolate 6269-BHL032417-GBD17228_2867-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAGGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTTAAATGTTATTGGAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTAGTGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607185 Chironominae sp. water mite diet isolate 6271-BHL032417-GBD26421_14871-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGCACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGATCTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTACTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCGCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCATTATCTCTACTTCTATCTTGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607186 Chironominae sp. water mite diet isolate 6273-BHL032417-GBD12639_12500-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTACATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGACCAAAATTAGGACATCCTGGAACTTTTATTGATGACGACCAAATTTATAATGTTACTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCGGATATAGCGTTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607187 Chironominae sp. water mite diet isolate 6276-BHL032417-GBD20674_2647-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGTACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGATCTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTGATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCATATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCATTATCTCTACTACTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607188 Chironominae sp. water mite diet isolate 6277-BHL032417-GBD28111_12463-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAGTTCTAATTCGAGCAGAATTAGGTCATCCTGGAACTCTTATTAGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGTACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTTTTCCTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607189 Chironominae sp. water mite diet isolate 6278-BHL032417-GBD4580_13788-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGACCAGAATTAGGTCATCCTGGATCTTTTATCGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATAGCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCGTCATTAACTCTTCTTCTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607190 Chironominae sp. water mite diet isolate 6281-BHL032417-GBD19564_21307-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCTTGATCAGGAATAGTGGGAACTTCTTTAAGAATGCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGTATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCCCTTCTTCTATCTAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607191 Chironominae sp. water mite diet isolate 6282-BHL032417-GBD7763_5888-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTTTATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATACTGGATCTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAATTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTACCCCCTTCATTAACTCTACTACTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607192 Chironominae sp. water mite diet isolate 6283-BHL032417-GBD29580_16095-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGATCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATAATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTCTGATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607193 Chironominae sp. water mite diet isolate 6285-BHL032417-GBD21778_22252-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATCTTTGGAGCCTGATCAGGAATAGTTGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTCTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTGTCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607194 Chironominae sp. water mite diet isolate 6286-BHL032417-GBD21545_25554-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGTACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATCCTGGATCTTTTATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCTTTAACTCTACTACTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607195 Chironominae sp. water mite diet isolate 6292-BHL032417-GBD21906_26559-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTATTTAAGAATTTTAATTCGAGTAGAATTAGGACATCCAGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATAATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCTGATATAGCATTTCCTCAAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607196 Chironominae sp. water mite diet isolate 6293-BHL032417-GBD3577_14285-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACATTATATTTCATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATATTAATTTGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607197 Chironominae sp. water mite diet isolate 6295-BHL032417-GBD17441_3992-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACAGCCTGGAACTTTTATTGGTGACGACCATATTTATAATGTTATTGTAACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATAACCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTACATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTCTTGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607198 Chironominae sp. water mite diet isolate 6296-BHL032417-GBD27543_10818-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGAAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACCTCCCCCTTCATTAACTCTTCTTCTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607199 Chironominae sp. water mite diet isolate 6299-BHL032417-GBD25698_17580-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCTTTAAGTATTCTAATTCGAGCAGAATTTGGACATCCTGGTACTTTTATTGGTGACGACCAAATTTACAATGTAATTGTAACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCATTAACTCTTCTACTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607200 Chironominae sp. water mite diet isolate 6300-BHL032417-GBD7040_13784-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGTTGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAACTTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGACTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTCCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACCCTACAACTTTCTAGTGCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607201 Chironominae sp. water mite diet isolate 6301-BHL032417-GBD22008_13197-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAAAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTAGATATCTTCTTCTGACTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607202 Chironominae sp. water mite diet isolate 6302-BHL032417-GBD10575_3082-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGCACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGCTCTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTGATATTAGAAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTACCCCCTTCATTAACCCTTCTTCTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607203 Chironominae sp. water mite diet isolate 6303-BHL032417-GBD3641_17558-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATCTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTTAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATGTCCTCGAATAAATAATATAAGATACTGATTACTTCCCCCTTCTTCATCTCTTCATCTGTCTAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607204 Chironominae sp. water mite diet isolate 6304-BHL032417-GBD17215_28237-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACTTTATATTTTATTTTTGGAGCCTGGTCAGGAATAATTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGGCATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCCGATATAGCTTTTCCTCGAATAAATAACATAAGATTCTGATTACTTCCCCCTTCTTTATCCCTTCTTCTATCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607205 Chironominae sp. water mite diet isolate 6306-BHL032417-GBD13773_9808-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGATCACGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTTGGGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCAAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTGTAACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607206 Chironominae sp. water mite diet isolate 6307-BHL032417-GBD22642_18754-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGACATCCTGGCACTTTTATTGGTGGCGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTACTTTCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607207 Chironominae sp. water mite diet isolate 6308-BHL032417-GBD9238_15375-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAGTTCGAGCAGAATTAGGACATCCTGGTTCTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTTTTCTACTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607208 Chironominae sp. water mite diet isolate 6311-BHL032417-GBD24967_13451-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTCGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCCAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607209 Chironominae sp. water mite diet isolate 6313-BHL032417-GBD2687_10460-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTGAATTTTTGGAGACTGATCAGGAATAGTGGGAACTTCTTGAAGAATTCTACTTCGAGTAGAATTAGGATATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATCGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCTGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607210 Chironominae sp. water mite diet isolate 6314-BHL032417-GBD27548_11404-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGAATTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATAAAGCATTTCCTCGAATAAAAAAAAAAAAAATTCTGATTACTTCCCCCTTCTTTAACTCTACTTCTTTCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607211 Chironominae sp. water mite diet isolate 6316-BHL032417-GBD10631_9448-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTTTTTAAGAATTTTAATTCGAGCAGAATTAGGACCTCCTGGTACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAGTTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCGTCTTTATCTCTACTACTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607212 Chironominae sp. water mite diet isolate 6317-BHL032417-GBD9217_4322-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACATTACATTTTATTTTCGGAGCCTGATCTGGAATAGTTGGAACTTCTCTAAGTATTTTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607213 Chironominae sp. water mite diet isolate 6318-BHL032417-GBD27590_14549-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACCTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACAACCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCCCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTA-ACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607214 Chironominae sp. water mite diet isolate 6319-BHL032417-GBD27851_11955-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCAGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607215 Chironominae sp. water mite diet isolate 6320-BHL032417-GBD21155_3562-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGAAGAATTAGGACATCCTGGAACTTTTATTGTTGACGACCAAATGTATGATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAGATTGATTAGTTCCTCTTATATTAGGAGTACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAATTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607216 Chironominae sp. water mite diet isolate 6321-BHL032417-GBD14672_26755-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607217 Chironominae sp. water mite diet isolate 6322-BHL032417-GBD16089_3568-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGTACATCCTGGAACTTTTATTGGTGACGTCCATATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACACCTTTTAATTGCAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607218 Chironominae sp. water mite diet isolate 6324-BHL032417-GBD24101_18851-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGTTTTTTTATGGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCTCTTCTTTAACTCTACTTCTATCTAGTTCTATTGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607219 Chironominae sp. water mite diet isolate 6325-BHL032417-GBD10342_19528-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAAAATTGGGACATCCTGGAACTTTTATTGATGACGACCAAATTTGTAATGTTATTGTAACAGCTCATGTTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCACTTCCTCGAATAAATAATATAAGATTCTGATTGCTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTTTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607220 Chironominae sp. water mite diet isolate 6326-BHL032417-GBD28241_17946-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGTACTTCTTTATGAATTTTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTACGTTATCTCTTCTTCTTTCTAGTTCTAGTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607221 Chironominae sp. water mite diet isolate 6327-BHL032417-GBD6537_6419-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGTAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAACTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGTATCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACATCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGGAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607222 Chironominae sp. water mite diet isolate 6328-BHL032417-GBD10159_6768-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTCATTCAAGCAGAATTAGGACATCCTGGAACTTTTATTGGTTACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATCTTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCGTCTTCTTTCTAGTTCTATTGTAGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607223 Chironominae sp. water mite diet isolate 6329-BHL032417-GBD7547_10754-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACCCTGGTTCTTTAATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCGTCTTTATCTCTACTACTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607224 Chironominae sp. water mite diet isolate 6330-BHL032417-GBD11999_11229-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTGGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGAAGGATTTGGAAATTGATTAGTTCCCCTTATATTAGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGATTTCTTCCCCCCTCTTTATCTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607225 Chironominae sp. water mite diet isolate 6331-BHL032417-GBD5252_20922-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTCGGACATCCTGGTACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCCATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCACTTCCCCGAATAAATAATATAAGATTCTGATTACTTCCCCCGTCTTTAACTCTACTACTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607226 Chironominae sp. water mite diet isolate 6333-BHL032417-GBD12597_22094-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATCGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGTTGACGACCAAATTTATGATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACGTCCCCCTTCTTTAACACTTCTTCAATCTAGTGCTAGAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607227 Chironominae sp. water mite diet isolate 6334-BHL032417-GBD20696_20596-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTTTATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGATCTTTTATTGGTGACGACCAAATTTATATTGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCATCTTTATATCTACTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607228 Chironominae sp. water mite diet isolate 6336-BHL032417-GBD5873_25082-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGAAGAACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCGATCTAGGTCTATTGTAGAAAATGGCGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607229 Chironominae sp. water mite diet isolate 6337-BHL032417-GBD12680_25669-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAATTGGAACTTCCTTAAGAATTTTAATTCGAGCAGAATTAGGACACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCCCTTCTTCTATCTAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607230 Chironominae sp. water mite diet isolate 6338-BHL032417-GBD27435_18960-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGGGCCTGATCAGGAATAGTTGGAACTTCTTTAAGGATTCTAATTCGAGCAGAATTAGGACATCATGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGACATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATATCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607231 Chironominae sp. water mite diet isolate 6339-BHL032417-GBD23503_5617-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTAGATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCATATATTAGGAGCACCAGATATGGCGTTTCCTCGAATAAATAATATAAGATTCTGATTACGTCCCCCTTCTTTATCTCATCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607232 Chironominae sp. water mite diet isolate 6341-BHL032417-GBD20417_25327-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAAAATTAGGACATCCTGGAACATTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTATCATAGTTATACCCATTCTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACCCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607233 Chironominae sp. water mite diet isolate 6346-BHL032417-GBD20600_3065-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATATCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGTATAAATAATATAAGGTTCTGATTACTACCCCCTTCTTTAACTCTTCTTCTGTCTAGTTCTACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607234 Chironominae sp. water mite diet isolate 6347-BHL032417-GBD12892_15613-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAACTAGGACATCCTGGAACTTTTATTGATGACGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTCTAACTCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607235 Chironominae sp. water mite diet isolate 6349-BHL032417-GBD24501_10094-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTATGACAACCAGGAACTTTTATTGGTGAAGACCAAATATATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTACTACTTTCTAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607236 Chironominae sp. water mite diet isolate 6352-BHL032417-GBD19571_21123-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACATTATATTTTATTTTTGGAGTCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAACAAATAATATAAGATTCTGATTACTTCCCCCTGCTTTAACTCTTCTTCTTGCTAGTGCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607237 Chironominae sp. water mite diet isolate 6353-BHL032417-GBD25930_9999-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGTATTCTAATTCGAGCAGAATTAGGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCACGAATAAATAATATAAGATTCTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607238 Chironominae sp. water mite diet isolate 6354-BHL032417-GBD4319_9773-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTATTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATGAGATTCTGATTACTTCCCCCCTCTTTAACTCTTCTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607239 Chironominae sp. water mite diet isolate 6355-BHL032417-GBD5263_12894-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACATCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTATTACCCCCATATCTTACTCTACTTCTTTCAAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607240 Chironominae sp. water mite diet isolate 6359-BHL032417-GBD9999_6863-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTATTTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATCTCCTCGAATAAACAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607241 Chironominae sp. water mite diet isolate 6360-BHL032417-GBD5006_12549-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGGGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTTATTCGAGCAGAATTAGGACATCCTGGAACCTTTATTGGTGACGACCAAATTTATAATGTTGTTGTAACTGCTCATGCTTTTATTATAATTTTTTTCACAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTCTATCTCTTCATCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607242 Chironominae sp. water mite diet isolate 6361-BHL032417-GBD4362_13585-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGTAGAATTAGGACAACCTGGCACTTTTCTTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATATTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAAGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTACTTCTATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607243 Chironominae sp. water mite diet isolate 6363-BHL032417-GBD25893_10945-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGTCATCCTGGAACTTTTATTGGTGACGGCCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATCTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTACTTCTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607244 Chironominae sp. water mite diet isolate 6364-BHL032417-GBD24111_6321-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGTAGCCTGATCAGGAATAGGTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTGTAATTGGAGGATATGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCGTCTTCTATCTAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607245 Chironominae sp. water mite diet isolate 6367-BHL032417-GBD23788_25394-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTCTTATAATTTTTTTCATAGTTATACCCATGTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTGTATCTCTTCTACTTGCTAGTTCGAGTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607246 Chironominae sp. water mite diet isolate 6368-BHL032417-GBD4542_12725-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTTATATTTGGAGCACCAGACATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCTTCTCTAACGCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607247 Chironominae sp. water mite diet isolate 6369-BHL032417-GBD25273_9840-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCAGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATATTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAAAAAATAATATAAGAGTTTGATTATTACCACCAACTCTTACTTTATTACTTACAAAAAGAATATTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607248 Chironominae sp. water mite diet isolate 6371-BHL032417-GBD5939_15579-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGTGACGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCGCGAATAAACAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607249 Chironominae sp. water mite diet isolate 6372-BHL032417-GBD6056_25173-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCCCCAGATATAGCATTTTCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTCCTTTACCCCTCCTCCTTTCTAGTCCTATTGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607250 Chironominae sp. water mite diet isolate 6375-BHL032417-GBD29082_16530-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTTTTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATGTGGAAATTGATTAGTTCCTCTAATATCAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTGCATTAACTGTACTACTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607251 Chironominae sp. water mite diet isolate 6376-BHL032417-GBD6295_22017-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTTTTTTGGAGTCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAACTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTACTTCTTTCTAGTAGAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607252 Chironominae sp. water mite diet isolate 6378-BHL032417-GBD7748_5903-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACACCCTGGAACTTTTATTGGAGAAGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAATTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACCCTTCTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607253 Chironominae sp. water mite diet isolate 6379-BHL032417-GBD17443_9655-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGAGCCTGATCAGGCATAGTTGGCACTTCTTTAAGATTTCTAATTCGAGCAGAATTCGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCGCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCGTCATTAACTCTACTACTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607254 Chironominae sp. water mite diet isolate 6380-BHL032417-GBD29639_16646-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAGTTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTGTACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTGTAGCGCGGCGTCTTGCTAATTCTATTGTAGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607255 Chironominae sp. water mite diet isolate 6382-BHL032417-GBD20433_20226-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATCCTGGAATTTTTATTGGTGACGACCAAATTTATAATGTTAATGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGTACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTACTTCTTTCTAGATCTATTGTAGAAAATGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607256 Chironominae sp. water mite diet isolate 6383-BHL032417-GBD19338_22043-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCTGGAATAGTTGGTACTTCTTTAAGTATTCTAATTCGAGCAGAATTAGGACATCCTGGTACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTTATTATCTCTTCTTCCTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607257 Chironominae sp. water mite diet isolate 6384-BHL032417-GBD6194_23605-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGAAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTATATAACTCATCTTCTTACTAGTTCAATTGTAGAAAATGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607258 Chironominae sp. water mite diet isolate 6386-BHL032417-GBD8939_27048-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTATGACATCCTGGAACCTTTATTGGTGACGATCAAATTTATAATGTTCTTGTAACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTACTTTCTAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607259 Chironominae sp. water mite diet isolate 6387-BHL032417-GBD12701_23398-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAAGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGTCATCCTGGTACTTTTATTGGTGACGATCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCTGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCATTAACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607260 Chironominae sp. water mite diet isolate 6389-BHL032417-GBD28323_17650-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCACTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCTCCCTTCTCTATCACTACTTCTTTCTAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607261 Chironominae sp. water mite diet isolate 6390-BHL032417-GBD7484_8235-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTGGGAGCACCAGATAAAGCCTTTCCTCCAATAAAAAATAAAAGATTCTGATTACTTCCCCCCTCTTTATCTCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607262 Chironominae sp. water mite diet isolate 6392-BHL032417-GBD5271_7226-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGCGCTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAATAAAAGATTCTGATTACATCCCCCTTCTTTAACTCTACTTCTTTCTAGTGCTATTGTAGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607263 Chironominae sp. water mite diet isolate 6394-BHL032417-GBD18503_7585-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGATCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGAAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCTTCTTTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607264 Chironominae sp. water mite diet isolate 6395-BHL032417-GBD23348_4977-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTAGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGTAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTATTATAACTTTTTTCATAGTTATACCCATATTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCATCTTCTTTCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607265 Chironominae sp. water mite diet isolate 6396-BHL032417-GBD27056_11593-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACATTTATTGGTGACGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTACTATAATTTTTTTCATAGTTATACCCATTTTAATTGGGGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTATTGCCCCCTTCTTTATCTCTACTACTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607266 Chironominae sp. water mite diet isolate 6397-BHL032417-GBD9430_10848-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGGACTTCTTTAAGAATTCTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTTTACCCATTTTAATTGGAGGATTTGGAAATTGATTAATTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTCCTTTATCTCTTCTTCTTTCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607267 Chironominae sp. water mite diet isolate 6398-BHL032417-GBD20009_27300-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTCTATTGGAGACGACCAAATTTATAATATTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCGTCTTTAACTCTACTACTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607268 Chironominae sp. water mite diet isolate 6400-BHL032417-GBD24935_23836-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTAACTCTATTACTTTCAAGGTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607269 Chironominae sp. water mite diet isolate 6406-BHL032417-GBD25007_25759-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGGACTTCGTTAAGAATACTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGACATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCTTCTTTAACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607270 Chironominae sp. water mite diet isolate 6408-BHL032417-GBD3104_18017-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTATTTAAGAATTCTAATTCGAGCAGAATTAGGATATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTCACAGCTCATGCTTTTATTATAATTTTTTTCATAGTCATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAATATTCTGATTGCTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607271 Chironominae sp. water mite diet isolate 6409-BHL032417-GBD5014_18142-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCCCGAATAAAAAAAAAAAAGATTCTGATCACTTCCCCCTCCTTCATCCCCTCCTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607272 Chironominae sp. water mite diet isolate 6410-BHL032417-GBD23520_24576-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGTATTCTAATTCGAGCAGAATTAGGACATCCCGGAACTTTTATTGGTGACGACCAATTTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGAATACTTCCCCCTTCATTAACACTACTTCTGTCTAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607273 Chironominae sp. water mite diet isolate 6411-BHL032417-GBD13353_2166-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGCATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTACAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTGATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAATTCTATTCTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607274 Chironominae sp. water mite diet isolate 6412-BHL032417-GBD28114_21547-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCTTGACCAGGAATAGTTGGAACTTCTTTAAGAATACTAATTCGAGCAGAATTAGGACATCCTGAAACTTTTAGTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAGTATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607275 Chironominae sp. water mite diet isolate 6413-BHL032417-GBD28905_15021-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTATGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTACCTTATCTCATCCTCTTACTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607276 Chironominae sp. water mite diet isolate 6415-BHL032417-GBD24679_18027-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATACTAATTCGAGCTGAATTAGGCCAACCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTAGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTACTTTCTAATTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607277 Chironominae sp. water mite diet isolate 6416-BHL032417-GBD2322_16216-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATCCTGGATCTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCTGATATAGCATTCCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTATTACTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607278 Chironominae sp. water mite diet isolate 6417-BHL032417-GBD13265_5598-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACACTATATTTTATTTTTGGAGCATGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACAACCAGGAACTTTTATTGGTGACGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTACTTTCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607279 Chironominae sp. water mite diet isolate 6418-BHL032417-GBD5180_9125-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAATTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTACCCCTTCTTCTTTCAAGTTCTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607280 Chironominae sp. water mite diet isolate 6420-BHL032417-GBD22627_20316-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGAAGGATTTGGAAATTGATTGGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTACGTCCCCCTTCTTTAACTCGGCTTCGTTCTAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607281 Chironominae sp. water mite diet isolate 6422-BHL032417-GBD24893_20222-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCTTGATCGGGAATAGTTGGAACTTCTTTAAGAATATTAATTCGAGCAGAATTAGGACATCCTGGACCTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607282 Chironominae sp. water mite diet isolate 6423-BHL032417-GBD24753_14106-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGTACTTCTTTAAGTATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATATCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCTCTATCTCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607283 Chironominae sp. water mite diet isolate 6425-BHL032417-GBD18237_4351-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATACTAATTCGAGCAGAATTAGGACATCCTGTAACATTTATTGGAGACGACCAAATTTATAATGGAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCCTTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607284 Chironominae sp. water mite diet isolate 6427-BHL032417-GBD22084_16422-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATTCTAATTCGAGCAGAACTAGGACATCCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACAGATCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607285 Chironominae sp. water mite diet isolate 6428-BHL032417-GBD21040_27331-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCATGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATGCCCATTTTAATTGGAAGATTTGGAAATTGATTAGTTTCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAAAATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607286 Chironominae sp. water mite diet isolate 6430-BHL032417-GBD22932_23613-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGCATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGTCATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATACTTTTTTTCATAGTTATACACATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCATCTACTTTCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607287 Chironominae sp. water mite diet isolate 6432-BHL032417-GBD24288_23866-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTGATTCGAGCAGAATTAGGACAACCTGGAACCTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTTATACTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTACCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607288 Chironominae sp. water mite diet isolate 6433-BHL032417-GBD18701_20842-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGTCTGATCAGGAATAGTTGGAACTTCTTTTAGAATTCTAATTCGAGCAGAATTAGGACAACCTGGAACTTTCATTGGTGACGAGCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTACCCCCTTCTTTAACTCTACTACTTTCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607289 Chironominae sp. water mite diet isolate 6434-BHL032417-GBD21075_12260-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATATTTGGAACTTCTTTTAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTCTTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAGTATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCTCTTCTTTAACTCTTCTTCTTTCTAGTGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607290 Chironominae sp. water mite diet isolate 6435-BHL032417-GBD9792_7809-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGTGCCTGATCTGGTATAGTTGGAACTTCTTTAAGAATTCTTATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCATCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCCCTACTACCATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607291 Chironominae sp. water mite diet isolate 6436-BHL032417-GBD12296_25249-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCAAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTGACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607292 Chironominae sp. water mite diet isolate 6437-BHL032417-GBD5831_19870-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGAGCAGGAATAGTTGGAACTGCTTTAAGAATACTAATTCGAGTAGAATTAGTACATCCAGGAACTTTTATTGGTGACGACCAATTTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGACTAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607293 Chironominae sp. water mite diet isolate 6438-BHL032417-GBD10568_14657-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAGCTTCTTTAAGAATTCTAATTCGAGCAGCTTTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTCTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATACAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAGCTCGACATCTGTCTAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607294 Chironominae sp. water mite diet isolate 6440-BHL032417-GBD24642_16221-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATCCTAATTCGAGCAGAATTAGGACATCCTGGAACATTAATTGGAGATGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607295 Chironominae sp. water mite diet isolate 6441-BHL032417-GBD11289_15430-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTATGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATATTAATCCGAACGGGATTAGGTCATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607296 Chironominae sp. water mite diet isolate 6442-BHL032417-GBD21173_21008-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGATCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGGGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCCGATTACTCCCCCCTTCTTGATCTCTTCTACTATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607297 Chironominae sp. water mite diet isolate 6443-BHL032417-GBD8150_15092-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGTATTCTTATTCGAGCAGAATTAGGTCAACCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTTTTTGTAACAGCTCATGCTTTTATTATAATTTTATTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTCTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607298 Chironominae sp. water mite diet isolate 6444-BHL032417-GBD22676_20232-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGAAACTTTTAGTGGTGACAACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTCTTATATTAGGAGCATTAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607299 Chironominae sp. water mite diet isolate 6446-BHL032417-GBD2166_13457-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTGTATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCCCCAGATACAGCTTTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTCGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607300 Chironominae sp. water mite diet isolate 6447-BHL032417-GBD7100_11005-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTTAGAATTATAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTCTTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTAATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAACATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCACCTTCTTTAACCCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607301 Chironominae sp. water mite diet isolate 6449-BHL032417-GBD12241_13501-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGTCTGATCAGGAATAGTTGGAACTTCATTGAGAATGCTTATTCGAGCAGAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTAATATAATTTTTTTCATAGTTATACCAGTTTTATATGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607302 Chironominae sp. water mite diet isolate 6450-BHL032417-GBD10246_5793-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTTAGAATTTTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTGTTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATGGCATTCCCTCGAATAAATAATATAAGATTCTGATTTCTTCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607303 Chironominae sp. water mite diet isolate 6451-BHL032417-GBD27471_19042-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTTTTTTTGGAGCCTGATCAGGAATAGGTGGAACTTCTTTAAGAATTCTAATTCGCGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGTTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTGATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGGGTAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCGTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607304 Chironominae sp. water mite diet isolate 6452-BHL032417-GBD20298_25068-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTCGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATATCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCATCATTAACTCTACTACTATCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607305 Chironominae sp. water mite diet isolate 6454-BHL032417-GBD4826_18376-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATCGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607306 Chironominae sp. water mite diet isolate 6461-BHL032417-GBD24860_14388-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTCATTTTTGGAGCCTGATCAGGAATAGTGGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATCCTGGAATTTTTATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTTTACTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607307 Chironominae sp. water mite diet isolate 6462-BHL032417-GBD15157_12808-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTTTATTTTATTTTTGGAGCCTTATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATCTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTGCCCCCTTCATTAACGTTACTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607308 Chironominae sp. water mite diet isolate 6464-BHL032417-GBD7451_18491-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGGACTTCTTTAAGAATACTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTTCTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607309 Chironominae sp. water mite diet isolate 6465-BHL032417-GBD19134_5849-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAAGGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 93.4% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607310 Chironominae sp. water mite diet isolate 6467-BHL032417-GBD28331_9397-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCCGGAACTTTTATTGGTGACGACCAATTTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCGTCTTTAACTCTTTTACTATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607311 Chironominae sp. water mite diet isolate 6469-BHL032417-GBD20921_23909-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAACAGTTGGAACTTCTTTAAGAATTCTAATTAGAGCAGAACTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATGATGTTATTGTAACAGCTCATGCTTTTATTATAACTTTTTTCATAGTTATACCCATTTTAGTTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATATTATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607312 Chironominae sp. water mite diet isolate 6470-BHL032417-GBD26895_11689-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTTAGAATATTAATTCGAGTAGGATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGTACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTACTACTTTCTAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607313 Chironominae sp. water mite diet isolate 6471-BHL032417-GBD9207_12444-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGTATTCTAATTCGAGCAAAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAACATAAGATTCTGATTACTTCCCCCTTCTTTATCCCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607314 Chironominae sp. water mite diet isolate 6475-BHL032417-GBD15284_2443-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGAAGCCTGATCAGTAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTTGAACTTTTATTGGTGACGACCAAATTTATAATGGTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTTGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACCTCCCCCTTCTTTATCTCTTCTTCTTTCTAATTCTATTGTCGAAAATGGAGCTGGACCAG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607315 Chironominae sp. water mite diet isolate 6478-BHL032417-GBD16172_9829-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTTTAAGAATTCTTATTCGAGCTGAATTAGGACGTCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACGGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGTGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCCTCTTTGACTCTTCTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607316 Chironominae sp. water mite diet isolate 6481-BHL032417-GBD16647_26495-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGACTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGAAATCCTGGAACTTTTATTGGTGACGACCCAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTTGAGGATTTTGAAATTGATTAGTTACTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTTGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607317 Chironominae sp. water mite diet isolate 6484-BHL032417-GBD10712_23540-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGTCTGATCAGGAATAGTTGGAACTTCTTTTAGAATTCTAATTCGAGTTGAATTGTGACATCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGCTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607318 Chironominae sp. water mite diet isolate 6485-BHL032417-GBD25765_11545-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTCATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGTATTCTAATTAGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGTACCAGATATAGTATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607319 Chironominae sp. water mite diet isolate 6487-BHL032417-GBD3057_10669-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGCCTAAATCATATAAGATTCTGATTCCTTCCCCCTTCTTTCTCTCTTCTTCTTTCTTGTTCTTTTGT	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607320 Chironominae sp. water mite diet isolate 6488-BHL032417-GBD19368_24231-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTGTATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCAAGCAGAATTAGGACATCCTGGAACTTTTATTTGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCAGCCTCTTTCTAGTACGAGAGTAGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607321 Chironominae sp. water mite diet isolate 6489-BHL032417-GBD10691_18842-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGTAGAATTAGGACATCCAGGATTTTTCATTGGTGACGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATAATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACCCTACTTCTTTCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607322 Chironominae sp. water mite diet isolate 6490-BHL032417-GBD10601_4294-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCATTTTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAATTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCCCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCGCCTTCTTTCTAGTGCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607323 Chironominae sp. water mite diet isolate 6491-BHL032417-GBD7743_6060-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTCTATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATAGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATTCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATGTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCTTTCTTTATCTCTGCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607324 Chironominae sp. water mite diet isolate 6492-BHL032417-GBD23300_26283-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCCGGAATAGTTGGAACTTCTTTAAGAATTCTTTTTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTAATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATCTCCTCGAATAAATAATATAAGATTCTGATTACTACCCCCCTCTCTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607325 Chironominae sp. water mite diet isolate 6493-BHL032417-GBD7564_5526-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTATTTTTGGATCCTGATCTGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTAATACCCATTCTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATACTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACACTACTACTATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607326 Chironominae sp. water mite diet isolate 6494-BHL032417-GBD23322_26020-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACACTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCTAGCAGAATTAGGACATCCTGGATCTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTAATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607327 Chironominae sp. water mite diet isolate 6496-BHL032417-GBD24031_17690-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACGGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCCATTTTAATTGGGGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTACTACTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607328 Chironominae sp. water mite diet isolate 6497-BHL032417-GBD2051_17397-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGCTTATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAACAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607329 Chironominae sp. water mite diet isolate 6499-BHL032417-GBD27864_18893-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGGACTTTTATTGATGATGACCAAATTTATAATGTTATTGTACCAGCTCATGTTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAAGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607330 Chironominae sp. water mite diet isolate 6500-BHL032417-GBD23380_18472-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTAATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTGATATTAGGAGCACCGGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTACCCCCTTCATTAACCCTACTTCTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607331 Chironominae sp. water mite diet isolate 6502-BHL032417-GBD18978_2556-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGACACCCTGGTACTTTTATCGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATAATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607332 Chironominae sp. water mite diet isolate 6503-BHL032417-GBD26134_14649-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATTTTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCTGAATTATGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCTTCTTTAACCCTACTACTTTCTAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607333 Chironominae sp. water mite diet isolate 6504-BHL032417-GBD26241_22468-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTATGAATTCTAATTCGAGCAGTATTAGGACATCATGGAACTTTTATTGGTGACGACCAAATTTACAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTACTTGCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607334 Chironominae sp. water mite diet isolate 6506-BHL032417-GBD21495_4670-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACCTTTATTGGTGACGACCAAATTTATATTGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACATCCCCCTTCTATATCTCTGCGTCGTACTAGGACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607335 Chironominae sp. water mite diet isolate 6507-BHL032417-GBD14381_18650-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGGGCTTGATCGGGAATAGTGGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGTACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTATGATTAGTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607336 Chironominae sp. water mite diet isolate 6511-BHL032417-GBD8321_13899-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTCGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTCTTATTCGAGCAGAATTAGGACAACCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGATATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTTCTTCCCCCTTCTTTGACTCTTCTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607337 Chironominae sp. water mite diet isolate 6512-BHL032417-GBD17814_24126-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTCGGACATCCTGGTATGTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATATCCATTTTAATTGGAGGATTTGGAAATTGATTAATTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTACTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607338 Chironominae sp. water mite diet isolate 6514-BHL032417-GBD18051_11710-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTCGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTCATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCTTCGAATAAATAATATAAGATTCTGATTACTTCCCCCGTCTTTAAATCTACTTCTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607339 Chironominae sp. water mite diet isolate 6515-BHL032417-GBD14404_7014-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTTGGCACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGTTCTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAAAAATATAAGATTCTGATTACTTCCCCCGTCATTATCTCTTCTTCTATCTAATTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607340 Chironominae sp. water mite diet isolate 6516-BHL032417-GBD17304_2647-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCATATTTATAATGGTATTGTAACAGCGCATGCCTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATGGGAGGATTTGGAGATTGATTAGTTCCTCTTATATTAGGAGCACAAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607341 Chironominae sp. water mite diet isolate 6517-BHL032417-GBD23287_25331-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATACTTGTAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTAGTGACGACCAAATTTATATTGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATATCTTCTTCGTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607342 Chironominae sp. water mite diet isolate 6518-BHL032417-GBD8443_25181-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACGGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTATTTCCCCCTTCTTTAACTCTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607343 Chironominae sp. water mite diet isolate 6520-BHL032417-GBD24307_15754-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTCTATTTTATTTTTGGAGCATGATCAGGAATAGTTGGAACTTCTTTAAGTCTTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCTCCCTTCTTTATCTCTGCTTCTTTCGAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607344 Chironominae sp. water mite diet isolate 6521-BHL032417-GBD19031_10828-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATGATGTTATTGTAACAGCTCAAGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAAGAATTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATTACCTTTCCTCGAATAAATAAAAAAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607345 Chironominae sp. water mite diet isolate 6522-BHL032417-GBD21974_12963-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATACTTATTCGAGCAGAGTTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAGTTTTTTTCATAGTTACACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTCTATCTCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607346 Chironominae sp. water mite diet isolate 6524-BHL032417-GBD2417_16841-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATTCTGGTTCTTTAATTGGTGACGATCATATTTATAATGTTATTGTAATAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCAGATATAGCATTCCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTATTACTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607347 Chironominae sp. water mite diet isolate 6525-BHL032417-GBD13797_24254-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAAGATTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGTCATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTATGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607348 Chironominae sp. water mite diet isolate 6526-BHL032417-GBD18380_5272-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTTTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACTACCAAATTTATATTGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTTATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTGGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607349 Chironominae sp. water mite diet isolate 6527-BHL032417-GBD6314_24370-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCAAATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGTCTTTTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATATTAGGAGCACCAGATATAGCATTTCATCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTGCTAGTTCGATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607350 Chironominae sp. water mite diet isolate 6528-BHL032417-GBD21823_22520-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTACTATCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607351 Chironominae sp. water mite diet isolate 6529-BHL032417-GBD21925_4088-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGAAACTTCTTTAGGAATTCTAATTCGAGCAGAATTCGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCGTCTTTATCTCTTCTACTATCTGGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607352 Chironominae sp. water mite diet isolate 6532-BHL032417-GBD18944_27869-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTAACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCGTCTTTCTAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607353 Chironominae sp. water mite diet isolate 6533-BHL032417-GBD22494_9913-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTTGGAACTTCTATAAGAATTTTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGTTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAGCTCTACTTCTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607354 Chironominae sp. water mite diet isolate 6535-BHL032417-GBD26163_23251-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTGGGAACTTCATTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTAATAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607355 Chironominae sp. water mite diet isolate 6536-BHL032417-GBD6646_15744-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGCTTTAGTACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTAGAGGATTTGGAAATTGATCAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATACTGATTACTTCCCCCTTCTTTATCACTACTGCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607356 Chironominae sp. water mite diet isolate 6538-BHL032417-GBD26594_17094-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGTATTCTAATTCGAGCATATTTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACATCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGAGTCTGATTACTTCCCCCTTCTTTATCTCAGCTACTTTCTAGTACTAGAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607357 Chironominae sp. water mite diet isolate 6540-BHL032417-GBD13484_4625-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGACCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGTCCTAATTTATAATGTTATGGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATAACCATTTTAATTGGAGGATTTGGAAATTGATTTGTTCATCTTATATTAGGAGCACAAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607358 Chironominae sp. water mite diet isolate 6541-BHL032417-GBD16501_4569-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGTAACTTTTAATGGTGACGACCATTTTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTTGAAATTGATTAGTTCCTCTTATATTAGGAGCCCAAGATATAGCATTTCCTCTAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607359 Chironominae sp. water mite diet isolate 6542-BHL032417-GBD15733_3665-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATACTAATTCGAGCAGAACTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTGCCTCTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTTTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607360 Chironominae sp. water mite diet isolate 6543-BHL032417-GBD15278_2765-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGTAACTTTTATTGGGGACGACCATATTTATAATGGTATTGGAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTGATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTCCTTTATCTCTTCTTCTTTCTAGTTCCATTGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607361 Chironominae sp. water mite diet isolate 6549-BHL032417-GBD9876_17675-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATACTTTATTTTTGGAGCCTGATCAGGAATAGTGGGAACTTCTTTAAGAATTCTTATTCGAGCAGAATTAGGACAACCCGGAACTTTCATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTATTTCCCCCTTCTCTAACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607362 Chironominae sp. water mite diet isolate 6551-BHL032417-GBD4578_11625-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGAGCCTGATCAGGAATAATTGGAACTTCTTTAAGAACTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTGTATTGGTGACGACCAAGTTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCACTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607363 Chironominae sp. water mite diet isolate 6552-BHL032417-GBD26033_18855-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGTTGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGCTATTGTAACAGCTCATGCTTTTATTATAATTTTTCTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTCCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607364 Chironominae sp. water mite diet isolate 6553-BHL032417-GBD4327_8567-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGTCCAGGAATAGTTGGAACTTATTTAAGAATTCTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTACTGTATCTCTGCTTCTTGCTAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607365 Chironominae sp. water mite diet isolate 6555-BHL032417-GBD21083_3122-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGTCATCCTGGATCTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTAATATTAGGAGCACCAGATATAGCATTTCCACGAATAAATAATATAAGATTCTGATTACTTCCCCCGTCTCTAACTCTACTACTTTCTAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607366 Chironominae sp. water mite diet isolate 6560-BHL032417-GBD5753_16003-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGCCATGCTGGTTCTTTAATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTTGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTATCTAGTTCTCTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607367 Chironominae sp. water mite diet isolate 6561-BHL032417-GBD24412_20642-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGACTAGTTGGAACTTCTTTAAGAATTCTACTTCGAGCAGAATTATGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTACTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTGCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607368 Chironominae sp. water mite diet isolate 6562-BHL032417-GBD9801_19866-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAGTTCGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCACCAGATATATCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTACTTCCATCTAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607369 Chironominae sp. water mite diet isolate 6563-BHL032417-GBD14212_19945-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGCATTATGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAGCACTTCAGCTGTCTAGTGCTATTGTAGAAAATGGAGCTGAAACAG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607370 Chironominae sp. water mite diet isolate 6565-BHL032417-GBD9456_27229-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACTTTATATTTTATTTTTGGAGCTCGATCAGGAATAGTTGGAACTTCTTTAAGTATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTGACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTGTATCTCCTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607371 Chironominae sp. water mite diet isolate 6566-BHL032417-GBD28089_16993-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGAAATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCTCTTATATTAGGGGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTACTCCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607372 Chironominae sp. water mite diet isolate 6567-BHL032417-GBD18477_25661-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTAATGTAACATCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCAACAGATATAACATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCACATCATCTTTCTAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607373 Chironominae sp. water mite diet isolate 6572-BHL032417-GBD22882_24189-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATATGTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATTAGATTCTGATTACTTCCCCCTTCTATAACGCTTCTTCATTCTAGTTCTATTGTAGAAAAGGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607374 Chironominae sp. water mite diet isolate 6574-BHL032417-GBD12798_27056-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGTCATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACCCTACTACCTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607375 Chironominae sp. water mite diet isolate 6575-BHL032417-GBD28316_19947-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTTATTGTAACCGCTTATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCGTTAACTCTATTACTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607376 Chironominae sp. water mite diet isolate 6577-BHL032417-GBD11374_15135-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTACCCCCTTCTTTAACTCTTTTTCTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607377 Chironominae sp. water mite diet isolate 6578-BHL032417-GBD22591_26124-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCCGGAATAGTTGGAACTTCTTTAAGAATTCTTATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTAGCAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGGTTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAATTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607378 Chironominae sp. water mite diet isolate 6579-BHL032417-GBD24600_15412-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGAAAGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTTATTACTTCCCCCTTCTTCATCTCTACTTCTTTCTAGTACTATTGGAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607379 Chironominae sp. water mite diet isolate 6580-BHL032417-GBD5299_18466-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTTAGTATTTTAATTCGAGCAGAACTTGGACACCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607380 Chironominae sp. water mite diet isolate 6581-BHL032417-GBD17888_18628-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTATCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATGCTGATTACTTCCCCCTTCTTGAACACGTAGTCTTTCTAGTTCTTTTGTAGAAAAGGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607381 Chironominae sp. water mite diet isolate 6582-BHL032417-GBD4962_14553-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTGCTTTTAGAATTCTAATTCGAATAGAATTATGACATCCTGGAACTTTTATTGGTAACGACCAAATTTATAATATTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAGATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607382 Chironominae sp. water mite diet isolate 6583-BHL032417-GBD23627_6344-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACATTATATTTTCTTTTTGGAGTCTGATCAGGAATAGTTGGAACTTCTTTTAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTACGTTATCTCATCATCAATCTAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607383 Chironominae sp. water mite diet isolate 6584-BHL032417-GBD15826_19081-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCGTTAAGAATTCTAATTCGATCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATATCCATTTTAATTGGAGAATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAAGAATATAAGATTCTGATTACTTCCCCCTTCTATATCTCGGCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607384 Chironominae sp. water mite diet isolate 6586-BHL032417-GBD23238_19798-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGCATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGTCATCCCGAATCTTTTATTGGTGACGAACAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCGTCTTTAACTCTACTACTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607385 Chironominae sp. water mite diet isolate 6587-BHL032417-GBD3224_19827-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTGTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCAGGAACTTTTATTGGTGAAGACCAACTTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTTGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAACAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607386 Chironominae sp. water mite diet isolate 6588-BHL032417-GBD26700_20572-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTATTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTACCCCCTTCTTTATCTCTACTACTTTCTAGTACTATAGTAGGAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607387 Chironominae sp. water mite diet isolate 6589-BHL032417-GBD22535_24037-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGACATCCTGGATCTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATATTTTTTTTCATAGTAATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCATTAACTCTACTTCTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607388 Chironominae sp. water mite diet isolate 6597-BHL032417-GBD15208_5833-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATCTTATTTTTGGAGCCTGATCAAGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAACTAGGACATCCTGTAACTTTTATTGGTGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCATATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607389 Chironominae sp. water mite diet isolate 6600-BHL032417-GBD20305_16779-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGTTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607390 Chironominae sp. water mite diet isolate 6601-BHL032417-GBD25044_24343-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGTAGAGTTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTATTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCATTATCCCTACTTCTATCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607391 Chironominae sp. water mite diet isolate 6604-BHL032417-GBD13858_6508-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTTTTTTTGGACCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATCTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCATCTTTATCTCTTCTTCTTTCTAGTACTATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607392 Chironominae sp. water mite diet isolate 6605-BHL032417-GBD23634_25895-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAGATTTATAATGTTATTGTCACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCGTCGTTAGCTCTGCTTCTTTCTAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607393 Chironominae sp. water mite diet isolate 6606-BHL032417-GBD16506_22439-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGGATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTGCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCCGATTACTTCCCCCTTCGTTAACTCTTCTTCTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607394 Chironominae sp. water mite diet isolate 6608-BHL032417-GBD4025_16592-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTTAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTCTTGTAACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTCCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTTTACTACTTTCGAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607395 Chironominae sp. water mite diet isolate 6610-BHL032417-GBD21689_22273-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTTAGAATTCTAATTCGAACTGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAACTTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTCATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTATTTCTAGTGCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607396 Chironominae sp. water mite diet isolate 6611-BHL032417-GBD5689_22953-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATGCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGTTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATATGGAAATTGATTAGTTCCTCTTATATTAGGAGCCCCCGATCTAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607397 Chironominae sp. water mite diet isolate 6612-BHL032417-GBD6661_6919-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGATTAGTAGGAACTTCTTTAAGAATTCTAATTCGAGCGGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTACCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607398 Chironominae sp. water mite diet isolate 6615-BHL032417-GBD18536_28374-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTGAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCAAAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATAGAGCATTTCCTCGAATAAATAATATAAGATGCTGATTACGTCCCCCTTCTTTATCTCTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607399 Chironominae sp. water mite diet isolate 6616-BHL032417-GBD8747_12975-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCCGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTCATTGGTGACGACCAAATTTATAATGTTGTTGTAACTCCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGACACTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTCTATCTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607400 Chironominae sp. water mite diet isolate 6619-BHL032417-GBD27267_9204-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACAGTGTGTTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAAGTAGGACATCCCGGAACTTTTATTGGGGACGGCCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTGCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607401 Chironominae sp. water mite diet isolate 6621-BHL032417-GBD21868_13391-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGATGACGGCCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACTCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGCATAAATAACATAAGAGTCTGATTACTTCCCCCTTCTTTATCTCTGCCTCTTTCTAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607402 Chironominae sp. water mite diet isolate 6623-BHL032417-GBD3223_16335-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAACTTGATCAGGAATAGTTGGAATTTCTTTAAGCATTTTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGACGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCTGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607403 Chironominae sp. water mite diet isolate 6624-BHL032417-GBD22182_25568-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCATGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGCTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGACTAGTTCCACTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCATCTTTAACTCTACTACTTTCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607404 Chironominae sp. water mite diet isolate 6628-BHL032417-GBD9558_6377-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGCATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTTTTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAAAAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCCCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607405 Chironominae sp. water mite diet isolate 6629-BHL032417-GBD26372_20942-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAATTTTATATTTTATTTTTGGAGTCTGATCCGGAATAGTTGGAACTTCTTTAAGAATTCTTATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTTGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCCTCTCTAACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607406 Chironominae sp. water mite diet isolate 6630-BHL032417-GBD8149_11053-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACGTTGTATGTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGACCAGCATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCACTTCTTCTTTCTAGTTCTAGTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607407 Chironominae sp. water mite diet isolate 6632-BHL032417-GBD17944_4662-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGTCCTTATTTATAATGGTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTTGAGGATTTGGAAATTGATTAGTTACTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAACATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGATAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607408 Chironominae sp. water mite diet isolate 6633-BHL032417-GBD23512_6211-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTTATTCGAGCAGAATTAGGACATCCTGGAACTTTCATTGGTGATGACCAAATTTATAATGTTATTGTTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAAATGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTTCTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607409 Chironominae sp. water mite diet isolate 6634-BHL032417-GBD27581_20529-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGGACTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCCCCAGATACAGCATTTCCTCGAATAAACAATATAAGTTTCTGATTACTTCCCCCTTCTTTATCTCTTCTACTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607410 Chironominae sp. water mite diet isolate 6635-BHL032417-GBD10775_9860-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATTGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACCTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACATCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATCGGAGGATTTGGGTATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCTCCCTTCTTTATCTCTTCTTCTTTCTAGTCCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607411 Chironominae sp. water mite diet isolate 6636-BHL032417-GBD23918_10042-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGTCATACTGATTCTTTTATTGGTGACGAACAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATCATTTTTTTCATAGTGATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCATTAACTCTACTACTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607412 Chironominae sp. water mite diet isolate 6638-BHL032417-GBD11550_9107-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAAAATCAGGACATCCTGGAACTTTTATTAGTGACGACCAGATGTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTCTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGGTTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607413 Chironominae sp. water mite diet isolate 6639-BHL032417-GBD19753_18387-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGTAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCTATCAGAATTAGGACATCCTTGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCAAAGTTATACCCATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607414 Chironominae sp. water mite diet isolate 6641-BHL032417-GBD24667_16814-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGTCATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTTATATTAGGAGCACCAGATATAACATTTCCTCGAATAAATAAAAAAAGATTCTGATTACTTCCCCCTTCATTAACTCTACTACTATCTAGCTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607415 Chironominae sp. water mite diet isolate 6642-BHL032417-GBD14228_26568-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGGGCGGAATTAGGAAATCCTGGAACTTTTATGGGGGACGACAAAATTTATAATGTTATGGTAAAAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607416 Chironominae sp. water mite diet isolate 6643-BHL032417-GBD27463_22638-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACACCCTGGAACTTTTATAGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGACTAAATAATATAAGATTCTGATTACTGCCCCCTTCTGTATCTCTTCTTCTATCTAGTTCTACTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607417 Chironominae sp. water mite diet isolate 6644-BHL032417-GBD8503_14525-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACATCCCGGAACTTTTATTGGTGACGACCAAATTTATAATGTTGTTGTAACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTAATATTTGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTCTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607418 Chironominae sp. water mite diet isolate 6645-BHL032417-GBD11896_11127-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACATTATACTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGACATCCTGGAACTTTTATTGTTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607419 Chironominae sp. water mite diet isolate 6647-BHL032417-GBD13878_4314-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCATGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGGCGTCCTAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCCTTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607420 Chironominae sp. water mite diet isolate 6648-BHL032417-GBD6366_24251-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACCTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTATGACATCCTGGAACTTTTACTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTTCTATAATTTTTTTCATGGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTGCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607421 Chironominae sp. water mite diet isolate 6650-BHL032417-GBD14007_13006-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACACCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCCTTTCCTCGCATAATTAATATCAGATTCTGATTACTTCCCCCTTCTTGAACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607422 Chironominae sp. water mite diet isolate 6652-BHL032417-GBD19033_14613-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCATGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATACTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTGCCACTTTATAGTTCGATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607423 Chironominae sp. water mite diet isolate 6653-BHL032417-GBD13082_28980-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATACTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTAATAGTTATACCCATTTTAATTTGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTACTTCTTTCTAGTGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607424 Chironominae sp. water mite diet isolate 6654-BHL032417-GBD18145_5869-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGATATCCTGTAACTTTTATTGGAGACGACCAAATTTATAATGCAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607425 Chironominae sp. water mite diet isolate 6656-BHL032417-GBD16412_6865-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAATTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAATAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTCATTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTAGATCGCGTCTTCTTTCTAGTTCTATTGTAGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607426 Chironominae sp. water mite diet isolate 6658-BHL032417-GBD28699_17119-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGACATCCTGGTACTTTTATCGGTGACTACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAAGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTACTATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607427 Chironominae sp. water mite diet isolate 6936-BHL032417-GBD23959_14072-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGCAATTGTTACTGCTCATGCCTTTATTATAATTTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGAATGTGATTATTAACAACATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607428 Chironominae sp. water mite diet isolate 7020-BHL032417-GBD5704_19656-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTTCCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTTACTTTATTTCTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607429 Chironominae sp. water mite diet isolate 7038-BHL032417-GBD13230_24993-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTTTATTTTATTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACTGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATGACCCCCATCTCTTACATTATTTAAATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607430 Chironominae sp. water mite diet isolate 7094-BHL032417-GBD9285_19212-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTTTAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTATGAGCCCATGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTAGCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607431 Chironominae sp. water mite diet isolate 7126-BHL032417-GBD27698_10639-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCGGAATTAGGTCATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCTCTAATATTAGGAGCCCCTGATATGGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTAACTTTACTACTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607432 Chironominae sp. water mite diet isolate 7127-BHL032417-GBD9991_19082-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGAAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGAAGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607433 Chironominae sp. water mite diet isolate 7148-BHL032417-GBD19293_12106-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGACATCCTGGAACATTTATTGGTGATGAACAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGATACTGGTTAGTACCACTAATATTAGGAGCACATGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607434 Chironominae sp. water mite diet isolate 7185-BHL032417-GBD10223_10560-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTAAAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTTCCACTAATATTAGGAGCCCCTGAAAAGGCCTTTCCACGAAAAAATAATATAAAATTTTGATTATTACCACCATCTATTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607435 Chironominae sp. water mite diet isolate 7200-BHL032417-GBD12332_22715-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGTACCTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCACTAATATTAGGAGCCCCAGATATGGCATTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607436 Chironominae sp. water mite diet isolate 7226-BHL032417-GBD16846_27338-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGCTATAGTAGGAACTTCTTTAAGAATATTAATCCCAACGGAATTAGGTCATCCTGGATCATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCCAACTTTACTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607437 Chironominae sp. water mite diet isolate 7235-BHL032417-GBD29461_15325-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACTGAATTAGGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCTCTAATATTAGGAGCCCCTGATATGGCTTTTCCTCGAATAAATAATATAAGATTTTGACTATTACCCCCATCTCTAACTCTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607438 Chironominae sp. water mite diet isolate 7237-BHL032417-GBD11812_22747-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCTTTTAGTATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607439 Chironominae sp. water mite diet isolate 7241-BHL032417-GBD28946_18131-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGATCATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCTCTAATACTAGGAGCCCCTGATATAGCATTTCCACGAATAAATAATATAAGATTTTGATTAATACCACCATCACTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607440 Chironominae sp. water mite diet isolate 7252-BHL032417-GBD12018_24515-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTTGGAGCTTGATCGGGTATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTGGAATTAGGTCATCCTGGCACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTTGCTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607441 Chironominae sp. water mite diet isolate 7255-BHL032417-GBD13889_9797-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTTCACGAATAAATAATATAAGATTTTGACTACTACCACCATCTCTAACTTTATTACCTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607442 Chironominae sp. water mite diet isolate 7282-BHL032417-GBD12812_26819-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTATGAACTTCTTTAAGAATATTAATTCGAACTGAATTATGTCATCCTGGATCATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTAACACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607443 Chironominae sp. water mite diet isolate 7306-BHL032417-GBD21616_2922-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAATATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTTACTTTATTACTTTCAAGAATACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607444 Chironominae sp. water mite diet isolate 7337-BHL032417-GBD26787_19109-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTAGTACCACTAATATTGGGAGCCCCTGATATGGCATTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTTATTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607445 Chironominae sp. water mite diet isolate 7342-BHL032417-GBD12466_9469-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTTAGAATTTTAATTCGTACGGAATTAGGTCATCCTGGTACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACATTATTACTATCAAGAAGAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607446 Chironominae sp. water mite diet isolate 7346-BHL032417-GBD29306_17183-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGTAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTTGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCGCTGACGGGAGGACGGGCAAGAAGAAGAGGAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607447 Chironominae sp. water mite diet isolate 7359-BHL032417-GBD23285_17215-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTTTATTTTATTTTTGGAGCTTGATCAGGTATGGTAGGAACTTCTTTAAGTATATTAATCCGAACGGAATTAGGTCATCCTGGGACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCTCTAATATTGGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTAGCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607448 Chironominae sp. water mite diet isolate 7360-BHL032417-GBD2945_12027-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAAAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAAAGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTCATACCCATTTTAATTGGAGCATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607449 Chironominae sp. water mite diet isolate 7362-BHL032417-GBD25295_6114-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAATGGAATTAGGTCATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCTCCTGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTTACCTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607450 Chironominae sp. water mite diet isolate 7367-BHL032417-GBD26139_21706-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATGTTTATTCGAACGAAATTAGGTCATCCAGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTAATAGTAATACCTATTTTAATTGGAGGTTTTGGAAATTGGTTATTCCCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGACTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607451 Chironominae sp. water mite diet isolate 7374-BHL032417-GBD7308_13946-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTACTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGGATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607452 Chironominae sp. water mite diet isolate 7378-BHL032417-GBD25057_6704-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAATGGAATTAGGTCATCCAGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCTCTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607453 Chironominae sp. water mite diet isolate 7379-BHL032417-GBD21382_14900-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGGTCAGGTATAGTAGGTACTTCTTTAAGAATGTTAATTCGAGCGGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATTCCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCATGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607454 Chironominae sp. water mite diet isolate 7388-BHL032417-GBD16668_16155-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGATGATGACCAAATTTACAATGTAATTGTAACTGCTCATGCTTTTATTATAATTCTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607455 Chironominae sp. water mite diet isolate 7395-BHL032417-GBD12031_17625-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATGTTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATAGCATTTCCACGAATAAATAATATAAGATTTTGATTACTACCACCATCTCTAACTTTATTTCTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607456 Chironominae sp. water mite diet isolate 7398-BHL032417-GBD7757_18495-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAACGGAATTAGGTCATCCTGGCTCATTAATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTAACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607457 Chironominae sp. water mite diet isolate 7429-BHL032417-GBD27683_8640-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATCCGACTGGAATTAGGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTATTACTGCACATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCTCTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACCTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607458 Chironominae sp. water mite diet isolate 7445-BHL032417-GBD4970_10270-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAATTATATTTTATTTTTTGGAGCTTGATCAGGTAGAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTATGTTATCCTGTAACATTTATTGGATATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607459 Chironominae sp. water mite diet isolate 7467-BHL032417-GBD29508_16396-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGTGCTTGATCAGGTATAATAGGAACTTCTTTAAGAATATTAATCCGAACTGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTACTACCACCCTCTCTAACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607460 Chironominae sp. water mite diet isolate 7471-BHL032417-GBD20680_25495-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAACGGAATTAGGTCATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTTCCTCTAATATTAGGAGCACCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTTACTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607461 Chironominae sp. water mite diet isolate 7502-BHL032417-GBD5452_21570-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATGTTAATCCGAACGGAATTAGGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGACATGGCTTTTCCACGAATGAATAATATAAGATTTTGATTATTACCCCCCTCTCTTACTTTATTTCTTTCAAGAAGAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607462 Chironominae sp. water mite diet isolate 7513-BHL032417-GBD23410_23346-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGGTTATTTCCTCTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCATCACTTACTTTATTATTATCAAGAAGACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607463 Chironominae sp. water mite diet isolate 7584-BHL040517-GBD2266_13967-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCTTGATCTGGTATGGTAGGTACTTCTTTAAGTATGCTAATTCGAACAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR287664, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607464 Chironominae sp. water mite diet isolate 7586-BHL040517-GBD16256_8581-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACATTATTGTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTACACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607465 Chironominae sp. water mite diet isolate 7656-BHL040517-GBD23706_9295-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607466 Chironominae sp. water mite diet isolate 7661-BHL040517-GBD10271_24044-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607467 Chironominae sp. water mite diet isolate 7663-BHL040517-GBD5175_20851-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAGATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTAGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607468 Chironominae sp. water mite diet isolate 7678-BHL040517-GBD19279_23769-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTCTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607469 Chironominae sp. water mite diet isolate 7728-BHL040517-GBD8635_14304-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACAACCTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTTACAGCTTACGCTTTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTATTATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607470 Chironominae sp. water mite diet isolate 7750-BHL040517-GBD21235_23762-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAAATTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID MG449442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607471 Chironominae sp. water mite diet isolate 7774-BHL040517-GBD4580_10239-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAGATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTAGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607472 Chironominae sp. water mite diet isolate 7792-BHL040517-GBD15153_16033-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCAAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATTCGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCTAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607473 Chironominae sp. water mite diet isolate 7862-BHL040517-GBD12709_12348-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGGTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCGTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607474 Chironominae sp. water mite diet isolate 7938-BHL040517-GBD22940_5073-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGTATGCTACTTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAGATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTAGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607475 Chironominae sp. water mite diet isolate 8031-BHL040517-GBD8406_9011-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAACAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGTATACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTTCCCATAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTCAGTCTTCTTCTTTCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID MG448641, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607476 Chironominae sp. water mite diet isolate 8053-BHL040517-GBD19516_22215-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAAAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607477 Chironominae sp. water mite diet isolate 8121-BHL040517-GBD16523_7465-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTTCTTTTATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGATTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCATTAACACTTTTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607478 Chironominae sp. water mite diet isolate 8212-BHL040517-GBD17491_19263-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTTGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCGCCTTCATTAACTCTTTTACTTTCAAATTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607479 Chironominae sp. water mite diet isolate 8240-BHL040517-GBD16149_14567-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCTAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGA-TTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTGCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607480 Chironominae sp. water mite diet isolate 8269-BHL040517-GBD18362_7444-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGTTCTGGTATAGTAGGCACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTATTTGTTACAGCACACGCTTTTATTATAATTTTTTTTATACTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGGCCCAGATATGGATTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607481 Chironominae sp. water mite diet isolate 8370-BHL040517-GBD7512_19258-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGGATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID MG449215, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607482 Chironominae sp. water mite diet isolate 8420-BHL101416-GBD19963_2986-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607483 Chironominae sp. water mite diet isolate 8445-BHL101416-GBD5228_13850-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTGTAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607484 Chironominae sp. water mite diet isolate 8464-BHL101416-GBD11798_11015-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGCTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607485 Chironominae sp. water mite diet isolate 8481-BHL101416-GBD11762_10971-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCTTTAAGTATATTAATTCGAGCTGATCTTGGACGACCTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGATTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607486 Chironominae sp. water mite diet isolate 8517-BHL101416-GBD27283_9150-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTCGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCTCTCTTACTCATCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR287664, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607487 Chironominae sp. water mite diet isolate 8526-BHL101416-GBD20161_4427-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACGTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTGTTCGAGCAGAATTAGGACGACCCGGAACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTAATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTCTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607488 Chironominae sp. water mite diet isolate 8531-BHL101416-GBD19794_16197-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCTAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607489 Chironominae sp. water mite diet isolate 8543-BHL101416-GBD3666_15391-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATTTTTTATTTTTGGAGCTTGATCTGGTATAGCAGGTACTTCTTTAAGTATGCAAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607490 Chironominae sp. water mite diet isolate 8568-BHL101416-GBD21718_23956-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTATGTACTTCTTTTTGTATGCTAATTCGAGCAGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATTTCTATCTCTGCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KR287664, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607491 Chironominae sp. water mite diet isolate 8587-BHL101416-GBD27294_15109-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGAACCCTTAGTGGAGATGACCAATTTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTAATAGTTAGGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607492 Chironominae sp. water mite diet isolate 8596-BHL101416-GBD19995_9213-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCATCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCACTAATATTAGGAGCCCCTGATATGGCATTTCCACGAATAAATAATATAAGATTTTGACTATTACCACCATCTCTAACTTTACTACTTTCAAGAACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607493 Chironominae sp. water mite diet isolate 8608-BHL101416-GBD10195_9754-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAATTTGACTAGTGCCATTAATATTAGGAGCACCTGATATGGCATTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCTTCCTTAACATTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607494 Chironominae sp. water mite diet isolate 8645-BHL101416-GBD16049_3362-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCTGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATACTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607495 Chironominae sp. water mite diet isolate 8713-BHL101416-GBD5074_15077-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTTTAAGTATGCTAATTTGAGCAGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTTTTATAATTTTTTTAATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAACTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607496 Chironominae sp. water mite diet isolate 8723-BHL101416-GBD16757_22650-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAACTTGACTTGTCCCTTTAATATTAGGATCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTCTTGACTTCTCCCCCCATCCTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607497 Chironominae sp. water mite diet isolate 8766-BHL101416-GBD27666_8317-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTACTTCGAGCAGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTCGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607498 Chironominae sp. water mite diet isolate 8769-BHL101416-GBD11033_20746-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGTATGTTAATTAGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCAGAGCACAGGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGAAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCACAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607499 Chironominae sp. water mite diet isolate 8772-BHL101416-GBD14677_12282-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTTTGGATCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGCGGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAACACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGATTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607500 Chironominae sp. water mite diet isolate 8824-BHL101416-GBD12162_16119-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTTAGTATGCTAATTCGAGCAGAACTTTGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTATCCCCTTCTATATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607501 Chironominae sp. water mite diet isolate 8826-BHL101416-GBD9612_6705-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTCTGGGGCTTCATCCGGAATAGTGGGAACTTCATTAAGAATGCTTAATCGAGCAGAATTAGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607502 Chironominae sp. water mite diet isolate 8926-BHL032417-GBD26911_7982-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTACTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGTTCTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607503 Chironominae sp. water mite diet isolate 8929-BHL032417-GBD13273_4465-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGGGCGCCAGATATAGCTTTTCCTCGGATAAATAATATAAGTTTTTGATTACTCCCCCCTTCTCTTACTCTTCTTCTTCCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607504 Chironominae sp. water mite diet isolate 8938-BHL032417-GBD21073_24845-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGATGACCTGGTACGTTTCTTGGAGAGGACCAAATTTACAATTTAGTTGTCACAGCACACACTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGATGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTCACTTTCAAGTTCTATTGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607505 Chironominae sp. water mite diet isolate 8949-BHL032417-GBD24544_13758-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTTCTTTTACTGGAGATGACCAAATTTACAATGTAATTGTCACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCGTCATTAACTTTATTACTATCAAGTTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607506 Chironominae sp. water mite diet isolate 8991-BHL032417-GBD28175_15351-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATGATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTAACTCTACTACTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR287664, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607507 Chironominae sp. water mite diet isolate 9040-BHL032417-GBD24455_24683-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGAATGCTAATTCGAGCAGAACTCGGACGACCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTGTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCATTAACTCTTTTACTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607508 Chironominae sp. water mite diet isolate 9042-BHL032417-GBD27947_15583-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCTCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACCCTTTTACTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607509 Chironominae sp. water mite diet isolate 9045-BHL032417-GBD19007_3028-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGTATAATAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAGCTTGGACGACCTGGTACTTTTATTAGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTCCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607510 Chironominae sp. water mite diet isolate 9058-BHL032417-GBD20412_25571-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607511 Chironominae sp. water mite diet isolate 9062-BHL032417-GBD3204_18764-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTAGACCTGGAACTTTTATTGGTGACGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTTGAGGTTTTGGAAATTTACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG449215, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607512 Chironominae sp. water mite diet isolate 9081-BHL032417-GBD15328_26152-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTACATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATGGTTATGCCAATTTTAATTGGAGGTTTTGAAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAAGAATATAAGTTTTTGACTACTCCCCCCTTCATTAACTCTGTGACGTTCAAGTTCTATTGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607513 Chironominae sp. water mite diet isolate 9087-BHL032417-GBD3279_18006-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTACTGGATATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTATTTGGAGGGTTTGGAAATTGACTAGTTCCTTTAATATTGGTGGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTTTACCTCCTTCTTTAACTCTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607514 Chironominae sp. water mite diet isolate 9107-BHL032417-GBD9805_20329-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGAATGCTAATTCGAGCAGAACTTGGACGACCTGGTTCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTATTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607515 Chironominae sp. water mite diet isolate 9115-BHL032417-GBD26374_15044-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGCCGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCATCAGTAACTCTATTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607516 Chironominae sp. water mite diet isolate 9123-BHL032417-GBD5746_10473-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTATGTTTGCTAATTCGAGCAGAACTTGGACGACTTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGGCTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTCCCCCCTTCTCCTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGGACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607517 Chironominae sp. water mite diet isolate 9127-BHL032417-GBD16419_23824-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGTTAATTCGAGCAGAACTTGGTCGACGTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCTAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607518 Chironominae sp. water mite diet isolate 9130-BHL032417-GBD29229_16372-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTACTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTACAGTAACGCGGGGACGGGCAAGGGCGAGGGGAGAAAAGGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607519 Chironominae sp. water mite diet isolate 9133-BHL032417-GBD23009_12501-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACAACCTGGTTCTTTTATTGGAGATGATCAAATTTACAATGTAATTGTTACCGCACACGCTTTTGTTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCGTCATTAACTCTATTACTATCAAGTTCTCTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607520 Chironominae sp. water mite diet isolate 9161-BHL032417-GBD27739_16535-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTCGGACGAGCTGGTTCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTATTACTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607521 Chironominae sp. water mite diet isolate 9187-BHL032417-GBD27366_12300-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCTATTTTAATTGGAGGTTTTGGAAATTGACTTTTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCATTAACTCTTTTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607522 Chironominae sp. water mite diet isolate 9200-BHL032417-GBD17424_29044-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATTCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGGTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCATTCCCTCGAATAAATAATATAAGTTTTTGAATACTTCCCCCTTCATTAACTCTATTACTATCAAGCTCTCTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607523 Chironominae sp. water mite diet isolate 9254-BHL032417-GBD22188_24713-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACAACCTGTTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTGATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCACCAGATACGGCTTTCCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607524 Chironominae sp. water mite diet isolate 9288-BHL032417-GBD23483_6276-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATTCTAATTCGAGCAGAACTTGGTCTCCCTGGTACTTTTATTGGAGAAGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGAATTATTCCTTTAATGTTAGGAGCCCCAGATATGGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCATTAACTCTATTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607525 Chironominae sp. water mite diet isolate 9291-BHL032417-GBD9684_22065-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACAACGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCTCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTGCCCCCTTCATTAACTCTATTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607526 Chironominae sp. water mite diet isolate 9297-BHL032417-GBD11203_21780-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCGTTAAGTATGCTAATTCGAGCAGAACTAGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCATCATTAACCCTTTTACTATCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607527 Chironominae sp. water mite diet isolate 9301-BHL032417-GBD7165_18399-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGCACTTCTTTAAGTTTTCTAATTCGAGTAGAACTTGGACGACGTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCATTAACCCTTTTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607528 Chironominae sp. water mite diet isolate 9302-BHL032417-GBD15004_10059-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTCGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCACGAATAAATAACATAAGTTTTTGACTTCTTCCCCCATCATTAACCCTTTTACTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607529 Chironominae sp. water mite diet isolate 9304-BHL032417-GBD16914_17074-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAACATAAGATTTTGATTACTACCCCCTTCATTAACACTATTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607530 Chironominae sp. water mite diet isolate 9322-BHL032417-GBD13295_22134-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTCCTTCTTTAAGTATTCTAATTCGACCAGAACTTGGACAACCTGGTACTTTTACTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCGTCATTAACTCTATTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607531 Chironominae sp. water mite diet isolate 9323-BHL032417-GBD28971_15205-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTCTTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCATCATTAACTCTTTTACTATCAAGAACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607532 Chironominae sp. water mite diet isolate 9341-BHL032417-GBD18952_24564-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGTATGCTTATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTACCCCCTTCATTAACTCTTCTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607533 Chironominae sp. water mite diet isolate 9348-BHL032417-GBD10497_23687-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTTATTCGAGCAGAATTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTCTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCATCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607534 Chironominae sp. water mite diet isolate 9359-BHL032417-GBD5205_7911-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATTTGGACAACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTATACCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGACTACTACCACCATCATTAACTCTTTTACTTTCAAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607535 Chironominae sp. water mite diet isolate 9365-BHL032417-GBD17325_24211-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAACTTGATCTGGTATAGTAGGAACTTCTTTAAGTATTCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTGTTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607536 Chironominae sp. water mite diet isolate 9366-BHL032417-GBD8755_11835-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACAACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTTTAATATTAGGAGCACCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607537 Chironominae sp. water mite diet isolate 9373-BHL032417-GBD7720_10249-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGCTGAACTAGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGATTTATTCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607538 Chironominae sp. water mite diet isolate 9374-BHL032417-GBD27375_17539-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTGGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACATCCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCTATTTTAATTGGAGGTTTTGGAAACTGACTTATTCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607539 Chironominae sp. water mite diet isolate 9376-BHL032417-GBD16618_18355-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACCTGGACGACGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCCTCTTTAACTCTTCTACTATCTAGTTCTTTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607540 Chironominae sp. water mite diet isolate 9406-BHL032417-GBD24303_17764-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACATCCTGGTACTTTTATAGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTAATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTACCACCTTCATTAACACTATTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607541 Chironominae sp. water mite diet isolate 9407-BHL032417-GBD21154_24171-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACGAACTGGTTCTTTTATGGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTTGGAAATTGATTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCGTCATTAACTCTACTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607542 Chironominae sp. water mite diet isolate 9408-BHL032417-GBD3218_20831-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGTTTGCTAATTCGAGCAGAATTTGGACAACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATACCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTTACTCTATTACTTTCAAGATCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607543 Chironominae sp. water mite diet isolate 9419-BHL032417-GBD21879_3511-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGTCGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACCGCACACGCTTTTTTTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCATTAACTCTTTTACTATTAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607544 Chironominae sp. water mite diet isolate 9454-BHL032417-GBD13672_27961-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATTCTAATTCGAGCAGAACTTGGACAACGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACCGCACACGCTTTTGTTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGATTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTTTTTTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607545 Chironominae sp. water mite diet isolate 9455-BHL032417-GBD19895_18439-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACCTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACACCCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCACTAACTCTATTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607546 Chironominae sp. water mite diet isolate 9460-BHL032417-GBD10695_17008-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGGTCAGGAATAGTAGGAACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACCCTTTTACTATCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607547 Chironominae sp. water mite diet isolate 9476-BHL032417-GBD7702_3997-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTTATTCGAGCCGAATTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTAATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607548 Chironominae sp. water mite diet isolate 9480-BHL032417-GBD7914_19003-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGCACTTCTTTAAGTTTGCTAATTCGAGCAGAATTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTGTTCCTTTAATATTAGGTGCCCCAGATATGGCTTTCCCGCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACCCTTTTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607549 Chironominae sp. water mite diet isolate 9489-BHL032417-GBD15440_18310-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACTACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTAATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATACCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCATTAACTCTATTACTTTCAAGTAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607550 Chironominae sp. water mite diet isolate 9496-BHL032417-GBD20336_17095-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTATGTTTGCTAATTCGAGCAGAACTTGGACGAAGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATACGGCTGTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCAGTAACTCATTCACTTTCAAGTACTATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607551 Chironominae sp. water mite diet isolate 9498-BHL032417-GBD25435_10792-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACGACGTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATAAGGGTTTCCCTCGAATAAAAAATATAAATTTTTGGCCTCCTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607552 Chironominae sp. water mite diet isolate 9516-BHL032417-GBD27078_23041-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACGTCCTGGTTCTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTATTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607553 Chironominae sp. water mite diet isolate 9527-BHL032417-GBD23399_22799-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACAACCTGGTACTTTTATTGGAGATGACCAAATTTACAGTGTAATTGTCACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGGTTAATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTACCTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607554 Chironominae sp. water mite diet isolate 9757-BHL040517-GBD26085_15238-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTAGAGGATTCGGAAATTGACTAGTCCCATTGATGATTAGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGACTTTTACCCCCCTCTTTAACTCTTCTACTATCTAGTTCTTTCACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607555 Chironominae sp. water mite diet isolate 9758-BHL040517-GBD20632_17230-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTGCTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCTTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607556 Chironominae sp. water mite diet isolate 9786-BHL040517-GBD23770_22293-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATTTTAATTCGAGTAGAACTTGGACGACCTGGTTCTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCACCAGATATGGCTTTCCCGCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTACTATCAAGTTCTAGTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607557 Chironominae sp. water mite diet isolate 9804-BHL040517-GBD25564_15277-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACGAGCTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTTACCGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCTGATATGGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607558 Chironominae sp. water mite diet isolate 9806-BHL040517-GBD10721_12803-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATATTAGGTACTTCTTTAAGTATGTTAATTCGAGCGGAACTTGGACAACCTGGTACTTTCATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTATTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607559 Chironominae sp. water mite diet isolate 9814-BHL040517-GBD3061_20357-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGTAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGTGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCGTTAAC---CTTACTTTTATCAAAATCAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607560 Chironominae sp. water mite diet isolate 9925-BHL040517-GBD10390_3502-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAGTATAAGCTTTTGATTATTACCTCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.0% identical to accession ID KR765094, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607561 Chironominae sp. water mite diet isolate 9948-BHL040517-GBD22379_14463-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGCTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCACGAATAAATAATATAAGTTTCTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAGAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607562 Chironominae sp. water mite diet isolate 9961-BHL040517-GBD6196_15085-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR765094, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607563 Chironominae sp. water mite diet isolate 9973-BHL040517-GBD25504_20091-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGGACTTCCTCAAGTATACTAATTCGAGCTGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.7% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607564 Chironominae sp. water mite diet isolate 9983-BHL040517-GBD4605_8779-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGAGGTCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KR765094, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607565 Chironominae sp. water mite diet isolate 9988-BHL040517-GBD11467_2617-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCATGGAACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTCTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCCTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATGATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID MG449442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607566 Chironominae sp. water mite diet isolate 9996-BHL040517-GBD22838_6952-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATACGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607567 Chironominae sp. water mite diet isolate 10015-BHL040517-GBD7547_22576-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607568 Chironominae sp. water mite diet isolate 10025-BHL040517-GBD15123_16072-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAACAATATAAGCTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR765094, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607569 Chironominae sp. water mite diet isolate 10056-BHL040517-GBD17908_4223-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCTGG-ACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR765094, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607570 Chironominae sp. water mite diet isolate 10073-BHL040517-GBD21675_12755-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATACGAGCAGAACTTGGACAACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAACTGACTTATTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607571 Chironominae sp. water mite diet isolate 10083-BHL040517-GBD6704_20712-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATACGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGGAATTGACTTATCCCTTTAATGTTAGGAGCCCCAGATATGGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607572 Chironominae sp. water mite diet isolate 10129-BHL040517-GBD15265_28499-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607573 Chironominae sp. water mite diet isolate 10133-BHL040517-GBD12750_28654-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGAAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATGTGGTAATTGACTATTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTACTCGAATAAATAATATAAGTTTTTGATTATTACCTCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KR765094, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607574 Chironominae sp. water mite diet isolate 10174-BHL040517-GBD22243_22020-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATACGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAACACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR765094, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607575 Chironominae sp. water mite diet isolate 10177-BHL040517-GBD18093_12138-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAAACGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATCAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR765094, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607576 Chironominae sp. water mite diet isolate 10199-BHL040517-GBD24284_8757-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATACGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCTCCAGATATGGTCTTTCCTCGAATAAATAATATGAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607577 Chironominae sp. water mite diet isolate 10318-BHL040517-GBD16564_4314-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTACTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCATCCTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR765094, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607578 Chironominae sp. water mite diet isolate 10332-BHL040517-GBD5742_10750-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTCATTATAATTTTTTTTATAGTTATACTAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR765094, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607579 Chironominae sp. water mite diet isolate 10338-BHL040517-GBD13393_15830-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACCTCTTTAAGTATGCTAATACGGGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGCCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGGAACTGA-TTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607580 Chironominae sp. water mite diet isolate 10352-BHL040517-GBD8228_6733-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATACGAGCAAAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATCGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607581 Chironominae sp. water mite diet isolate 10355-BHL040517-GBD8631_24549-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATACGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607582 Chironominae sp. water mite diet isolate 10397-BHL040517-GBD18190_6123-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGTATGCTAATACGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG449442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607583 Chironominae sp. water mite diet isolate 10420-BHL040517-GBD17686_14688-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATACGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607584 Chironominae sp. water mite diet isolate 10439-BHL040517-GBD4409_14014-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTTGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607585 Chironominae sp. water mite diet isolate 10444-BHL040517-GBD28194_19580-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACAACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTCATAGTTATACCTATCTTAATTGGAGGATTTGGGAACTGA-TTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAACAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTGTCAAGTAGAACAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607586 Chironominae sp. water mite diet isolate 10460-BHL040517-GBD10261_13166-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAAAATAAGTTTTTGATTATTACCTCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR765094, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607587 Chironominae sp. water mite diet isolate 10498-BHL040517-GBD14487_21487-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATACGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAGTGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607588 Chironominae sp. water mite diet isolate 10597-BHL040517-GBD18399_25458-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTTGGAGCTTGATCGGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATCAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607589 Chironominae sp. water mite diet isolate 10709-BHL101516-GBD13036_13386-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGCACTTCCTTAAGTATACTTATTCGAGCAGAGTTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTAACCGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCGATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR751654, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607590 Chironominae sp. water mite diet isolate 10764-BHL101516-GBD26306_22653-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGCACTTCCTTAAGTATACTTATTCGAGCAGAGTTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTAACCGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTGCTGTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR751654, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607591 Chironominae sp. water mite diet isolate 10805-BHL101516-GBD16976_25767-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGCACTTCCTTAAGTATACTTATTCGAGCAAAGTTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTAACCGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCGATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGGGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR751654, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607592 Chironominae sp. water mite diet isolate 10900-BHL101516-GBD14453_28061-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCAGAGTTAGGACATCCAGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTTACCGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCGATTTTAATTGGAGGTTTTGGAAATTGATTAGTACCTTTAATATTAGGGGCCCCTGATATAGCCTTCCCGCGAATAAATAATATAAGATTTTGACTTCTCCCACCGTCTCTTTCTCTTCTTCTTTCTAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR751654, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607593 Chironominae sp. water mite diet isolate 11260-BHL110116-GBD25951_11872-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCCTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACTTTTATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTGATTGGAGGCTTTGGAAATTGACTATTACCACTTATACTTGGAGCCCCTGATATGGCCTTTCCTCGAATAAATAAAATAAGATTCTGGTTACTTCCCCCGTCTATTTCTTTGCTTCTATCAAGAACAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR765681, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607594 Chironominae sp. water mite diet isolate 11338-BHL110116-GBD11935_15808-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTCTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607595 Chironominae sp. water mite diet isolate 11353-BHL110116-GBD4493_14880-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGAACTTCTTTAAGTATATTTATTCGTGCTGAATTAGGACATCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATGCCTATTTTGATTGGAGGCTTTGGAAATTGGCTATTACCACTAATACTTGGAGCCCCTGATATGGCCTTTCCTCGAATAAATAACATAAGATTCTGGTTACTACCTCCGTCTATTACTTTGCTTCTGTCTAGAACAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR765681, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607596 Chironominae sp. water mite diet isolate 12059-BHL040517-GBD19963_2986-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607597 Chironominae sp. water mite diet isolate 12084-BHL040517-GBD5228_13850-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTGTAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607598 Chironominae sp. water mite diet isolate 12103-BHL040517-GBD11798_11015-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGCTATTGTAACTGCTCATGCATTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607599 Chironominae sp. water mite diet isolate 12120-BHL040517-GBD11762_10971-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCTTTAAGTATATTAATTCGAGCTGATCTTGGACGACCTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGATTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607600 Chironominae sp. water mite diet isolate 12156-BHL040517-GBD27283_9150-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTCGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCATCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR287664, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607601 Chironominae sp. water mite diet isolate 12165-BHL040517-GBD20161_4427-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACGTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTGTTCGAGCAGAATTAGGACGACCCGGAACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTAATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTCTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607602 Chironominae sp. water mite diet isolate 12170-BHL040517-GBD19794_16197-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCTAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607603 Chironominae sp. water mite diet isolate 12182-BHL040517-GBD3666_15391-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATTTTTTATTTTTGGAGCTTGATCTGGTATAGCAGGTACTTCTTTAAGTATGCAAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607604 Chironominae sp. water mite diet isolate 12207-BHL040517-GBD21718_23956-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTATGTACTTCTTTTTGTATGCTAATTCGAGCAGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATTTCTATCTCTGCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KR287664, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607605 Chironominae sp. water mite diet isolate 12226-BHL040517-GBD27294_15109-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGAACCCTTAGTGGAGATGACCAATTTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTAATAGTTAGGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607606 Chironominae sp. water mite diet isolate 12235-BHL040517-GBD19995_9213-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCATCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCACTAATATTAGGAGCCCCTGATATGGCATTTCCACGAATAAATAATATAAGATTTTGACTATTACCACCATCTCTAACTTTACTACTTTCAAGAACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607607 Chironominae sp. water mite diet isolate 12247-BHL040517-GBD10195_9754-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAATTTGACTAGTGCCATTAATATTAGGAGCACCTGATATGGCATTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCTTCCTTAACATTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607608 Chironominae sp. water mite diet isolate 12284-BHL040517-GBD16049_3362-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCTGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATACTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607609 Chironominae sp. water mite diet isolate 12352-BHL040517-GBD5074_15077-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTTTAAGTATGCTAATTTGAGCAGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTTTTATAATTTTTTTAATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAACTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607610 Chironominae sp. water mite diet isolate 12362-BHL040517-GBD16757_22650-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAACTTGACTTGTCCCTTTAATATTAGGATCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTCTTGACTTCTCCCCCCATCCTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607611 Chironominae sp. water mite diet isolate 12405-BHL040517-GBD27666_8317-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTACTTCGAGCAGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTCGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607612 Chironominae sp. water mite diet isolate 12408-BHL040517-GBD11033_20746-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGTATGTTAATTAGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCAGAGCACAGGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGAAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCACAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607613 Chironominae sp. water mite diet isolate 12411-BHL040517-GBD14677_12282-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTTTGGATCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGCGGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAACACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGATTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607614 Chironominae sp. water mite diet isolate 12463-BHL040517-GBD12162_16119-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTTAGTATGCTAATTCGAGCAGAACTTTGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTATCCCCTTCTATATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607615 Chironominae sp. water mite diet isolate 12465-BHL040517-GBD9612_6705-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTCTGGGGCTTCATCCGGAATAGTGGGAACTTCATTAAGAATGCTTAATCGAGCAGAATTAGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607616 Chironominae sp. water mite diet isolate 12561-BHL040517-GBD19166_3114-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTGATTGTCACAGCACACGCTTTTGTAATAATTTTTTTTATAATGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTTCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607617 Chironominae sp. water mite diet isolate 12621-BHL040517-GBD3278_13873-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTTCTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607618 Chironominae sp. water mite diet isolate 12708-BHL040517-GBD4562_20734-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGATGACCAAATTTCCAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTGCATTAACTCTTTTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607619 Chironominae sp. water mite diet isolate 12747-BHL040517-GBD25377_17410-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTACTTTATTTTTGGAGCTTGATCCGGAATAGTAGGAACATCTTTAAGAATATTAATTCGAGCAAAATTAGGGCACCCAGGAACATTGATTGGAGATGATCAAATTTACAATGTAATTGTAACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607620 Chironominae sp. water mite diet isolate 12759-BHL040517-GBD16914_4813-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607621 Chironominae sp. water mite diet isolate 12808-BHL040517-GBD29407_14447-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGCACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTCATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAGATTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607622 Chironominae sp. water mite diet isolate 12870-BHL040517-GBD10530_8437-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGTCATGCTGGATCTTTTATTGGTGACGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGTTTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCGTCTTTAACTCTACTACTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607623 Chironominae sp. water mite diet isolate 12887-BHL040517-GBD7625_23230-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCGTCATCAACTCTACTATTATCTAGTTCTATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607624 Chironominae sp. water mite diet isolate 13226-BHL040517-GBD7499_25576-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTATTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTATTTCCCCCATCTCTAACACTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR285570, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607625 Chironominae sp. water mite diet isolate 13328-BHL040517-GBD10076_22231-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGTATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGTAATTGACTTTTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAACATAAGTTTTTGATTACTACCCCCATCTCTAACACTACTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR285570, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607626 Chironominae sp. water mite diet isolate 13329-BHL040517-GBD26718_22316-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGGGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTTATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAGTTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTTCCCCTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR285570, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607627 Chironominae sp. water mite diet isolate 13445-BHL040517-GBD8288_8980-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTCGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCGTCTTTAACATTATTACTTTCAAGAAGAATTGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR285570, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607628 Chironominae sp. water mite diet isolate 13947-BHL040517-GBD10315_15546-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCTTTTAGTATATTAATTCGAGCAGAATTTGGTCACCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCTGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR654792, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607629 Chironominae sp. water mite diet isolate 14226-BHL040517-GBD26557_8626-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGCTGATCAAATTTACAATGTTATTGTCACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCAATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTATGTTCTAGCGCAAGAGTAGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607630 Chironominae sp. water mite diet isolate 14268-BHL040517-GBD23236_18878-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACCTCACTTAGTATTTTAATTCGAGCAGAACTTGGTCACACTGGATCTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTAACACTACTACTATCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607631 Chironominae sp. water mite diet isolate 14292-BHL040517-GBD6815_25658-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCTAGGCTCATTGATCGGAGACGACCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAACTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR764241, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607632 Chironominae sp. water mite diet isolate 14293-BHL040517-GBD18959_23422-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAAAACTTGGTCACCCTGGAACTTTTATTAGTGGTGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATGAATAATATAAGTTTTTGATTACTACCTCCTTCTCTTACCT-TACTTTTAGTAAACAGTATACTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR174905, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607633 Chironominae sp. water mite diet isolate 14295-BHL040517-GBD20932_7190-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGTACATCCCTTAGTATATTAATTCGAACAGAACTTGGTCACCCTGGAACTTTTATTGATGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAAAATGAGATTTTGATTACGTCCCCCGTCTTTATCTCGTCTTCTTTCTAGCGCAAGTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR286005, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607634 Chironominae sp. water mite diet isolate 14307-BHL040517-GBD26077_7607-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCATTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTGCTTCCCCCTTCTTTAACTCTTCTTCTATCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607635 Chironominae sp. water mite diet isolate 14317-BHL040517-GBD6232_7956-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATCGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCGCGAATAAATAATATGAGATTTTGATTACTTCCTCCATCACTTACATTACTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607636 Chironominae sp. water mite diet isolate 14318-BHL040517-GBD23365_24586-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCATTTAGTATATTAATTCGAGTAGAATTTGGTCACCCTGGCACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCATTAACCCTTCTTCTATCAAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM988908, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607637 Chironominae sp. water mite diet isolate 14321-BHL040517-GBD17033_27877-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGTACATCACTTAGTATATTAATTCGAGCAGAACTCGGTCACCCTGGTACTTTTATTGGTGATTATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATCATTTTTTTTATAGTGATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTAACTCTACTTCTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607638 Chironominae sp. water mite diet isolate 14335-BHL040517-GBD3206_18828-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCTGGTTCTTTAATTGGAGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGTTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGGATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR689936, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607639 Chironominae sp. water mite diet isolate 14341-BHL040517-GBD7696_5719-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACATCATTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGTTCTTTAATTGGTGATGATCAAATTTATAATGCTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTAACTCTACTTCTATCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR159655, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607640 Chironominae sp. water mite diet isolate 14359-BHL040517-GBD12663_27069-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACTTTATATTTTATTTTCGGAGCTTGACCTGGAATAGTAGGTACATCATTTAGTATATTAATTCGAGCAGAACTCGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCATTAACTCTACTACTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR159655, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607641 Chironominae sp. water mite diet isolate 14372-BHL040517-GBD23186_16644-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGGACTTCTTTTAGTATGCTAATTCGAGCAGAACTTGGACACCCTGGTACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR746550, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607642 Chironominae sp. water mite diet isolate 14378-BHL040517-GBD25923_21682-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCACTTAGAATATTAATTCGAGCAGAACTAGGACACCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATCTTAATTGGTGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGACTACTTCCCCCTTCTTTATCTCTTCTACTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR642580, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607643 Chironominae sp. water mite diet isolate 14384-BHL040517-GBD29455_16448-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTCGATCTGGAATCGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCATGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCGGTAGCGCGGCGGCGGGCGAGCGCAAGGGGAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607644 Chironominae sp. water mite diet isolate 14390-BHL040517-GBD12944_8520-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCTCTTAGCATATTAATTCGAGCAGAACTTGGTCACCCTGGTACTTTTATTGGTGATAATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCGTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCGTCATTAACTCTTCTACTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR286005, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607645 Chironominae sp. water mite diet isolate 14392-BHL040517-GBD14044_15597-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCACTTAGTATATTAATTCGACTAGAACTTGGTCGCCCAGGCACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCGCGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCCCTTCTTCTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR764241, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607646 Chironominae sp. water mite diet isolate 14393-BHL040517-GBD18942_14568-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCACTTAGTATATTAATTCGAGCAGAACTTGGACACCCTGGCACCTTTATTGGTGATGATCAAATTTACAATGTTATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTACCCCCTTCTTTAACCCTTCTTCTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607647 Chironominae sp. water mite diet isolate 14395-BHL040517-GBD26144_15457-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTTTATTTTATTTTCGGAGCTTGATCTGGAATAGTTGGAACTTCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTTTTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTGCCCCCTTCATTAACTCTACTACTATCTAGCTCAATTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR159655, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607648 Chironominae sp. water mite diet isolate 14417-BHL040517-GBD13907_13780-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGGTCTGGAATAGTAGGAACTTCTTTTAGTATTTTAATTCGAGCAGAACTCGGTCACCCTGGTACTTTTATTGGTGATGATCAAATTTATAATGCTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTGATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTAACTCTACTACTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KM921023, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607649 Chironominae sp. water mite diet isolate 14420-BHL040517-GBD19360_25115-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTCTTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCATCCTGGAACTTTTATTGGAGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTAACCCTTCTTCTAGCTAGCGCAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607650 Chironominae sp. water mite diet isolate 14421-BHL040517-GBD13527_22564-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCCCTTAGTATATTAATTCGAGCAGAACTTGGCCACCCTGGTACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATACGAGATTTTGAATACGTCCCCCTTCTTTAGCACTACTTCTGTCTAGCGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR286005, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607651 Chironominae sp. water mite diet isolate 14424-BHL040517-GBD9548_10248-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCTTTTAGTATTTTAATTCGAGCAGAATTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCTGATATAGCATTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR617721, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607652 Chironominae sp. water mite diet isolate 14439-BHL040517-GBD3030_11140-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGAAGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAATTTTATAATGTAATTGTTACAGCTAACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTGTATCTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR289910, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607653 Chironominae sp. water mite diet isolate 14441-BHL040517-GBD18281_27827-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCCTGATCTGGAATAGTAGGAACATCATTTAGTATATTAATTCGAGCAGAACTCGGTCACCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTTATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAATATTTTGATTACTTCCCCCTTCTTTATCTCTACTTCTATCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988908, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607654 Chironominae sp. water mite diet isolate 14442-BHL040517-GBD19253_2491-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTCATTTTCGGAGCCTGATCTGGAATAGTAGGAACTTCCCTTAGTATATTAATTCGAGCTGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTCATAGTTATACCTATCCTAATTGGAGGATTTGGGAATTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCAAGCACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR286005, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607655 Chironominae sp. water mite diet isolate 14444-BHL040517-GBD22795_4539-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCATTTAGTATATTAATTCGAGCAGAACTAGGTCACCCTGGAACTTTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGATTTGGAAATTGATTACTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATGAGATTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCTAGCACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR642580, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607656 Chironominae sp. water mite diet isolate 14449-BHL040517-GBD11988_13612-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATATTTTATTTTCGGAGCCTGATCTGGAATAGTAGGAACTTCTTTTAGTATTTTAATTCGAGCAGAACTTGGTCACCCTGGTTCTTTAATCGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTGATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTAACTCTACTTCTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KJ444382, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607657 Chironominae sp. water mite diet isolate 14451-BHL040517-GBD14890_12748-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCTCTTAGTATATTTATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATCTTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGATTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR642580, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607658 Chironominae sp. water mite diet isolate 14457-BHL040517-GBD17338_7614-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGTTCTGGAATAGTCGGAACATCATTTAGTATATTAATTCGAGCAAAATTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAACATGAGATTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607659 Chironominae sp. water mite diet isolate 14458-BHL040517-GBD13614_22285-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACTTTATATTTTATTTGCGGAGCTTGATCTGGAATAGTAGGAACTTCACTTAGTATATTTATTCGAGCAGAATTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGCTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607660 Chironominae sp. water mite diet isolate 14462-BHL040517-GBD5389_23432-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACATCTTTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGATCTTTTATTGGAGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATACTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCACCTTCTTTAACTCTACTACTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM960768, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607661 Chironominae sp. water mite diet isolate 14463-BHL040517-GBD26207_16011-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCCTGATCTGGAATAGTTGGAACTTCTCTTAGTATTTTAATTCGAGCAGAATTTGGACACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR654792, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607662 Chironominae sp. water mite diet isolate 14478-BHL040517-GBD27935_11750-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTTACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCATTTAATACTAGTGGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTTACATTACTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607663 Chironominae sp. water mite diet isolate 14479-BHL040517-GBD15007_22638-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAATTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTATGATTACTTCCCCAATCTTTAACCCTTCTTCTATCTAGCTGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607664 Chironominae sp. water mite diet isolate 14485-BHL040517-GBD8762_23711-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCTTTTAGTATATTAATTCGAGCAGATCTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTACTTCTATCTAGCTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607665 Chironominae sp. water mite diet isolate 14489-BHL040517-GBD15962_27392-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCATTTAGTATATTTATTCGAGCAGAATTAGGACACCCTGGAACTTTTATTGGTGATGACCAATTTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATACTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM988908, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607666 Chironominae sp. water mite diet isolate 14490-BHL040517-GBD25937_10289-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCATGATCTGGAATAGTAGGAACATCTCTTAGAATATTAATTCGAGCAGAACTTGGACACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACCTCCCCCTTCTTTAACTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607667 Chironominae sp. water mite diet isolate 14493-BHL040517-GBD3890_10669-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTTGGAACTTCATTTAGTATTTTAATTCGAGCAGAATTTGGTCATCCTGGAACCTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATGTAGCATTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR289910, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607668 Chironominae sp. water mite diet isolate 14497-BHL040517-GBD25043_12711-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KT115418, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607669 Chironominae sp. water mite diet isolate 14504-BHL040517-GBD21330_5736-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATTTTAATTCGAGCAGAACTTGGTCATCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGAATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTGCTTCCCCCATCATTAACTCTACTTCTATCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607670 Chironominae sp. water mite diet isolate 14508-BHL040517-GBD19432_16791-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTTGGAACTTCTCTTAGTATATTTATTCGAGCAGAGCTTGGTCAACCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTAACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR654792, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607671 Chironominae sp. water mite diet isolate 14522-BHL040517-GBD16636_17410-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTTTATTTTATTTTCGGAGCTTGATCTTGAATAGTAGGAACTTCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGCACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCAATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCATTAACTCTACTTCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607672 Chironominae sp. water mite diet isolate 14560-BHL040517-GBD19926_3280-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTAACATGGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGGACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KR166401, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607673 Chironominae sp. water mite diet isolate 442-BHL040517-GBD14042_8283-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACCTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607674 Chironominae sp. water mite diet isolate 535-BHL040517-GBD17796_14824-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACCTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607675 Chironominae sp. water mite diet isolate 583-BHL072216-GBD10709_6043-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTAATGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTTTATAGTTATGCAAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACGTCTTCCCTCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607676 Chironominae sp. water mite diet isolate 606-BHL072216-GBD15192_16271-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGATACTTCTTTAAGTATGCTAAATCAAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAGATTGACTTATTCCTTTAATGTTAGGAGCCCCAAATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607677 Chironominae sp. water mite diet isolate 709-BHL072216-GBD23129_9091-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGATACTTCTTTAAGTATGCTAATTCGAGTGGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTCATTATAATTTTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGGACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607678 Chironominae sp. water mite diet isolate 763-BHL040916-GBD23032_13376-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACTTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGATAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACCCTTTTACTATCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607679 Chironominae sp. water mite diet isolate 769-BHL040916-GBD9201_4105-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAGCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607680 Chironominae sp. water mite diet isolate 778-BHL040916-GBD5255_23434-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTTATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATATGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATCCTGATTACTTCCACCTTCTTTATCTCTTCTTCTATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607681 Chironominae sp. water mite diet isolate 786-BHL040916-GBD19230_17797-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGTTTGGTCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACGCCCAGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTTATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTTTACCACCCTCTTTAACTCTTTTACTTTCAAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR289362, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607682 Chironominae sp. water mite diet isolate 850-BHL100916-GBD13863_10628-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCTTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607683 Chironominae sp. water mite diet isolate 877-BHL100916-GBD22498_8575-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCATCTTTAACCCTACTACTTTCTAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607684 Chironominae sp. water mite diet isolate 882-BHL100916-GBD24272_15273-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACGACCAGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTTATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGACTATTACCACCCTCTTTAACTCTATTACTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR289362, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607685 Chironominae sp. water mite diet isolate 896-BHL100916-GBD4433_17735-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAACTGGTTATTACCACTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607686 Chironominae sp. water mite diet isolate 1139-BHL110116-GBD15657_27990-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KM988908, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607687 Chironominae sp. water mite diet isolate 1157-BHL110116-GBD18914_7425-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCTCTTAGTATATTAATTCGAGCAGAACTTGGTCACCCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTACCCCCTTCTTTATCTCTTCTTCTATCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KT115418, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607688 Chironominae sp. water mite diet isolate 1266-BHL110116-GBD9352_18286-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAATAGGTACTTCATTTAGTATATTAATTCGAGCAGAACTTGGTCACCCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR642580, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607689 Chironominae sp. water mite diet isolate 1279-BHL110116-GBD17863_2003-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACTTCACTTAGTATTTTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTAACTCAACTACTATCTAGCACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR754526, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607690 Chironominae sp. water mite diet isolate 1294-BHL110116-GBD28312_18952-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACATCATTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTCTAACTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM988908, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607691 Chironominae sp. water mite diet isolate 1303-BHL110116-GBD20364_26422-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACTTCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTTGTTCCTTTAATATTAGGATCCCCTGATATAGCTTTTCCACGAATAAATAATATTAGATTCTGATTACTTCCCCCTTCTTTATCTCGTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR754526, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607692 Chironominae sp. water mite diet isolate 1315-BHL110116-GBD5820_11347-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTACTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAACCCCTGATATAGCTTTTCCACGAATAAATAATACGAGATTTTGATTACTTCCCCCTGCTTTAACTCTTCTTCTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR754526, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607693 Chironominae sp. water mite diet isolate 1317-BHL110116-GBD9038_8534-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACATCTTTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGTACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTTCCACGAATAAGTAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR754526, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607694 Chironominae sp. water mite diet isolate 1324-BHL110116-GBD15971_4061-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAAGAGTAGGGACATCACTTAGTATATTAATTCGAGCAGAACTTGTTCACCCTGTAACTTTTATTGGTTATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR754526, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607695 Chironominae sp. water mite diet isolate 1331-BHL110116-GBD6802_24257-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCCCTTAGTATATTTATTCGAGCAGAACTTGGTCAGCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTACCCCCTTCTTTAACTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR286005, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607696 Chironominae sp. water mite diet isolate 1334-BHL110116-GBD25964_21264-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATTTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCATGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTAACACTTCATCAATCTAGCTCAAGTGTAGAAAATGAAGCTGAAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR754526, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607697 Chironominae sp. water mite diet isolate 1356-BHL110116-GBD28493_15932-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACTTCATTTAGTATATTAATTCGAGTAGAACTTGGTCACCCTGGAACATTAATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTTCTATCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR754526, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607698 Chironominae sp. water mite diet isolate 1365-BHL110116-GBD24394_5145-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCAAGATATAGCTTTCCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTAACTCTACTTCTTTCTAGCTCAGTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KM988908, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607699 Chironominae sp. water mite diet isolate 1366-BHL110116-GBD8299_18270-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTCTCCCCGAATAAATAATATGAGATTTTGATTACCTCCCCCTTCTTTAACTCGTCGTCGTTCTAGCGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR754526, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607700 Chironominae sp. water mite diet isolate 1369-BHL110116-GBD24761_25798-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGGACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCACGAATAAATAGTATGAGATTTTGATTACTTCCCCCTTCTTTATCTCATCTTCTTTCTAGCACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR754526, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607701 Chironominae sp. water mite diet isolate 1370-BHL110116-GBD14932_3519-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTAGAATAGTAGGGACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTTATGCTCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCACTTGTAGAAAATGGAGCTGGACCAG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR754526, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607702 Chironominae sp. water mite diet isolate 1373-BHL110116-GBD20912_8757-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACATCACTTAGTATATTTATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCCGTCTAGAACAATTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ444382, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607703 Chironominae sp. water mite diet isolate 1382-BHL110116-GBD10448_10323-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTCGGAGCTTGATCTGGAATAGTCGGGACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAACATGAGATTTTGATTACTTCCCCCATCTTTAACTCTTCTTCTATCAAGCACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR754526, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607704 Chironominae sp. water mite diet isolate 1388-BHL110116-GBD16177_13753-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACATCACTTAGTATATTAATTCGAGTAGAATTTGGTCACCCAGGAACTTTTATAGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR754526, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607705 Chironominae sp. water mite diet isolate 1405-BHL110116-GBD25306_23558-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGGACATCATTTAGTATATTAATTCGAGCAGAATTTGGTCACCCTGGAATTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCCCCTGATATAGCATTTCCACGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KM988908, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607706 Chironominae sp. water mite diet isolate 1518-BHL110116-GBD19693_5460-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCTTTTAGTATATTAATTCGAGCAGAACTAGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR654792, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607707 Chironominae sp. water mite diet isolate 1619-BHL110116-GBD7747_7307-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCAGGATCTTTTATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTCCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCGTCTTTATCTTTTCTTCTATCTAGCTCAAAAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR159655, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607708 Chironominae sp. water mite diet isolate 1623-BHL110116-GBD24777_15097-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTCGGTCACCCTGGAACTTCTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTAACTCTACTACTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR159655, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607709 Chironominae sp. water mite diet isolate 1628-BHL110116-GBD6177_12809-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACATCCTTTAGTATATTAATTCGAGCAGAATTAGGACACCCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR286005, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607710 Chironominae sp. water mite diet isolate 1640-BHL110116-GBD27672_9565-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACTTTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCCTTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTAACCCTTCTTCTATCAAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR286005, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607711 Chironominae sp. water mite diet isolate 1673-BHL110116-GBD9348_26563-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTTGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR159655, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607712 Chironominae sp. water mite diet isolate 1771-BHL110116-GBD21812_18384-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCACTTAGTATATTTATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGCTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTAACTCTTTTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607713 Chironominae sp. water mite diet isolate 1783-BHL110116-GBD24935_11452-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAGCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTCCCATTAATATTAGGAGCACCAGATATGGCCTTCCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCGCTTACTCTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607714 Chironominae sp. water mite diet isolate 1806-BHL101516-GBD10096_25843-Ldc86 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGATACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGTTGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTCATTATAATTTTTTTTATAGTTATGCCAGTTTTAATTGGAGGTTTTGGAAATTGACTTTTTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATATTATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTGTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607715 Chironominae sp. water mite diet isolate 1844-BHL072216-GBD12149_26102-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTATTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR670143, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607716 Chironominae sp. water mite diet isolate 1852-BHL072216-GBD22783_11539-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATACTTTATTTTTGGAGCTTGATCTGGTATTGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCATTAACTCTTTTACGATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607717 Chironominae sp. water mite diet isolate 1858-BHL072216-GBD16637_26780-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATATTAATTCGAGCGGAATTAGGTCATCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCTCTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607718 Chironominae sp. water mite diet isolate 1859-BHL072216-GBD11366_8124-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAACGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607719 Chironominae sp. water mite diet isolate 1867-BHL072216-GBD11807_11141-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACGCCCAGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTTATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCACCAGATGTAGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTTTACCACCCTCTTTAGCTCTTTTACTTTCAAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR289362, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607720 Chironominae sp. water mite diet isolate 2135-BHL072216-GBD11680_14599-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCAGGAACTTTTATTGGTGACGACCAAATTTGTAATGTTATTGTAACAGCTCATGCTTTTATAATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTACCTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607721 Chironominae sp. water mite diet isolate 2162-BHL072216-GBD16598_4479-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGATGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGTAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTGATATTAGGAGCACAAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607722 Chironominae sp. water mite diet isolate 2164-BHL072216-GBD25064_25357-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATCTTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGTATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCGTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607723 Chironominae sp. water mite diet isolate 2198-BHL072216-GBD6960_4424-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATACTTTATTTTTGGAGCCTGATCCGGAATAGTTGGAACTTCTTTAAGAATTCTTATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607724 Chironominae sp. water mite diet isolate 2240-BHL072216-GBD12958_4935-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGCATTAGGACATCCTGGAACTTTTATTGGCGACGACCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCACGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCCCTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607725 Chironominae sp. water mite diet isolate 2241-BHL072216-GBD14445_27862-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTGTTTAAGAATTCTAATTCGAGTAGACTTAGGACATCCTGGATCTTTTATTGGTGACGACCAAATTTATAATGTTATTGTATCAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607726 Chironominae sp. water mite diet isolate 2286-BHL072216-GBD22355_17515-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTATATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTAACGCTACTTCGATCTAGCTCAATTGTAGAAAATGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607727 Chironominae sp. water mite diet isolate 2306-BHL072216-GBD29198_16954-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCT	Using NCBI BLASTN in June 2018, this sequence was 98.6% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607728 Chironominae sp. water mite diet isolate 2307-BHL072216-GBD20658_25493-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCTTTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTAACTCTACTACTTTCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM921023, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607729 Chironominae sp. water mite diet isolate 2320-BHL072216-GBD19111_28568-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAAAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607730 Chironominae sp. water mite diet isolate 2378-BHL072216-GBD25674_22307-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTCGGAACTCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTACTTTATCTCATCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607731 Chironominae sp. water mite diet isolate 2388-BHL072216-GBD20729_12966-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTAGGTCACCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGCGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KM988908, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607732 Chironominae sp. water mite diet isolate 2438-BHL072216-GBD12403_28044-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAACAGAATTAGGACATCCTGGAACTTTTATTGTTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGGTTAGTTCCTCTTATATTAGGAGCAACAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607733 Chironominae sp. water mite diet isolate 2485-BHL072216-GBD28942_17072-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTTTATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCCCTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCATTAACTCTTCTTCTATCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR286005, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607734 Chironominae sp. water mite diet isolate 2537-BHL072216-GBD27670_12817-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCTTTAAGAATATTAATCCGAGCGGCATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607735 Chironominae sp. water mite diet isolate 2546-BHL072216-GBD11323_5663-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATGAGATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTGTAATTCGAGCAGAATTAGGATATCCTGGAACTTTTATTGGTGACGACCAATTTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607736 Chironominae sp. water mite diet isolate 2548-BHL072216-GBD13691_4451-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCGAAATTAGGACATCCTGGAACATTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGATATAGCATTTCCTCGTATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607737 Chironominae sp. water mite diet isolate 2561-BHL072216-GBD17900_17271-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCATTAAGAATATTAATTCGAATGGAATTATGTCAACCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607738 Chironominae sp. water mite diet isolate 2577-BHL072216-GBD13276_16938-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTGGTGCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCTTCTTTAACTCTTCCTCTTTCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607739 Chironominae sp. water mite diet isolate 2629-BHL072216-GBD24167_24681-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACTTTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTCTAATTTGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCACGAATAAATAACATAAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTTCTATCTAGCACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR174905, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607740 Chironominae sp. water mite diet isolate 2640-BHL072216-GBD22989_25355-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGTACATTAATTCGAGCCGAATTAGGACGCCCAGTTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTGTAATTTTTTTATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTTTACCACCCTCTTTAACTCTTTTACTTTCAAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR289362, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607741 Chironominae sp. water mite diet isolate 2649-BHL072216-GBD8451_10823-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTGTATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGGGACGACCAAATTTATAGTGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATACAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTCATCTCTTCTTCTTTCTAGTTCTATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607742 Chironominae sp. water mite diet isolate 2768-BHL032417-GBD20582_18935-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607743 Chironominae sp. water mite diet isolate 2820-BHL032417-GBD7862_4342-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTATTTTTTTAGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGTACATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAGGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607744 Chironominae sp. water mite diet isolate 2858-BHL032417-GBD27404_15287-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTGGAGCCTGATCAGGTATTGTAGGAACTTCTTTTAGAATATTAATCTGGACGGAATTTGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607745 Chironominae sp. water mite diet isolate 2885-BHL032417-GBD10592_3283-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTTGTTCGAACTGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTGTCGAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607746 Chironominae sp. water mite diet isolate 2888-BHL032417-GBD18703_27612-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCAAGCAGAACTTGGATGACCTGGTACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACCCTTTTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607747 Chironominae sp. water mite diet isolate 2902-BHL032417-GBD3850_8887-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTTAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTACTTGTTACTGCTCATGCATTTATAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATCACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACCTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607748 Chironominae sp. water mite diet isolate 2945-BHL032417-GBD27470_15251-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAACTAGGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGAATTTGATTATTACCCCCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607749 Chironominae sp. water mite diet isolate 2983-BHL032417-GBD10174_19926-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCTAACGGAATTAGGTTATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTAGCACCATCTCTTACTTTATTACTTTCAAGAAGATTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607750 Chironominae sp. water mite diet isolate 2991-BHL032417-GBD15409_2508-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATACTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGTAACATTTATTGTTTATGACCAAATTTATAATGAAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607751 Chironominae sp. water mite diet isolate 3018-BHL032417-GBD15737_4961-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATATTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGGATTAGGTCATCCTGGTACATTTATTGGTTATGACCAAATTTATAATGTAACTTTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607752 Chironominae sp. water mite diet isolate 3031-BHL032417-GBD9794_16281-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATATTAATCCGAACGAAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607753 Chironominae sp. water mite diet isolate 3034-BHL032417-GBD19236_4451-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGGACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGCAATTATTACTGCTCATGCTTTTATTATAATTTTTTTTATGGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607754 Chironominae sp. water mite diet isolate 3043-BHL032417-GBD9460_16512-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTTATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGGGTTAGGTCATCCTGGAACGTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTGTTTTAATTGGAGGATTTGGAAATTTGTTATTACCACTAATATTAGGAGTCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607755 Chironominae sp. water mite diet isolate 3049-BHL032417-GBD18604_12546-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGAAACTTCTTTAAGAATATTTATCCAAACGGAATTAGGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTCTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607756 Chironominae sp. water mite diet isolate 3058-BHL032417-GBD8345_8189-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTGGAGCCTGATCAGGCATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTAGTTCCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607757 Chironominae sp. water mite diet isolate 3064-BHL032417-GBD21063_2485-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCCGGTATAGTTGCAACTTCTTTCAGAATATTAATCCGACCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATGACCACCATCGCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607758 Chironominae sp. water mite diet isolate 3068-BHL032417-GBD24086_8434-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGTTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTCCTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGACCCTGATATGGATTTTCCACGAATAAATAATATAGGATTTTGATTATTACCACCATCTCATACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607759 Chironominae sp. water mite diet isolate 3088-BHL032417-GBD24054_21978-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTCATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTAATGACCAAATCTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAAATGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCAGCTCATACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607760 Chironominae sp. water mite diet isolate 3089-BHL032417-GBD27727_14344-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACAACCTGGCACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607761 Chironominae sp. water mite diet isolate 3092-BHL032417-GBD5554_22548-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATACTAATTCGAACGGGATTAGGTCATCCTGGAACATTCATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGATGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607762 Chironominae sp. water mite diet isolate 3093-BHL032417-GBD25984_19025-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTTAGCATATTAATTCGAGCGGAATTAGGTCAACCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTAGCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607763 Chironominae sp. water mite diet isolate 3116-BHL032417-GBD26694_13458-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTTTATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAATGGAATTAGGTCATCCTGGATCATTTATTGGTGATGACCAAATTTATAATGCAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGAAAATTGGTTATTACCACTAATATTAGGAACCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACATTCAAGAAGAATAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607764 Chironominae sp. water mite diet isolate 3120-BHL032417-GBD21940_10892-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAATAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGAGTAATACCACCATCTCTTACTTGATGACTATCAAGAAGAATAGTAGACAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607765 Chironominae sp. water mite diet isolate 3134-BHL032417-GBD20763_18321-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTTTATTAATTGGAGGATTTGCAAATTGGTTATTACCACTAATATTAGGAGCTCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTATCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607766 Chironominae sp. water mite diet isolate 3144-BHL032417-GBD21393_5409-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTATTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTCGAACATTTACTGGTGATAACCAAATTTATAATGTAATTATTACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTAGTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607767 Chironominae sp. water mite diet isolate 3159-BHL032417-GBD15861_24716-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTTAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGAACAAATTTTTAATGTAATTGTTACTGATCATGCTTTTATTGTAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAAGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607768 Chironominae sp. water mite diet isolate 3161-BHL032417-GBD7909_6038-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCCGGTATAGTAGGAACTTCTTTAAGAATATTCATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTGTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAA	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607769 Chironominae sp. water mite diet isolate 3180-BHL032417-GBD17870_2713-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTGTATTTTTTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTTATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCTCTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607770 Chironominae sp. water mite diet isolate 3186-BHL032417-GBD10539_14619-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTCTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGGATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAACTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGAAATTGGTTATTACAACTAATATTAGGAGCCCCTGATATGGCCTTTCCACGGATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607771 Chironominae sp. water mite diet isolate 3204-BHL032417-GBD3313_13431-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATGCTGGAACATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTTCCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607772 Chironominae sp. water mite diet isolate 3206-BHL032417-GBD16144_4096-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTTGGAGCTTGATCAGGAATAGAAGGAACTTCTTTAGGAATATTAATCGGAACGGAATTAGGTCATCCTGGAACATTTATTGGGGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGATGATTTGGAAATTGGTTATTATCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607773 Chironominae sp. water mite diet isolate 3214-BHL032417-GBD13694_9239-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTCTTTTGGAGCTCGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATCTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTAGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAACCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGAATATTACCATCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607774 Chironominae sp. water mite diet isolate 3222-BHL032417-GBD20008_2431-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTGTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCATGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTATTTGGAGGATTTGGAAATTGGTTATTATCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATACAAGATTTTGAGTATTACCACCATCTCTTACTTTATTACGTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607775 Chironominae sp. water mite diet isolate 3223-BHL032417-GBD19178_17651-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTTTATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATCCGAGCGGAATTAGGTCATCCTGGATCATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTGCCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607776 Chironominae sp. water mite diet isolate 3224-BHL032417-GBD19669_20580-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTTTACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607777 Chironominae sp. water mite diet isolate 3231-BHL032417-GBD17765_7561-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACTGAAATAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCCCATGCTTTTATTATAATTTTTTTTATAGTATTACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACATTATTACGTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607778 Chironominae sp. water mite diet isolate 3234-BHL032417-GBD11730_19160-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCGTTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTACTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACCAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTATTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607779 Chironominae sp. water mite diet isolate 3236-BHL032417-GBD5624_9378-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCGGAATTAGGTCATCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGAAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTTCCACCATCTCTTACTTTATTACTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607780 Chironominae sp. water mite diet isolate 3240-BHL032417-GBD17784_2483-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCTTGATCAGGGATAGGAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGTAACATTTAATGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGACTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607781 Chironominae sp. water mite diet isolate 3243-BHL032417-GBD7353_22222-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCCTTATATATTTTTTTTGGAGCTTGATCAGATATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATGCCTATTTTAATTGGAGGATTTGGAAATTGGTTAGTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACATTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607782 Chironominae sp. water mite diet isolate 3244-BHL032417-GBD16680_7527-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGATGATGACCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGATACTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATATGATTTTGATTATTACCACCATCCCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607783 Chironominae sp. water mite diet isolate 3251-BHL032417-GBD22103_21842-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTCTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAAACCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607784 Chironominae sp. water mite diet isolate 3255-BHL032417-GBD15217_2815-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGTTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAAGTAGGTCATCCTGGAACATTTATTGGGGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGTGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTTCTTTATTACTTTCAAGAAGAATAGTAGAAAATGGCGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607785 Chironominae sp. water mite diet isolate 3257-BHL032417-GBD24547_24467-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATACTAGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAGTAATAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAGGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607786 Chironominae sp. water mite diet isolate 3263-BHL032417-GBD24625_20576-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTCATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGTAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTACCACCATCTCTAACTTTATTACTTGCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607787 Chironominae sp. water mite diet isolate 3267-BHL032417-GBD2737_10598-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTGAATTTTTGGAGATTGATCAGGTATAGTAGGAACTTCTTGAAGAATATTAATCCGAAGGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTACTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607788 Chironominae sp. water mite diet isolate 3273-BHL032417-GBD26815_10215-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTCTTTTGGAGCTTGATTAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAATGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGTAGCCCCTGATATGGCTTTTCCACGAAAAAATAAAATAAGATATTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607789 Chironominae sp. water mite diet isolate 3274-BHL032417-GBD13778_18371-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGAAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAACTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTATGAGCCCCTGATATGGCTTCTCCACGAATAAATAATATAAGATTTTGATTAATACCACCATCTCTTACTTTATCACTTTCAGGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607790 Chironominae sp. water mite diet isolate 3283-BHL032417-GBD2133_16538-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCCCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCATTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAAAATAAGATTTTGAATATTACCCCCATCTCTTACTCTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607791 Chironominae sp. water mite diet isolate 3287-BHL032417-GBD24516_21329-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGAGCAGGTATAGTAGGAACTTCTTTAAGTATATTAATTCGAACGGAATTAGGTAATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATAGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTTCCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTGACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607792 Chironominae sp. water mite diet isolate 3337-BHL032417-GBD7820_21012-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATTAGGTATAGTAGGTACTTCTTTAAGACTTTTAATCCGAACGGAATTAGGTCGTCCTGGAACATTTATTTGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTTTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607793 Chironominae sp. water mite diet isolate 3351-BHL032417-GBD23579_16224-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCCTTATCTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTATGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTTTAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGCTATTACCACTAATATTAGGAGTCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTGCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607794 Chironominae sp. water mite diet isolate 3353-BHL032417-GBD28648_15971-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTGGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTGGACCACGAATAAATAATATAAGATTTTGATTATGACCACCATCTCTTACTTTATTACATTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607795 Chironominae sp. water mite diet isolate 3356-BHL032417-GBD17637_23307-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGACCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGTACGGAATTAGGTCATCCTGGAACATTTCTTGGTACTGACCAAATTTATAATGCTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607796 Chironominae sp. water mite diet isolate 3369-BHL032417-GBD6215_14780-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAAGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGCCATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGTTTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607797 Chironominae sp. water mite diet isolate 3383-BHL032417-GBD3420_20668-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTTATGCTTTTATTATAATTTTTTTTATAGTAATTCCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCCCGAATAAATAATATAAAATTTTGATTATTACCCCCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607798 Chironominae sp. water mite diet isolate 3385-BHL032417-GBD27783_19431-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGCAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGGTGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAGATTGGTTAATACCACTAATATTAGGAGTCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAAGGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607799 Chironominae sp. water mite diet isolate 3392-BHL032417-GBD23732_8277-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTTAGTATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGATTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATGAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTGGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607800 Chironominae sp. water mite diet isolate 3393-BHL032417-GBD27385_15075-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTACATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGATGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATGCCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTTACTTTATTACTCTCACGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607801 Chironominae sp. water mite diet isolate 3403-BHL032417-GBD27035_18406-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCCTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTCTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCATTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTCTGATTATTACCACCAACTCTTACTTGAGTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607802 Chironominae sp. water mite diet isolate 3404-BHL032417-GBD10518_14537-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATGTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATACTGGAACATTTATTGGTGCTGACCAAATTTATAATGTAATTGTTAATGATCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTTGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTAACACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607803 Chironominae sp. water mite diet isolate 3406-BHL032417-GBD26296_8089-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTTAGAATATTAATCCGAACGAAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTTTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGGAATACCTATTTTAATTGGAGGCTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGACTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607804 Chironominae sp. water mite diet isolate 3410-BHL032417-GBD14467_18061-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGGGCTTGATCAGGTATAGTAGGAATTTCTTTATGAATATTAATCCGAACGGAATTAGGTCTTCCTGGAACATTTATTGGTGATGACAAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAAGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607805 Chironominae sp. water mite diet isolate 3420-BHL032417-GBD15023_7338-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGACTATTAATCCGTACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTAGTACCACTAATATTAGGAGCACATGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607806 Chironominae sp. water mite diet isolate 3441-BHL032417-GBD26262_9228-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTATTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAGATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTATCACCATCGCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607807 Chironominae sp. water mite diet isolate 3444-BHL032417-GBD26219_13035-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAAGGGAATTAGGTCATCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGATCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATATTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607808 Chironominae sp. water mite diet isolate 3462-BHL032417-GBD20310_8988-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGTTTGAACAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATATAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATGGTAATACCTATTTTAATTGGAGGATTTGGAAAATGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAGTAATATAAGATTTTGATTATTACCATCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607809 Chironominae sp. water mite diet isolate 3469-BHL032417-GBD15836_2760-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACAGAATTAGGTCATCCTGTAACATTTATTGGTTATGATCAATTTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATATGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607810 Chironominae sp. water mite diet isolate 3485-BHL032417-GBD15428_23209-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTTTTTAAGAATTTTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTATTTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607811 Chironominae sp. water mite diet isolate 3590-BHL032417-GBD9233_10264-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGCTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCTCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGACTACTACCACCATCTCTGACTGTATTACTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607812 Chironominae sp. water mite diet isolate 3591-BHL032417-GBD9077_4733-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607813 Chironominae sp. water mite diet isolate 3702-BHL032417-GBD29105_19089-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAATGGAATTAGGTCATCCTGGATCATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTAACCTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607814 Chironominae sp. water mite diet isolate 3770-BHL032417-GBD26980_8507-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACTGTTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGACTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607815 Chironominae sp. water mite diet isolate 3791-BHL032417-GBD20811_14024-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGAGCTTGATCCGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGCCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTATTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTGATTTCTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607816 Chironominae sp. water mite diet isolate 3876-BHL032417-GBD14307_3453-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGTAACATTTATTGGGGATGACCATATTTATAATGTAATTTTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607817 Chironominae sp. water mite diet isolate 3899-BHL032417-GBD23988_10666-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGAATTTGAATAATAACACCATCTCGAACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607818 Chironominae sp. water mite diet isolate 3915-BHL032417-GBD4754_23802-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATATGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTCCCCCCTTCATTAACTCTTTTACTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607819 Chironominae sp. water mite diet isolate 4118-BHL032417-GBD16589_12611-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTTATTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCGCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATAGGATGTTTTGGAAATTGATTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACGTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607820 Chironominae sp. water mite diet isolate 4183-BHL032417-GBD9074_4735-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCTGGTATAGTTGATACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGTAACCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607821 Chironominae sp. water mite diet isolate 4184-BHL032417-GBD25578_21754-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTCTTTTTGGAGCTTGATCTGGTATCGTAGGTACTTCTTCAAGTATGCTAATTCGAGCAGTACTTGGACGACCTGGTACTTTTATTGGAGATGAACAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTGCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607822 Chironominae sp. water mite diet isolate 4220-BHL032417-GBD20112_28211-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACATTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607823 Chironominae sp. water mite diet isolate 4258-BHL032417-GBD19177_10021-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCATAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607824 Chironominae sp. water mite diet isolate 4354-BHL032417-GBD9902_4384-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATACTAATTCGAGCAGAATTAGGACGACCTGGTACTTTTATTGGAGATGAGCAAATTTATAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGGCTTCTTCCCCCTTCATTAACCCTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607825 Chironominae sp. water mite diet isolate 4388-BHL032417-GBD26617_8353-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATCTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCAAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTGATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGATTTATTCCTTTAATGTTAGGTGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607826 Chironominae sp. water mite diet isolate 4390-BHL032417-GBD13164_28466-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGAATGCTTATTTGAGCAGAATTTGGACGACCTGGTACTTTCATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607827 Chironominae sp. water mite diet isolate 4393-BHL032417-GBD27606_17656-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGAATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTAGGACATCCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACCCTTCTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607828 Chironominae sp. water mite diet isolate 4413-BHL032417-GBD14878_5815-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCAAGCAGAACTTGGACTACCTGGTACTTTTATTGGAGATGAGCATATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCACTTTTACTTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCAAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607829 Chironominae sp. water mite diet isolate 4414-BHL032417-GBD27819_10746-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGATCTTGGACGACCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGATTTATACCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607830 Chironominae sp. water mite diet isolate 4429-BHL032417-GBD20862_15106-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACAACCTGGTACTTTTACTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAATTTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACCCTTTTACTTTCAAGTACTAAAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607831 Chironominae sp. water mite diet isolate 4822-BHL032417-GBD27242_19231-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAACGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATGGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGCTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607832 Chironominae sp. water mite diet isolate 4841-BHL032417-GBD21593_19042-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTATAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCTTTTTAATTGGAAGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTACCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607833 Chironominae sp. water mite diet isolate 4876-BHL032417-GBD14900_25712-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR641103, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607834 Chironominae sp. water mite diet isolate 4925-BHL032417-GBD24667_13068-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATATTGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGGTTATTACCACTAATATTAGGAGCTCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAA	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607835 Chironominae sp. water mite diet isolate 5011-BHL032417-GBD9226_19770-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCAAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607836 Chironominae sp. water mite diet isolate 5127-BHL032417-GBD15149_12461-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATGATAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTATCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTTAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607837 Chironominae sp. water mite diet isolate 5230-BHL032417-GBD23410_15878-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAGTTCGAGCAGAACTTGGTCACCCCGGATCTTTTATTGGTGATGATCAAATTTATAATGTTATTGTTACCGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTATCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR159655, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607838 Chironominae sp. water mite diet isolate 5260-BHL032417-GBD17624_28721-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGTTGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTAATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCATTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTAACCTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607839 Chironominae sp. water mite diet isolate 5415-BHL032417-GBD23868_15266-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTTAGAATATTAATCCGAATGGAATTATCTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCATGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607840 Chironominae sp. water mite diet isolate 5730-BHL032417-GBD21181_14847-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTATTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAACGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTTTATGGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607841 Chironominae sp. water mite diet isolate 5780-BHL032417-GBD5558_6972-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGATCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGTAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607842 Chironominae sp. water mite diet isolate 5986-BHL032417-GBD17948_24871-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACATCTTTAAGAATTCTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCCTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607843 Chironominae sp. water mite diet isolate 5987-BHL032417-GBD5535_13243-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATGGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607844 Chironominae sp. water mite diet isolate 6034-BHL032417-GBD10465_15607-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGTATTAGGACATCCTGTTACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAAAAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCGCTTCTTCTTTCTAGTTCCATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607845 Chironominae sp. water mite diet isolate 6060-BHL032417-GBD9208_6394-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCATCTTTATCTCTTCTTCTATCAAGTTCTATTGCAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607846 Chironominae sp. water mite diet isolate 6120-BHL032417-GBD22515_24116-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGTACTTTTATTGGAGACGACCAAATTTATAATTTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAATTCCTCTTATATTAGGAGCACCAGATGTAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCATTAACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607847 Chironominae sp. water mite diet isolate 6137-BHL032417-GBD10445_5797-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGTTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATCTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCACTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607848 Chironominae sp. water mite diet isolate 6207-BHL032417-GBD21671_27889-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATTTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTTGAGGTTTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607849 Chironominae sp. water mite diet isolate 6237-BHL032417-GBD26255_21505-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGACGACCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTACTACCCCCTTCTCTATCTCTTCTTCTTTCTAGCTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607850 Chironominae sp. water mite diet isolate 6247-BHL032417-GBD20176_6019-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTTTAACAGCTCATGATTTTATTATAATTTTTTTCATAGTTATACACATTTTAATTGGAGGATTTGGAAATTGATTAGTTTCTCTTATATTAGGAGCACCTGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607851 Chironominae sp. water mite diet isolate 6345-BHL032417-GBD26773_22883-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTGTAATGTTATTGTAACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607852 Chironominae sp. water mite diet isolate 6351-BHL032417-GBD29264_17564-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTATTTTTGGAGTCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATGCTCATTTTAATTGGATGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCT	Using NCBI BLASTN in June 2018, this sequence was 96.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607853 Chironominae sp. water mite diet isolate 6357-BHL032417-GBD18465_13029-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGCACTTCTTTAAGAATTCTTATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATAGCATTTCCTTGAATAAATAATATAAGATTCTGACTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607854 Chironominae sp. water mite diet isolate 6373-BHL032417-GBD17025_12936-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTAGATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACCTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGATCACCAGATATAGCATTTCCTCGAATAGATAATATAAGATTCTGATTACTTCCCCCTTCTTTAGCACTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607855 Chironominae sp. water mite diet isolate 6393-BHL032417-GBD8128_14850-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGTCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTATGACATCCTGGAACTTTTATTGGAGACGATCAAATTTATAATGTTCTTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGACTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACCCTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607856 Chironominae sp. water mite diet isolate 6419-BHL032417-GBD10793_25933-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGAAACTTCTTTAAGTATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGAACAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCTTCTTTAACCCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607857 Chironominae sp. water mite diet isolate 6445-BHL032417-GBD26823_13829-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGATCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAAATAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATATTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCACTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCTTCTTTACCACTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607858 Chironominae sp. water mite diet isolate 6457-BHL032417-GBD2155_15855-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAACGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCCCTACTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607859 Chironominae sp. water mite diet isolate 6463-BHL032417-GBD28258_20381-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATATTAATCCGAGCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCAGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTAACTTTATTACTAACAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607860 Chironominae sp. water mite diet isolate 6479-BHL032417-GBD27141_9602-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGGGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGACTAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACCCTACTAATTTCTAGTTCTACTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607861 Chironominae sp. water mite diet isolate 6495-BHL032417-GBD16821_4204-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCCTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGAACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCTTCTCTATCTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607862 Chironominae sp. water mite diet isolate 6513-BHL032417-GBD8348_10630-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTATGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTTATTGTAACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTCATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATACTATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607863 Chironominae sp. water mite diet isolate 6603-BHL032417-GBD18661_7848-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCGATATCGCTTCGTCGTTCTAATTCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR287540, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607864 Chironominae sp. water mite diet isolate 6617-BHL032417-GBD10476_11456-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTTATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGGTATTTTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCCTTATCCCTTATTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607865 Chironominae sp. water mite diet isolate 6646-BHL032417-GBD15259_6522-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTACTTTTGTAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGAATACTCCCCCCTTCTTTATCTCTTCGTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607866 Chironominae sp. water mite diet isolate 6651-BHL032417-GBD26956_20954-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATACTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATCCTAATTCGAGTTGAATTAGGACATCCTGGAACTTTTATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAAAATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAAAATAAGATTCTGATTACTTCCCCCTTCTTTATCCCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607867 Chironominae sp. water mite diet isolate 7018-BHL032417-GBD12997_5166-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATCTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607868 Chironominae sp. water mite diet isolate 7080-BHL032417-GBD26534_12327-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGTATATTAATCCGAACGGAATTAGGTCATCCTGGTACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCTCTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACGTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607869 Chironominae sp. water mite diet isolate 7083-BHL032417-GBD9770_24810-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTATATTTTATTTTTGGAGCTTGATCCGGGATATTAGGAACCTCATTAAGCATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607870 Chironominae sp. water mite diet isolate 7098-BHL032417-GBD19949_12491-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGGTTATTACCACTAATATTAGGAACCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGAATATTACCACCATCTCTTACTGTATTACTTTCAAGAAGAATAGGAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607871 Chironominae sp. water mite diet isolate 7101-BHL032417-GBD11969_7521-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTTATTAGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCCTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTTCCACCATCTCTTACTTTATTACTTTCAAGAAGAATAATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607872 Chironominae sp. water mite diet isolate 7112-BHL032417-GBD21821_19459-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTTTATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTGATCCGAACGGAATTAGGTCATCCTGGTACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGGTTATTACCACTAATATTGGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTGTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607873 Chironominae sp. water mite diet isolate 7114-BHL032417-GBD26265_23683-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTTATTTTTGGAGCTTGATCAGGTATTGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTTATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTGTTACCACTAATATTAGGAGCCCCTGATATGGTTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCAGCTCTTACTTTAGTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607874 Chironominae sp. water mite diet isolate 7133-BHL032417-GBD13051_17902-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTGGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATAATAATTCGAACGGAATTAGGTCATCCTGGAACATTTACTGGTGATGACCAAATTTTTAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607875 Chironominae sp. water mite diet isolate 7141-BHL032417-GBD20182_8812-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTAGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCGTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTAGTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTATCACCATCTCTTACTTTATTACCTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607876 Chironominae sp. water mite diet isolate 7155-BHL032417-GBD24359_6827-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTTATACTGGAACATTTATTGGTGATGACAAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607877 Chironominae sp. water mite diet isolate 7158-BHL032417-GBD4315_17704-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTGTATTTTATTTTTGGAGCTTGATCAGGTATAGTATGAACTTCTTTATGTATATTAATCCGAACTGAATTAGGTCATCCTGGAACATTTATTTGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTGGGAGCCCCTGATATGGCTTTTCCACGAATAAAAAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607878 Chironominae sp. water mite diet isolate 7163-BHL032417-GBD17196_5254-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCTTCCTGTAACATTTATTGTTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTGGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACTACCATCTCTTACTTTATTAATTTCAAGAAGAATAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607879 Chironominae sp. water mite diet isolate 7169-BHL032417-GBD29551_16588-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTCTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACGGGAGGACTTGCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607880 Chironominae sp. water mite diet isolate 7181-BHL032417-GBD20223_7219-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTCTATTTTTTGGAGCTTGATCAGATATAGTAGGAACTTCTTTTATCATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAGATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTGGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607881 Chironominae sp. water mite diet isolate 7183-BHL032417-GBD27261_19875-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATGATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACACTACTACTTTCTAGTTCTATTGTAGAAAATGTAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607882 Chironominae sp. water mite diet isolate 7184-BHL032417-GBD26914_16878-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAGTCCGAACGGAATTAGAACATCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607883 Chironominae sp. water mite diet isolate 7189-BHL032417-GBD16246_2978-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCAGCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATGGTTACTGCTCATGCTTTTATTATAATTTTTTTAATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAACATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607884 Chironominae sp. water mite diet isolate 7190-BHL032417-GBD26905_19847-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCATGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTTGGAGCCCCTGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGACTATTACCCCCCTCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607885 Chironominae sp. water mite diet isolate 7199-BHL032417-GBD24679_12308-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGACATCCTGGATCATTTATTGGTGATGACCAAATTTATAATGTAATTGCTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCATGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTTACCTTATTACTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607886 Chironominae sp. water mite diet isolate 7203-BHL032417-GBD6498_25423-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGATCTTGATCAGATATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTATGTCTTCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATCATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTAGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607887 Chironominae sp. water mite diet isolate 7231-BHL032417-GBD13611_2955-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCTTGATCAGGGATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGGCAACCTGTAACATTTATTGGTTATGACCAAATTTATGATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607888 Chironominae sp. water mite diet isolate 7236-BHL032417-GBD5345_17998-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTGTATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAGTCCGAACGGAATTAGGTCATCTTGGAACATTTATTGGTGTTGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGATCCCCTGATATGGCTGTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607889 Chironominae sp. water mite diet isolate 7243-BHL032417-GBD23278_24562-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGTAACTTCTTTAAGTATATTAATCCGAACGGAATTAGGTAATACTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCATGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACATTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607890 Chironominae sp. water mite diet isolate 7244-BHL032417-GBD23512_18768-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTGCTTCTTTAAGTATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCATTTTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607891 Chironominae sp. water mite diet isolate 7247-BHL032417-GBD22770_23622-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607892 Chironominae sp. water mite diet isolate 7257-BHL032417-GBD5240_21329-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCACGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTAGTGATGCCCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTTGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGGTTATTACCACCATTTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607893 Chironominae sp. water mite diet isolate 7258-BHL032417-GBD19427_22459-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGAATTTAGGTCATCCTGGAACATTTATTGGTTATGACCAAAATTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGCAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTATCACCATCTCTTACCTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607894 Chironominae sp. water mite diet isolate 7259-BHL032417-GBD15470_27442-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATGCTAGTACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTTATATGGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTTCCCCCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607895 Chironominae sp. water mite diet isolate 7263-BHL032417-GBD6274_17007-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGAAGATGACCAAATTTATAATGTAATTGCTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAAATGGTTATTACCACTAATATTAGGAGCCCCTGATATGGTTTTTCCAGGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACCTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607896 Chironominae sp. water mite diet isolate 7272-BHL032417-GBD18923_4051-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGATTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTTCTTCTTTCATGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607897 Chironominae sp. water mite diet isolate 7273-BHL032417-GBD17732_3151-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGAAATTAGGTCATCCTGGAACATTTATTGGTTATGACCATATTTATAATGGAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCATGATATGGCTTTTCCACGAATAAATAAAATAAGATTTTGATTATTACCCCCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607898 Chironominae sp. water mite diet isolate 7277-BHL032417-GBD19422_28533-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGTTTGATCCGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGATTTAGGTCATCCCGGAACATTCATTGGTGATGACCAAATTTATAATATAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607899 Chironominae sp. water mite diet isolate 7278-BHL032417-GBD23041_9921-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTTAGAATATTAATCCGAACGGAATTAGATCATCCTGTAGCATTTATTTGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGACCCTGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607900 Chironominae sp. water mite diet isolate 7280-BHL032417-GBD20936_19530-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTATTTATGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTGATACCTATTTTAATTGAAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTGATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607901 Chironominae sp. water mite diet isolate 7288-BHL032417-GBD14028_11712-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTCGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGTAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTAGTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATGTGGAAATTGGTTATTACCACTAATATTAGGAGCCACTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTAGTACGTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607902 Chironominae sp. water mite diet isolate 7291-BHL032417-GBD6855_13797-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATATTAATCCGAACGGAATTAGGTCACCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCCTACATTATTACAATCAAAAAGAATAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607903 Chironominae sp. water mite diet isolate 7294-BHL032417-GBD23866_24163-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATCTTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATATTAATCCGAACGGAATTAGGTTATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCGCTTACTTTATTATTTGCAAGAAGAAGAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607904 Chironominae sp. water mite diet isolate 7297-BHL032417-GBD11528_4531-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGTTCAGGTATAGTAGGAACTTCTTTATGAATATTAATCCGAACGGAATTAGGTAATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGTTTTTCCACGAATAAATAATATAAGATTGTGATTATTACCACCATATCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607905 Chironominae sp. water mite diet isolate 7304-BHL032417-GBD17988_10628-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTTTATTTTCTTTTTGGAGCTTGATCCGGAATAGTATGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGGCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACATTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607906 Chironominae sp. water mite diet isolate 7311-BHL032417-GBD13316_13893-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCGTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGATATTGGTTATTACCACTAATATTAGGAGCCCCTGAAATGGCATTTCCACGAATAAATAATATAAGATTTTGATTATTAACACCATCTCTTACTTTATTACTTTCAAGAAGAATAGGAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607907 Chironominae sp. water mite diet isolate 7314-BHL032417-GBD20888_8670-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGGGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTACTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTACAGTAATACCTATTTTAATTGGAGGATTTAGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGTTTTTCCACGAATAAATAATATAAGATTTTGATTATTACTACCATCTCTTACTTTATTATTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607908 Chironominae sp. water mite diet isolate 7328-BHL032417-GBD5050_22657-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTTGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTACTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGATATTACCGCTAATATTAGGAGCCCCTGATATGGCTGTTCCACGCATAAATAATATAAGATTTTGATTAGTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607909 Chironominae sp. water mite diet isolate 7332-BHL032417-GBD26231_7287-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTATGAGACCATGATATGGCTTTTCCACGAATGAATAATATAAGATTTTGATTATGACCACCATATCTTACTTTATTACGATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607910 Chironominae sp. water mite diet isolate 7334-BHL032417-GBD22438_3788-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATCATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATTCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTAGAAATTGGTTATTACCACTGATATTAGGAGCCCATGATATGGCTTTTCCACGAATGAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607911 Chironominae sp. water mite diet isolate 7336-BHL032417-GBD17639_20285-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATGTTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATACTGGAAAATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGACCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTCGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAAAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607912 Chironominae sp. water mite diet isolate 7341-BHL032417-GBD11185_17563-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTTATCCGAACGGAATTAGGACATCCTGAAACATTTATTGGTGATGACCAAATTTATAATGTAGTTGTTACTGCTCATGCTTTTATTATAATTTTTCTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCTTCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607913 Chironominae sp. water mite diet isolate 7353-BHL032417-GBD16370_4595-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAATATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTTATGACCACATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACAACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGGTTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607914 Chironominae sp. water mite diet isolate 7356-BHL032417-GBD3821_9251-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCGTTAAGAATATTAATCCGAACGGAATTACGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTGTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607915 Chironominae sp. water mite diet isolate 7357-BHL032417-GBD18685_21996-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTTATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATCTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATCACTTTCAAAAAGAATAGTAGAAAAAGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607916 Chironominae sp. water mite diet isolate 7358-BHL032417-GBD21462_10840-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTCTATTTTATTTTTGGTGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGTTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACATTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607917 Chironominae sp. water mite diet isolate 7371-BHL032417-GBD23905_19804-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTCTATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGCATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATCATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGACTATTACCACCATCTCTTACGTTAGTACTGTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607918 Chironominae sp. water mite diet isolate 7376-BHL032417-GBD8542_3862-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAACGGAACTAGGTCATCCTGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTAGTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTTTTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607919 Chironominae sp. water mite diet isolate 7377-BHL032417-GBD11716_11061-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGGGCTTGATCAGGTATAGTAGGAACTTCTTTAAGCATATTCATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCCCTGATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGTTTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607920 Chironominae sp. water mite diet isolate 7391-BHL032417-GBD25159_24521-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGAAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTTATGATTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGGTCATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCAGCACTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607921 Chironominae sp. water mite diet isolate 7392-BHL032417-GBD25832_6102-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTTAGAATATTAATCCGAACGAAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTATTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTAGAAATTGATTATTACCACTAATATTAGGAGCCTCTGATATGGCTTTTCCACGAGTAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607922 Chironominae sp. water mite diet isolate 7393-BHL032417-GBD21466_16721-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTATGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAAAAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCACGAAAAATAGTAGAAAATGGAGCTAGAACTGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607923 Chironominae sp. water mite diet isolate 7400-BHL032417-GBD2127_14708-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGGTCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGATATTAAGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTAGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATATTGATTATTACCACCAGCTCTTACTTTATTACTGTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607924 Chironominae sp. water mite diet isolate 7404-BHL032417-GBD29571_16229-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCAGAACGAAATTAGGTCATCCTGGAACATATATTGGTGATAACCAAATTTATAATGTAATTGTTACTGATCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATACTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATCATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607925 Chironominae sp. water mite diet isolate 7405-BHL032417-GBD16502_5618-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTTGTTATTACCACTAATATTAGGAGCCCCTGATATGTCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTCGAAACTG	Using NCBI BLASTN in June 2018, this sequence was 98.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607926 Chironominae sp. water mite diet isolate 7410-BHL032417-GBD21820_7515-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACTGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCATGATATGGCATTTCCACGAATAAATAATATAAGATTTTGACTATTGCCACCATCACTTACTTTATTACTTGCAAGAAGAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607927 Chironominae sp. water mite diet isolate 7420-BHL032417-GBD25331_20580-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTCATTCGAGCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGCAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607928 Chironominae sp. water mite diet isolate 7421-BHL032417-GBD9957_17083-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAACTAGGTCATCCTGGATCATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCTACGAATAAATAATATAAGATTTAGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607929 Chironominae sp. water mite diet isolate 7424-BHL032417-GBD23595_25330-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTACGAATATTAATCCGAATGGCATTCGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTGATTACCACTAATATTAGGATCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATGTTGATTATTACCACCATCTCTTACTTGATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607930 Chironominae sp. water mite diet isolate 7441-BHL032417-GBD18766_15653-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATCCGAACGGAATTAGGACATCCTGGAACATTAATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCTCTAATATTAGGAGACCCTGATATGGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTACCACCATCTCTTACATTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607931 Chironominae sp. water mite diet isolate 7442-BHL032417-GBD13586_12020-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCATATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATATTGATTATGACCACCATCTCTTGCGTTATTACTGTCAAGAAGAATAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607932 Chironominae sp. water mite diet isolate 7443-BHL032417-GBD16205_20363-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGGGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGTTCATGCTTTTATTATAATTTTTTTATAGTAATACCTACTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGTCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGACTATTACCACCATCTCTTACTTTATTACGTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607933 Chironominae sp. water mite diet isolate 7451-BHL032417-GBD24797_15238-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATAATAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTAATGACCAAATTTATAATGTTATTGTTACTACTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATATTAATTGGAGGATTTGGAAATTGATTATTACCTCTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTAATACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607934 Chironominae sp. water mite diet isolate 7453-BHL032417-GBD8931_14781-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCCTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAGTACCTATTTTAATTGGAGGGTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACAAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAGGAAGAATAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607935 Chironominae sp. water mite diet isolate 7456-BHL032417-GBD19438_26398-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAATTTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGATATTGGTTATTACCACTAATATTAGTAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCTCCATCTCTTACTTTATTACTGTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607936 Chironominae sp. water mite diet isolate 7458-BHL032417-GBD7437_24680-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGTTATAGTAGGAACTTCTTTAAGTATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTTTTGGTGATGACCAAATTTATAATGTAATTGTTACTGTTCATGCTTTTATTATAATTTTTTTAATAGTACTACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607937 Chironominae sp. water mite diet isolate 7464-BHL032417-GBD14753_4054-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATGTTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACTACCATCTCTTACTTCATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607938 Chironominae sp. water mite diet isolate 7470-BHL032417-GBD23843_4143-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGTAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGATCATTCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATGTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTGATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607939 Chironominae sp. water mite diet isolate 7472-BHL032417-GBD15734_6484-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCGTTCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGATCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACCTTCAAGAAGAATAGTAGCAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607940 Chironominae sp. water mite diet isolate 7473-BHL032417-GBD16992_2215-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCCTTTATTATAATTTTTTTAATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGGTTATTACCACTATCTCTTACTTTATTTCTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACCGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607941 Chironominae sp. water mite diet isolate 7474-BHL032417-GBD19602_13428-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTATTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATATATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGTAGTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCATGATATGGCTTCTCCACGAATAAATAATATAAGATTTTGATTATTACCACCTTCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607942 Chironominae sp. water mite diet isolate 7483-BHL032417-GBD20497_4839-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAATAATATTAATTTGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAGATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGTTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607943 Chironominae sp. water mite diet isolate 7485-BHL032417-GBD5593_7114-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAATGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAGTTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCTCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACCTTATTAATTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607944 Chironominae sp. water mite diet isolate 7486-BHL032417-GBD29166_18597-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGATCATTTATTGGTGACGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTAGTACCACTAATATTAGGAGCCCCTGATATAGCTTTACCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTGCTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607945 Chironominae sp. water mite diet isolate 7488-BHL032417-GBD26564_18826-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAACTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGACTATTACCACCATCTCTAACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607946 Chironominae sp. water mite diet isolate 7511-BHL032417-GBD19643_13418-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCCGGTGTAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGACCATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCATCATCTCTTACTTTATTACGTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607947 Chironominae sp. water mite diet isolate 7515-BHL032417-GBD2253_14461-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTAGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCATATTTATAATGTAAGTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTCATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAATTAATATATGATTTTGATTATTTCCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607948 Chironominae sp. water mite diet isolate 7642-BHL040517-GBD18331_3462-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAATTTTACAATGTAATTGTCACAGCAGACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAAATGACTTTTTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTTCTTTCAAGTTCTATTGTAGAAAATGGCGCTGGACCAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607949 Chironominae sp. water mite diet isolate 7681-BHL040517-GBD22746_9964-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTGAGTATGTTAATTCGAGCAGAACTTGGACAACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCCGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACCCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607950 Chironominae sp. water mite diet isolate 7707-BHL040517-GBD25719_15438-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGAATGCTAATTCGAGTAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCCTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607951 Chironominae sp. water mite diet isolate 7744-BHL040517-GBD9071_10099-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATTTGGACGACCTTGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCATACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTTTTACCTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607952 Chironominae sp. water mite diet isolate 7752-BHL040517-GBD24691_23057-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACATTATTTTTGGGGCTTGATCTGGTATAGTAGGTTCTTCTTTACGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGTAGATGACCAAATGTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607953 Chironominae sp. water mite diet isolate 7788-BHL040517-GBD26981_21108-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGTCCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTCACAGCATATGCTTTTATTATAATTTTTTTCATAGTTATGCCCATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGCTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607954 Chironominae sp. water mite diet isolate 7816-BHL040517-GBD6943_19462-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTATGTATACTAATTCGTGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAACTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCATTAATGTTAGTAGCCCCAGATATGGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACACTTTTACTTTCAAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607955 Chironominae sp. water mite diet isolate 7825-BHL040517-GBD5166_23608-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCCGGTATAGTGGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGAGATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607956 Chironominae sp. water mite diet isolate 7833-BHL040517-GBD17765_27076-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTGCCTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607957 Chironominae sp. water mite diet isolate 7895-BHL040517-GBD28561_19865-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATTCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGCTTTTGGAAATTGATTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTATTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607958 Chironominae sp. water mite diet isolate 7899-BHL040517-GBD16914_10466-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCCTGCTCGGGGATAGTAGGGACATCCCTATGAATACTAATTCGTGCTGAATTAGGTCAACCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACATCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTGTTACTTTCGAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR670143, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607959 Chironominae sp. water mite diet isolate 7939-BHL040517-GBD29232_17770-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGTAGAACTTGGACGACCTGGCACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGTTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGGTTTTGACTACTTCCCCCTACATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607960 Chironominae sp. water mite diet isolate 7944-BHL040517-GBD27141_8181-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGTCCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACTGCATACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCATTAACTCTATTACTTTCAAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607961 Chironominae sp. water mite diet isolate 7948-BHL040517-GBD7519_10228-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGGATATTAGGTACTTCTTTAAGTATATTAATTCGAGCAAAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTGATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGAAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607962 Chironominae sp. water mite diet isolate 7959-BHL040517-GBD20870_8804-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCATACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCATTTGGAAATTGATTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTTGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607963 Chironominae sp. water mite diet isolate 7978-BHL040517-GBD13726_27498-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATCCCTCTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTCTTCCCCCTTCATTAACTCTTTTTCTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607964 Chironominae sp. water mite diet isolate 7995-BHL040517-GBD28694_15107-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTATTTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGGTTCTGATTACTCCCTCCTACTCTATCTCAGGTACTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR670143, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607965 Chironominae sp. water mite diet isolate 8005-BHL040517-GBD8362_25074-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGTCTGATCGGGGATAGTAGGGACATCCCTTAGAATACTAATTCGTGTTGAATTAGGTCACCCAGGAACATTAATTGGAGACGACCAAATTTATAATGCAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAACTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTACTCTTTTACTTTCTAGTGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR670143, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607966 Chironominae sp. water mite diet isolate 8006-BHL040517-GBD26361_14896-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATTCTAATTCGAGCAGAACTTGGACGCCCTGGTTCTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCTTACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACGGTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607967 Chironominae sp. water mite diet isolate 8011-BHL040517-GBD6473_24183-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAATAATACTAATTCGTGCTGAATTATGTCACCCAGGAACATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATCCCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGATTACTCCCACCTTCTCTTTCTCTTTTACTGTCTAGTGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR670143, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607968 Chironominae sp. water mite diet isolate 8073-BHL040517-GBD22066_22118-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACTTCCCTAAGAATATTAATTCGTGCTGAATTAGGTCACGCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGCTTTGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTATTACTTTATAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR658416, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607969 Chironominae sp. water mite diet isolate 8081-BHL040517-GBD22101_5566-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAAGTACTTCTTTTTGTATGCTAATTCGAGCAGAACTTGGTCGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATGTAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTGTTACTTTCAAGTTCTAGTGTAGAAGATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607970 Chironominae sp. water mite diet isolate 8135-BHL040517-GBD29241_13313-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGTATACTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAAATGATCAAATTTATAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607971 Chironominae sp. water mite diet isolate 8168-BHL040517-GBD14825_4527-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACAATATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAAATTTTTTCATAGTTATTCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATTTGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607972 Chironominae sp. water mite diet isolate 8176-BHL040517-GBD23098_27125-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTGTATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGTGCAGAACTTGGACGACCTGGTACTTTTATTGGATATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATGAACAATTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607973 Chironominae sp. water mite diet isolate 8178-BHL040517-GBD19028_18432-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACAATATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTATTTAAGTATGCTATTTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAGAATTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTAGAGGTTTTGGAAATTGACTTGTTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACGGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607974 Chironominae sp. water mite diet isolate 8180-BHL040517-GBD25219_21068-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATATTAATTCGAGCTGAGTTAGGTCACCCAGGAACATTTATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATTCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCGGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR670143, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607975 Chironominae sp. water mite diet isolate 8181-BHL040517-GBD9861_5610-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCTGATATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCTTACGCTTTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGAGCTTTTGGGAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607976 Chironominae sp. water mite diet isolate 8192-BHL040517-GBD12007_6908-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTTAGTATGCTAATTCGCGCAGAACTTGGACGACTTGGTACTTTTTTTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCATCATTAACTCTTTTACTTTCAAGTGCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607977 Chironominae sp. water mite diet isolate 8201-BHL040517-GBD29215_18126-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCAGTAACGCGGGGACTTGCAAATTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607978 Chironominae sp. water mite diet isolate 8224-BHL040517-GBD19819_15645-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAACAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTACTTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTCATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTTCTTCCCCCTTCATTAACTCTTTTACTCTCAAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607979 Chironominae sp. water mite diet isolate 8232-BHL040517-GBD21688_15577-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTCGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACATTGTAATTGTCACAGCTTACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATCTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTTTTACTTTCAAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607980 Chironominae sp. water mite diet isolate 8237-BHL040517-GBD19481_22646-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAGTGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGTCCCAGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTCCTTTCAAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607981 Chironominae sp. water mite diet isolate 8274-BHL040517-GBD12938_10193-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGCGCTTGATCTGGTATAGTAGGTACTTCTTTATGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTTGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTCACTTTCAAGTACGATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607982 Chironominae sp. water mite diet isolate 8276-BHL040517-GBD22727_21881-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTGAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCGTCCCCCTTCATTAACACATTTACAATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607983 Chironominae sp. water mite diet isolate 8278-BHL040517-GBD20117_22035-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGTCGACCTGGTTCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTCACAGCATACGCTTTTGTTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607984 Chironominae sp. water mite diet isolate 8292-BHL040517-GBD18764_15205-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTATGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAACGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTACTTTAATGTTAGGAGTCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCCGTTAGTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607985 Chironominae sp. water mite diet isolate 8377-BHL101416-GBD14042_8283-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACCTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607986 Chironominae sp. water mite diet isolate 8443-BHL101416-GBD25020_21069-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATCCTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCCTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATACCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607987 Chironominae sp. water mite diet isolate 8457-BHL101416-GBD21822_12813-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGCAATTGATTTGTTCCTCTTATATTAGGAGCACCAGATATAGCTTTTCCTCGCATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607988 Chironominae sp. water mite diet isolate 8559-BHL101416-GBD9541_20977-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATACTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTCTTGACTTCTCCCCCCATCCTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607989 Chironominae sp. water mite diet isolate 8567-BHL101416-GBD19335_10507-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTTAGTATATTAATTCGAGCCGAACTTTGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGATTTTGATTACTTCCTCCATCTCTAACTCTTCTTCTTTCAAGTGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607990 Chironominae sp. water mite diet isolate 8577-BHL101416-GBD28072_9561-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGACTTGTTCCTCTTATATTAGGAGCCCCTGATATAGCATTTCCTCGAAAAAACAATATAAGTTTTTGATTACTTCCTCCGTCTCTAACTCTTCTTCTTTCAAGGTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607991 Chironominae sp. water mite diet isolate 8594-BHL101416-GBD26842_19823-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTTATTCGAGCCGAACTTGGACATCCAGGTACCTTTATTGGAGATGACCAATTTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCACTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607992 Chironominae sp. water mite diet isolate 8687-BHL101416-GBD20804_11330-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACAAGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCCTTTACTTTCAAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607993 Chironominae sp. water mite diet isolate 8712-BHL101416-GBD12978_15963-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGATCCGAACTTGGACATCCAGGTACCTTTATTGGAGATGACCATATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATATTAGGAGCCCCTGATATAGCCTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCCCCATCTCTAACTCTTCTTCTTTCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607994 Chironominae sp. water mite diet isolate 8758-BHL101416-GBD13478_4062-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGAACAGGAATGGTAGGAACTTCTTTAACTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTATACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAAAAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607995 Chironominae sp. water mite diet isolate 8836-BHL101416-GBD20499_22477-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACACGCTTTTGTTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCCATTACTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW607996 Chironominae sp. water mite diet isolate 8845-BHL101416-GBD24350_13450-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATCAATTCGAGCCAAACTTGGCCATCCAGTTACCTTTATTGGAGATGACCAAATTTATAATGTTATTTTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATATCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607997 Chironominae sp. water mite diet isolate 8859-BHL101416-GBD12024_10063-Lq60 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATTCTAATTCGAGCAGAACTTGGACAACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCATTAACTCTTTTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607998 Chironominae sp. water mite diet isolate 8860-BHL101416-GBD6677_6768-Lq60 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KR765094, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW607999 Chironominae sp. water mite diet isolate 8868-BHL101416-GBD14385_12856-Lq60 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAGATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTTTTACTTTCAAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608000 Chironominae sp. water mite diet isolate 8913-BHL032417-GBD1918_17148-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTCCTTCTTTAAGTATGCTAATTCGAGCAGAACTTTGACGACCTTGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACAAGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGACCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCACCTTCATGAACGCTTTTACTTTCAAGTTCTATTGTAGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608001 Chironominae sp. water mite diet isolate 8925-BHL032417-GBD13069_5788-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTCTGGAAATTGACTCATTCCTTTAATGTTAGGAGCCCCAGATATGACTTTCCCTCGAATAAACAATATAAGTTTTTGACTTCTTCCCCCTTCATTATCTCTTTCACTTTCAAGTTCTATTGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608002 Chironominae sp. water mite diet isolate 8931-BHL032417-GBD28408_10021-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACAACCTGGTACTTTTACTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTTTTACTATCAAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608003 Chironominae sp. water mite diet isolate 8933-BHL032417-GBD15237_12236-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAACTTGATCAGGAATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGTAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608004 Chironominae sp. water mite diet isolate 8935-BHL032417-GBD8067_4625-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGGTGACCAAATTTACAATGTCATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG449442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608005 Chironominae sp. water mite diet isolate 8953-BHL032417-GBD29587_16233-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGACCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTAATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCGATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTATCAAGTTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608006 Chironominae sp. water mite diet isolate 8961-BHL032417-GBD21989_6556-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGAATGTTAATTCGAGCAGAACTTGGACTACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTATAATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTATTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608007 Chironominae sp. water mite diet isolate 8964-BHL032417-GBD10629_22769-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTACTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGATTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608008 Chironominae sp. water mite diet isolate 8968-BHL032417-GBD24783_10221-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAATTTGGACGACGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTTATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAACTGACTTATTCCTTTAATGTTAGGAGCCCCAGATAGAGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608009 Chironominae sp. water mite diet isolate 8969-BHL032417-GBD14043_12745-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAATTTGGACAACCAGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTACCCCCTTCATTAACTCTTTTTCTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608010 Chironominae sp. water mite diet isolate 8971-BHL032417-GBD16761_17696-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG449442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608011 Chironominae sp. water mite diet isolate 8974-BHL032417-GBD8673_21721-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGATTGCTAATTCGAGCAGAACTTGGACGACGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTGTTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTATTACTATCAAGTTCTGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608012 Chironominae sp. water mite diet isolate 8978-BHL032417-GBD23596_13742-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGAACTGGTACTTTTACTGGAGATGACCAAATTTACAATGTAATTGTCACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGGTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTGGCAAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608013 Chironominae sp. water mite diet isolate 8981-BHL032417-GBD9641_9711-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATTCTAATTCGAGCAGAACTTGGTCGAGCTGGTTCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTATTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608014 Chironominae sp. water mite diet isolate 8984-BHL032417-GBD15778_22569-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACCATTTCCCCCTTCATTAACCCTTTTACTATCAAGATCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608015 Chironominae sp. water mite diet isolate 8990-BHL032417-GBD19249_6474-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGCCCTGGTACATTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGTGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCTTCATTAACCCTTTTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608016 Chironominae sp. water mite diet isolate 8998-BHL032417-GBD10333_15435-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATTTGGACAGCCTGGTACTTTTATTGGTGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTTTTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCATTAACTCTATTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608017 Chironominae sp. water mite diet isolate 8999-BHL032417-GBD19108_18382-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACAACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCATTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTATACCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCATTAACTCTATTACTTTCATGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608018 Chironominae sp. water mite diet isolate 9003-BHL032417-GBD23813_3925-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTAGGACAACCTGGTACTTTTACTGGAGATGATCAAATTTACAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTAATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTCTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTATTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608019 Chironominae sp. water mite diet isolate 9006-BHL032417-GBD27515_16036-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATACTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACCGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCTATTTTAATTGGAGGTTTTGGAAATTGATTAATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608020 Chironominae sp. water mite diet isolate 9007-BHL032417-GBD27131_15104-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACATCCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTTATTGTCACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTAGTTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608021 Chironominae sp. water mite diet isolate 9008-BHL032417-GBD12000_18447-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGTGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTACTGGAGATGACCAAATTTACAATGTAATTGTCACAGCTCACGCTTTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608022 Chironominae sp. water mite diet isolate 9011-BHL032417-GBD26735_17731-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAATAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACAACCTGGTACTTTTATTAGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTACCCCCTTCACTAACTCTATTACTTTCAAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608023 Chironominae sp. water mite diet isolate 9019-BHL032417-GBD22886_5269-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATTCTAATTCGAGCAGAACTTGGTCGACCTGGTTCTTTTACTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTTTTTTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608024 Chironominae sp. water mite diet isolate 9025-BHL032417-GBD9188_14695-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACAACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTAAAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTTTTCCTTTAATATTAGGAGCCCCAGATATGGCCTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608025 Chironominae sp. water mite diet isolate 9031-BHL032417-GBD19983_17977-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCTGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACACGCATTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608026 Chironominae sp. water mite diet isolate 9034-BHL032417-GBD12164_17916-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTACTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCCCCAATAAAAAATATAAGTTTTTTACCTCCCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608027 Chironominae sp. water mite diet isolate 9036-BHL032417-GBD25934_11313-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGCGCTTGATCTGGTATAGTAGGTACTTCTTTATGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTACATTAACTCTGTTACCTTCAAGTTCTATTGTAGAAAATGGAGCTGAAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608028 Chironominae sp. water mite diet isolate 9038-BHL032417-GBD11848_23144-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTCTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608029 Chironominae sp. water mite diet isolate 9041-BHL032417-GBD19903_26659-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTACTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR159655, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608030 Chironominae sp. water mite diet isolate 9047-BHL032417-GBD21542_7101-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGAATGCTTATTCGAGCAGAATTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGTAGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608031 Chironominae sp. water mite diet isolate 9052-BHL032417-GBD8138_4440-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTATTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACGACGAGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTACAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACACTATTACTTTCAAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608032 Chironominae sp. water mite diet isolate 9055-BHL032417-GBD4743_8405-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATTTGGACGTCCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATACCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTCCCCCCATCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608033 Chironominae sp. water mite diet isolate 9059-BHL032417-GBD28547_11131-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGAATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGAACTGGAACATTTATTGGATATGACCAAATTTACAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACCCTTTTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608034 Chironominae sp. water mite diet isolate 9069-BHL032417-GBD7692_9732-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTCCTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGAAGGTTTTGGAAATTGACTAATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATAAAAGTTTTTGACTTCTTCCTCCTTCATTAACTCTTTTACTTCCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608035 Chironominae sp. water mite diet isolate 9070-BHL032417-GBD24855_15207-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTCTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACGACGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACTGCACACGCATTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608036 Chironominae sp. water mite diet isolate 9072-BHL032417-GBD2058_12406-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTACTTGTCACAGCACATGCTTTTATAATAATTTTTTTTATAGTTATTCCCATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTGCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608037 Chironominae sp. water mite diet isolate 9077-BHL032417-GBD28122_14951-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCATGATCTGGAATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTGTTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608038 Chironominae sp. water mite diet isolate 9079-BHL032417-GBD13413_18270-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTAGGAGCTTGATCTGGAATAATAGGTACTTCTTTAAGAATGCTAATTCGAGTAGAACTTGGACAACCTGGTACTTTTATTAGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608039 Chironominae sp. water mite diet isolate 9082-BHL032417-GBD26916_10132-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACTGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCACTAACTCTTTTACTTTCAAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608040 Chironominae sp. water mite diet isolate 9086-BHL032417-GBD24328_10274-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTTATTCGAGCAGAACTTGGACGACTTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGATTTTTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608041 Chironominae sp. water mite diet isolate 9092-BHL032417-GBD21548_25101-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCTTGACCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATCATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.1% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608042 Chironominae sp. water mite diet isolate 9093-BHL032417-GBD9848_12179-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGACTAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTGTTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATACCTTTAATGTTAGGTGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608043 Chironominae sp. water mite diet isolate 9101-BHL032417-GBD22149_10953-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATTTTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGTAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTATTACTTTCAAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608044 Chironominae sp. water mite diet isolate 9105-BHL032417-GBD18956_13287-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAATAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTAGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGACAATTTTAATTGGAGGGTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCATTCCCTCGAATAGATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTATTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608045 Chironominae sp. water mite diet isolate 9108-BHL032417-GBD20361_8040-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGCTCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTACTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTGTTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCGTCCCCCGTCAGTAACACTTTTACTGTCAAGTTCTAGTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608046 Chironominae sp. water mite diet isolate 9110-BHL032417-GBD16808_4565-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTACTGTAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTCTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTTCTTTCAAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608047 Chironominae sp. water mite diet isolate 9116-BHL032417-GBD19273_21299-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGAACTTTTACTGGAGACGACCAAATTTATAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATAGCTCTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608048 Chironominae sp. water mite diet isolate 9120-BHL032417-GBD16868_5397-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGAATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACTACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCCATTTTAATTGGAGGGTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATTGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTATCTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608049 Chironominae sp. water mite diet isolate 9122-BHL032417-GBD11547_13038-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACAAACTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTGCATTAACCCTTTTACTATCAAGTGCTACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608050 Chironominae sp. water mite diet isolate 9132-BHL032417-GBD20887_22971-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACGACGTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACACGCTTTTGTTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAGATTGATTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTACCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608051 Chironominae sp. water mite diet isolate 9135-BHL032417-GBD22801_18141-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACGACCTAGTACTTTTACTGGAGATGATCAAATTTACAATGTAATTGTCACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTATTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608052 Chironominae sp. water mite diet isolate 9142-BHL032417-GBD17176_26256-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATTTGGACGACCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTATTACTATCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608053 Chironominae sp. water mite diet isolate 9144-BHL032417-GBD16359_4662-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGCCCTGTTACTTTTACTGTAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTCCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTTGAACCGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608054 Chironominae sp. water mite diet isolate 9145-BHL032417-GBD21191_19095-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGAACTGGTACTTTTATTGGAAATGACCAAATTTATAATGTAATTGTCACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTGTTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608055 Chironominae sp. water mite diet isolate 9148-BHL032417-GBD11484_20941-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTACTGGAGATGACCAAATTTACAATGTAATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608056 Chironominae sp. water mite diet isolate 9152-BHL032417-GBD26499_8539-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACGACGTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAGATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCCTTCCCTCGAATAAAGAATATAAGATTTTGACTACTTCCCCCTTCATTAACCCTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608057 Chironominae sp. water mite diet isolate 9156-BHL032417-GBD22034_19644-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACGACGAGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTACTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATACAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTATCAAGTTCTATTGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608058 Chironominae sp. water mite diet isolate 9169-BHL032417-GBD25106_12169-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGTATGCTTATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTTGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608059 Chironominae sp. water mite diet isolate 9174-BHL032417-GBD6286_21324-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTCTGACTTCTTCCCCCTTCATTAACTCTATTGCTTTCAAGTGCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608060 Chironominae sp. water mite diet isolate 9179-BHL032417-GBD9094_21679-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGAAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTACTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACCACGTCCCCCTTCATTAACACTTTTTCTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608061 Chironominae sp. water mite diet isolate 9181-BHL032417-GBD25971_24191-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTTTATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGTCCTGGCACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCCATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTCCTTCCCCCTTCATTAACTCTTTTACGATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608062 Chironominae sp. water mite diet isolate 9183-BHL032417-GBD21755_22272-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACAACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCTCATGCTTTTATTATAATTTTTTTTATAGTCATACCAATTTTAATTGGAGGTTTTGGAAATTGATTTATTCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTGTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608063 Chironominae sp. water mite diet isolate 9185-BHL032417-GBD14330_3415-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGTACTACCTGGTACTTTTAATGGAGATGACCATAGTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGTAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAATTCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608064 Chironominae sp. water mite diet isolate 9188-BHL032417-GBD26474_20263-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGTTAATTCGAGCAGAACTTGGACGACCTGGTTCTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACCGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATTTTTGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCATTAACTCTTTTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608065 Chironominae sp. water mite diet isolate 9190-BHL032417-GBD4596_23615-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACCTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACAACCTGGTACTTTTATTGGAGATGACCAAATTTACAACGTAATTGTCACAGCTCACGCTTTTATTATAATTTTTTTTACAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGTCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608066 Chironominae sp. water mite diet isolate 9191-BHL032417-GBD23175_8216-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAATAGGCACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTAGAGATGACCAAATTTATAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608067 Chironominae sp. water mite diet isolate 9192-BHL032417-GBD26913_9613-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACGTCCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCACACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATGCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608068 Chironominae sp. water mite diet isolate 9196-BHL032417-GBD18555_13297-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTTGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATTTGGACGACCTGGTATTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAACAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608069 Chironominae sp. water mite diet isolate 9199-BHL032417-GBD14270_2893-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATCCGAGCAGAACTTGGACGACCTGTTACTTTTATTTGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTCTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAATTCTATTGTAGCAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608070 Chironominae sp. water mite diet isolate 9209-BHL032417-GBD17807_25978-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTCGGACGAACTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTATTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608071 Chironominae sp. water mite diet isolate 9213-BHL032417-GBD4773_11673-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTACTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCTGAACTTGGACGACCTGGTACCTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATCGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCCTTTACTTTCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608072 Chironominae sp. water mite diet isolate 9214-BHL032417-GBD24226_24806-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTAGAGATGACCAAATTTATAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTGTTCCTTTAATGTTAGGTGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACGCTATTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608073 Chironominae sp. water mite diet isolate 9216-BHL032417-GBD16922_26802-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGAATAGTAGGTACTTCTTTAAGAATGCTAATTCGAGCAGAATTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTAACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGATTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608074 Chironominae sp. water mite diet isolate 9218-BHL032417-GBD10822_19513-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTTTATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATTCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTGTTCCTTTAATATTAGGAGCCCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608075 Chironominae sp. water mite diet isolate 9219-BHL032417-GBD19291_21287-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGCTCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTACTGGAGACGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTCGCCCTCGAATAAATAATATAAGTTATTGACTTCTTCCCCCTTCATTAACTCTTTTACTGTCAAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608076 Chironominae sp. water mite diet isolate 9220-BHL032417-GBD23920_21569-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACATCCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGTGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGGTTTTGAATACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTACTATTGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608077 Chironominae sp. water mite diet isolate 9226-BHL032417-GBD6465_13834-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTTAGTATGCTAATTCGAGCAGAACTTTGACGACCAGGTACTTTTATTGGATATGACCAAATTTATAATGTAATTGTCACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608078 Chironominae sp. water mite diet isolate 9228-BHL032417-GBD19052_13301-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCTATTTTAATTGGTGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCATCATTAACTCTTTTACTATCAAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608079 Chironominae sp. water mite diet isolate 9230-BHL032417-GBD13002_13625-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCTCTAAGTATGTTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTCTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608080 Chironominae sp. water mite diet isolate 9240-BHL032417-GBD28520_19499-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTATTTAAGTATGCTAATTCGAGCAGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCACACGCTTTTTTTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCATTAACTCTATTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608081 Chironominae sp. water mite diet isolate 9242-BHL032417-GBD20593_11891-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACAACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTGTTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGCGCTACTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608082 Chironominae sp. water mite diet isolate 9243-BHL032417-GBD14741_15822-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGTGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATGAACTCTTGTACTGCCAAGTACGATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608083 Chironominae sp. water mite diet isolate 9246-BHL032417-GBD25726_5766-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATTTGGACGACCTGGTCCTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCATTAACTCTATTATTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608084 Chironominae sp. water mite diet isolate 9249-BHL032417-GBD17611_22492-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGAATTCTAATTCGAGCAGAACTTGGTCGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTCTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCATTAACTCTTTTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608085 Chironominae sp. water mite diet isolate 9261-BHL032417-GBD28208_9060-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGACCTGGAATAGTAGGTATTCTTTTAAGTATGTTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTAACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCCTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608086 Chironominae sp. water mite diet isolate 9265-BHL032417-GBD15796_26248-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGTAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCATTTATGATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTATTAATTTCAAGTTCTAGAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608087 Chironominae sp. water mite diet isolate 9267-BHL032417-GBD18726_19041-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATCTGGACAACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTGCCCCCATCATTAACTCTATTACTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608088 Chironominae sp. water mite diet isolate 9269-BHL032417-GBD16648_5074-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAAAACTTGGACGACGTGTGACTTTTATTGGAGATGACCATATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATTCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTACCTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608089 Chironominae sp. water mite diet isolate 9278-BHL032417-GBD20241_28018-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACGACTTGTTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGCTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAAGATAAGATTTTGACTACTTCCCCCTTCATTAACTCTATTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608090 Chironominae sp. water mite diet isolate 9279-BHL032417-GBD11995_6773-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACATCCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCATTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGCTTTTGAATTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608091 Chironominae sp. water mite diet isolate 9280-BHL032417-GBD17206_22985-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTACTGGAGATGATCAAATTTACAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTACTTCCTCCTTCACTAACCCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608092 Chironominae sp. water mite diet isolate 9283-BHL032417-GBD26383_20502-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGGTCTGGTATAGTAGGTACTTCTTTAAGTATGCTTATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTAATTCCTTTAATGTTAGGAGCTCCAGATATGGCTTTCCCTCGAATAAATAGTATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608093 Chironominae sp. water mite diet isolate 9286-BHL032417-GBD15622_3526-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGAACTGCTTTAAGAATGCTAATTCGAGCAGAACTAGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGCAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCTAGCTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608094 Chironominae sp. water mite diet isolate 9289-BHL032417-GBD9127_26760-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGACCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTTCTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACCCTTTTACTTTCTACTTCTACTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608095 Chironominae sp. water mite diet isolate 9293-BHL032417-GBD27420_18129-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACGACGTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTTATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTTCTCTCAAGTTCTATTGTAGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608096 Chironominae sp. water mite diet isolate 9294-BHL032417-GBD2011_16012-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAGCCGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAACAATATAAGATTTTGAGTACTTCCCCCTTCTTTAACGCTGCTTCGTTCTAGCGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM988908, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608097 Chironominae sp. water mite diet isolate 9299-BHL032417-GBD28286_10489-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGTATGCTTATTCGAGCAGAACTTGGACGACCTGGTACTTTTACTGGAGATGATCAAATTTACAATGTAATTGTCTCAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608098 Chironominae sp. water mite diet isolate 9300-BHL032417-GBD26056_17990-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATCGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACAACCTGGTACTTTTACTGGAGATGACCAAATTTACAATGTAATTGTAACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGTGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCATTAACTCTTTTACTTTCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608099 Chironominae sp. water mite diet isolate 9307-BHL032417-GBD25376_16683-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGTAGAACTCTGACGACCTGGAACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATACCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608100 Chironominae sp. water mite diet isolate 9317-BHL032417-GBD4640_9111-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAAAACTTGGACGACCTGGTACTTTTATAGGAGATGATCAAATTTACAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608101 Chironominae sp. water mite diet isolate 9319-BHL032417-GBD28460_11107-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATTTGGTATAGTAGGTACTTTTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAGAGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACCCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608102 Chironominae sp. water mite diet isolate 9328-BHL032417-GBD17458_9178-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACTATCTGTTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATACAAGTTTTTGACTTCTTCCCCCTGCATTAACTCTTTTACTGTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608103 Chironominae sp. water mite diet isolate 9329-BHL032417-GBD28009_9289-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGTTTATTAATTCGAGCAGAATTTGGACGACGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTACGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATAAAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608104 Chironominae sp. water mite diet isolate 9330-BHL032417-GBD18881_11392-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGGACTTCTTTAAGTATGCTTATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGTGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608105 Chironominae sp. water mite diet isolate 9335-BHL032417-GBD8429_14722-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTTGGTACTTCTTTAAGTATTCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTCTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608106 Chironominae sp. water mite diet isolate 9340-BHL032417-GBD24834_5424-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATATTATTTTTGGGGCTTGATCTGGAATAGTGGGTACTTCTTTAAGTTTGCTAATTCGAGCGGAACTTGGACGACGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCACTAACTCTTTTACTTTCAAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608107 Chironominae sp. water mite diet isolate 9342-BHL032417-GBD5463_9120-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTTGTTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGACATGGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTCTTCCCCCTTCATTACCTCTTTTACTTTCAAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608108 Chironominae sp. water mite diet isolate 9343-BHL032417-GBD13895_4816-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACAGTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCCTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCACGTTCTATTGTCGAAAATGGCGCTGGAACCGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608109 Chironominae sp. water mite diet isolate 9346-BHL032417-GBD23303_14042-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTGCCTCGAATAAATAATATAAGTTATGGACTTCGTCCCCCGTCAGTAACTCGTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608110 Chironominae sp. water mite diet isolate 9350-BHL032417-GBD3298_18387-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGGCTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTACCCCCTTCATTAACTCTTTTACTTTCAAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608111 Chironominae sp. water mite diet isolate 9352-BHL032417-GBD7177_6113-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGATTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCAGTAACTAATTTACTTTCAAGATCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608112 Chironominae sp. water mite diet isolate 9354-BHL032417-GBD25249_13706-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGCAGAACTAGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAAGAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608113 Chironominae sp. water mite diet isolate 9358-BHL032417-GBD26178_20374-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACATCGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGAGATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCGTCCCCCTTCATTAACTCTTTTACTTTCGAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608114 Chironominae sp. water mite diet isolate 9363-BHL032417-GBD6852_11575-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTCCTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACAACGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTATAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTATTACCATCAAGTTCTATTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608115 Chironominae sp. water mite diet isolate 9369-BHL032417-GBD16363_4546-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTGGGACTACGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATTCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTCGACAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608116 Chironominae sp. water mite diet isolate 9371-BHL032417-GBD13352_8515-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGTAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAGTTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCAAAAAAATAAAATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACATTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608117 Chironominae sp. water mite diet isolate 9375-BHL032417-GBD12689_4977-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGACCGGGAATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGGACTTGGACGACCTGGTACTTTTACTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCATCATTAACTCTTTTACCATCAAGTTCTATTGTAGAAAGTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608118 Chironominae sp. water mite diet isolate 9377-BHL032417-GBD17243_5223-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTAGGACGACCTGGTACCTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATTCCAATTTTAATTGGAGGTTTTGGAAATTGAATTTTTCCTTTAATATTAGGAGCCCTAGATATGGCTCTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608119 Chironominae sp. water mite diet isolate 9381-BHL032417-GBD22785_26053-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACAACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGTGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608120 Chironominae sp. water mite diet isolate 9382-BHL032417-GBD8150_25424-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGAACTTCTTTAAGTATGTTAATTCGAGCAGAACTAGGACAACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608121 Chironominae sp. water mite diet isolate 9385-BHL032417-GBD27908_11832-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTTTATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAAAACTAGGACGACCTGGTACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTCACTGCCCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCACTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608122 Chironominae sp. water mite diet isolate 9386-BHL032417-GBD13897_3353-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACTACCTTGTACTTTTATTGGAGATGACCATATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATTCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTTTTTTACTTCCAAATTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608123 Chironominae sp. water mite diet isolate 9387-BHL032417-GBD13868_2443-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGTACTACCTGTTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATGGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGTATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAATTCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608124 Chironominae sp. water mite diet isolate 9393-BHL032417-GBD10713_22959-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGTCGACCAGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACCCTATTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608125 Chironominae sp. water mite diet isolate 9395-BHL032417-GBD20488_20496-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCAGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608126 Chironominae sp. water mite diet isolate 9405-BHL032417-GBD5477_7312-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGAATAGTAGGTACTTCTTTAAGTATACTAACTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTAATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCACTAACTCTTTTGCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608127 Chironominae sp. water mite diet isolate 9414-BHL032417-GBD7310_25601-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTGGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACGACCTGGTTCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGGTTTGGAAATTGATTAATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTATTACTATCAAGCTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608128 Chironominae sp. water mite diet isolate 9421-BHL032417-GBD20026_12726-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGCAGAATTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTCAACCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608129 Chironominae sp. water mite diet isolate 9422-BHL032417-GBD25155_24489-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGTGATGACCAAATTTACAATGTAATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTAATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGGTTTTGACTACTTCCCCCTTCATTAACGCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608130 Chironominae sp. water mite diet isolate 9426-BHL032417-GBD26353_19602-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTTTATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTTCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTGTTCCTTTAATGTTAGGAGCCCCAGATACGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTATTACTGTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608131 Chironominae sp. water mite diet isolate 9428-BHL032417-GBD12634_24869-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAACTGACTTATTCCTCTAATATTAGGAGCCCCCGATATAGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTGTTACTTTCAAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608132 Chironominae sp. water mite diet isolate 9431-BHL032417-GBD3502_16048-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAATAGGTACTTCTTTAAGTATTCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTAGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATTCCTATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTCTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608133 Chironominae sp. water mite diet isolate 9432-BHL032417-GBD27177_22794-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACTTTATTTTTGGAGCTTGATCTGGTATAATAGGTACTTCTTTAAGTATGCTAATTCGAGCAGCATTTGGACGACCTGGTACTTTTTTTAGAGATGACCAAATTTACAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608134 Chironominae sp. water mite diet isolate 9445-BHL032417-GBD5263_9494-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGCAGAACTTTGACGACCTGGTACTTTTATTGGAGACGACCAAATTTACAATGTAATTGTCACAGCACACGCATTTATTATAATTTTTTTTATAGTTATGCCAGTTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTCCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608135 Chironominae sp. water mite diet isolate 9446-BHL032417-GBD8173_25999-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATTAGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCAAGTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACCTCTACCCCCTTCACTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608136 Chironominae sp. water mite diet isolate 9452-BHL032417-GBD21732_22063-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTTAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTACTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTCTAATGTTAGGAGCACCAGATATGGCTTTCCCTCGAATAAACAATATAAGTTTCTGACTTCTTCCCCCTTCATTAACCCTTTTACTTTCAAGTGCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608137 Chironominae sp. water mite diet isolate 9456-BHL032417-GBD24980_17118-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACAACCTGGTGCTTTTACTGGAGATGACCAAATTTACAATGTAATTGTCACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGGAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAAAAATAAAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608138 Chironominae sp. water mite diet isolate 9458-BHL032417-GBD28408_19442-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGAAGACCAAATTTACAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTGTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAACAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608139 Chironominae sp. water mite diet isolate 9461-BHL032417-GBD26774_17597-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTCGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTCACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTGTTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608140 Chironominae sp. water mite diet isolate 9463-BHL032417-GBD25881_24897-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTGGGTACTTCTTTATGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCATTCCCACGAATAAATAATATAAGTTTTTGACTACGTCCCCCTTCATTAACTCTATTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608141 Chironominae sp. water mite diet isolate 9465-BHL032417-GBD24761_14443-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCCGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTATTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608142 Chironominae sp. water mite diet isolate 9467-BHL032417-GBD13977_15364-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTTAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTTGGGGCCCCGGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACCCTATTACTTTCAAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608143 Chironominae sp. water mite diet isolate 9474-BHL032417-GBD23251_4439-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGTACTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTGTTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAACTGACTTATTCCTTTAATGTTAGGTGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCACTAACCCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608144 Chironominae sp. water mite diet isolate 9482-BHL032417-GBD8102_4392-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGGCTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAACAATATAAGTTTTTGAATACTACCCCCTTCATTAACTCTTTTTCTGTCAAGAACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608145 Chironominae sp. water mite diet isolate 9484-BHL032417-GBD26608_10438-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACAACCTGGTGCTTTTATTGGAGATGACCAAATTTACAATGCAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCGTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTATTACAATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608146 Chironominae sp. water mite diet isolate 9486-BHL032417-GBD10749_15823-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACGACGAGGTACTTTTCTTGGAGATGACCAAATTTACAATGCAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTCTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608147 Chironominae sp. water mite diet isolate 9487-BHL032417-GBD15621_4634-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACATCACACGTTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAACTTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGTCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTACCTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGCGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608148 Chironominae sp. water mite diet isolate 9490-BHL032417-GBD10309_3109-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGTACAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTATTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGGTCTCCCTCGAAAAAAAAAAAAAAGGTTTTGACTTCTTCCCCCTTCATTAACACTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608149 Chironominae sp. water mite diet isolate 9497-BHL032417-GBD23437_5424-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACTTCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTATTTGTCACAGTACACGCATTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGATTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCCTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608150 Chironominae sp. water mite diet isolate 9503-BHL032417-GBD9173_16691-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCTGGTACTTTTATTGGTGATGATCAAATTTACATTGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608151 Chironominae sp. water mite diet isolate 9504-BHL032417-GBD22862_3920-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTTTTTAAGTTTGCTAATTCGAGCAGAACTTGGATGACGTGTTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGTGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608152 Chironominae sp. water mite diet isolate 9507-BHL032417-GBD13158_23147-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACCACCTGGTACTTTTACTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATGCCTTTAATGTTAGGAGCCCCAGATATGGCCTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608153 Chironominae sp. water mite diet isolate 9513-BHL032417-GBD21888_20766-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTATGTTTGCTAATTCGAGCAGAACTTGGACGACGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGTGCCCCAGATATGACTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCAGTTACTTTCAAGTACTAGTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608154 Chironominae sp. water mite diet isolate 9514-BHL032417-GBD27332_13695-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGTATAATAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGAACTGGTACTTTTATTAGAGATGACAAAATTTACAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGGCTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACCACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608155 Chironominae sp. water mite diet isolate 9520-BHL032417-GBD18332_5470-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATCTTCGGAGCTTGATCGGGAATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACTACGGGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608156 Chironominae sp. water mite diet isolate 9523-BHL032417-GBD11128_13639-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTTTATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTACTGGAAATGACCAAATTTACAATGTAATTGTAACAGCACACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGATCCCCAGATATGGCTCTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAATTCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608157 Chironominae sp. water mite diet isolate 9524-BHL032417-GBD27262_16133-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTCGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAACTCGAGCAGAACTTGGACGACGTGGTACTTTTATTGGAGATGACCAAATCTACAATGTAATTGTCACAGCACACGCTTTTATTATAACTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCCCTCCCTCGAATAAATAAAAAAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608158 Chironominae sp. water mite diet isolate 9530-BHL032417-GBD11820_9206-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGTTGAACTTGGACGACGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCATTTATTATAATTCTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGTGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCATCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608159 Chironominae sp. water mite diet isolate 9533-BHL032417-GBD15365_15086-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGTCCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTTATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCGGATATGGCTTTCCCTCGAATAAATAATATAAGATTCTGACTTCTTCCCCCTTCATTAACTCTTTTTCTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608160 Chironominae sp. water mite diet isolate 9534-BHL032417-GBD4207_18007-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATCCTAATTCGAGCAGAACTTGGACAACCTGGTACTTTTACTGGAGATGACCAAATTTACAATGTAATTTTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACCACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608161 Chironominae sp. water mite diet isolate 9536-BHL032417-GBD25460_19358-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTTATTCGAGCAGAACTTGGACGACGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACAAGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTACATTAACGCTTTTACTGTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608162 Chironominae sp. water mite diet isolate 9538-BHL032417-GBD5084_10571-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCGGGTATAGTAGGTACTTCTTTAAGTTTTCTAATTCGAGCAGAACTTGGACGACGTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCTCCAGATATGGCTTTCCCTCGAATAGATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGATCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608163 Chironominae sp. water mite diet isolate 9558-BHL032417-GBD25872_7655-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGGACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608164 Chironominae sp. water mite diet isolate 9717-BHL040517-GBD8014_5155-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAAAACTTGGACGACCTGGTACTTTTATTGGAAATGACCAAATTTACGATTTAATTGTCACAGCACGCGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCCCGAATAAATAATATAGGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608165 Chironominae sp. water mite diet isolate 9724-BHL040517-GBD22075_4884-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAGTTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCTCACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGTAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTATTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608166 Chironominae sp. water mite diet isolate 9727-BHL040517-GBD9743_7772-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAATTATGCCAATTTTAATTGGAGATTTTGGAAATTGACTTATTCCTTTAATGTTATGAGCCCCAGATATGGCGTCCCCTCGAATAAATAATATAATTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTTAAGTTCTATTGTACAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608167 Chironominae sp. water mite diet isolate 9731-BHL040517-GBD17596_2988-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCGGGTATAGTAGGAACTTCTTTAAGAATGCTAATTCGAGCAGAACTGGGACGACCTGTTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTTTTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAGGTTCTATTGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608168 Chironominae sp. water mite diet isolate 9732-BHL040517-GBD28163_12184-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCTTTAAGTATTCTAATTCGAGCAGAACTAGGACAACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTTATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608169 Chironominae sp. water mite diet isolate 9734-BHL040517-GBD29575_16730-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATTTAATTGTCACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCACCTTCATTAACGCTTTTACGTTCAAGTTCTATTGTAGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608170 Chironominae sp. water mite diet isolate 9736-BHL040517-GBD26580_22290-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCATTAACTCTATTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608171 Chironominae sp. water mite diet isolate 9737-BHL040517-GBD24439_8031-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTTATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTCTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCACTAACTCTTTTACTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608172 Chironominae sp. water mite diet isolate 9738-BHL040517-GBD10390_18068-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTCTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAAAAATATAAGTTATTGACTTCGTCCCCCTTCATTAACTCTATTACTTTCAAGTGCTATTGTAGAAAATGGAGGTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608173 Chironominae sp. water mite diet isolate 9739-BHL040517-GBD8691_13714-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTCTTCCCCCTTCATTGACACTACTACTTCCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608174 Chironominae sp. water mite diet isolate 9743-BHL040517-GBD27296_16484-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTTAGTATGCTAATTCGAGCAAAACTTGGACGACCTGGTACTTTTATTGGACATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATCGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGTTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608175 Chironominae sp. water mite diet isolate 9745-BHL040517-GBD17719_5497-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTAGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATTCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTACCTCTTTTTCTTTCAAGTTCTATTGTAGAAAATGGCGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608176 Chironominae sp. water mite diet isolate 9746-BHL040517-GBD20056_17896-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGAAAGGCCTTTCCCTCGAATAAAAAATATAAGTTTTGGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608177 Chironominae sp. water mite diet isolate 9753-BHL040517-GBD25198_18970-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATTTGGACGACCTGGTACTTTTATTGGAGATGACCTAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTTGTTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608178 Chironominae sp. water mite diet isolate 9755-BHL040517-GBD15503_26617-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGTCATGCTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCACACGCTTTTGTTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608179 Chironominae sp. water mite diet isolate 9756-BHL040517-GBD28469_10860-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGTGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTACTATCAGGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608180 Chironominae sp. water mite diet isolate 9759-BHL040517-GBD6703_17013-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGAACTGGTTCGTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTGATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCATTAACTCTTTTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608181 Chironominae sp. water mite diet isolate 9760-BHL040517-GBD8242_7792-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGCAGGTACTTCTTTAAGAATGTTAATTCGAGCAGAATTTGGACAACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACCTGCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608182 Chironominae sp. water mite diet isolate 9764-BHL040517-GBD10169_14176-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAATAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAAAAATATAAGTTTTTGGCTTCTTCCCCCTTCATTAACCCTTTCACCTTCAAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608183 Chironominae sp. water mite diet isolate 9766-BHL040517-GBD26634_15728-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGGTCTGGAATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTACAATGTTATTGTAACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTCTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608184 Chironominae sp. water mite diet isolate 9769-BHL040517-GBD13641_28408-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATTCCAATTTTAATTGGAGGGTTTGGAAATTGACTTTTTCCTTTAATATTAGGAGCCCCAGATATGACTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608185 Chironominae sp. water mite diet isolate 9770-BHL040517-GBD12650_9007-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTATGTATGCTAATTCGAGCAGAACTTGGTCGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTCTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGGGTTTGACTTCTTCCCCCTTCAGTAACTCTTTTACTTGCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608186 Chironominae sp. water mite diet isolate 9774-BHL040517-GBD10046_11184-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGCAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATCACTTTTTGACTTCATCCCCCTTCATTAACACTTTTACTTTCAAGTTCTATTGTACAAAACGGAGCTGCAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608187 Chironominae sp. water mite diet isolate 9775-BHL040517-GBD16656_5930-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACCACCTGTTACTCTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATGATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCAAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608188 Chironominae sp. water mite diet isolate 9783-BHL040517-GBD29083_16444-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTATCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608189 Chironominae sp. water mite diet isolate 9785-BHL040517-GBD28799_13076-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGTAGAACTTGGACGACCTGGTACATTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCTTCATTAACTCTTTTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608190 Chironominae sp. water mite diet isolate 9787-BHL040517-GBD13825_5154-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGGATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACGTGGACGACCTGGTACTTTTATTGGAGATGACCATATTTACAATGGAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTCTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608191 Chironominae sp. water mite diet isolate 9789-BHL040517-GBD10665_19510-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGACGATCAAATTTACAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTGTTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTATTATTATCAAGTTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608192 Chironominae sp. water mite diet isolate 9790-BHL040517-GBD20780_18358-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCTATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACCCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608193 Chironominae sp. water mite diet isolate 9792-BHL040517-GBD27599_17909-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGCGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGTCCTGGTATTTTTATTGGATATGACCAAATTTACAATGTAATTGTCACAGCACACGATTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCAAGATATGGCTTTCCCTCGAATAAATAAAATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608194 Chironominae sp. water mite diet isolate 9793-BHL040517-GBD10266_3802-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACATGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTTTTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGGTTTGGAAATTGACTTATTCCTTTAATGTTGGGAGCACCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCCTCATTAACTCTTTTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608195 Chironominae sp. water mite diet isolate 9794-BHL040517-GBD15959_28141-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGCTCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTCGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGATTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608196 Chironominae sp. water mite diet isolate 9797-BHL040517-GBD26431_19396-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTAATTCCTTTAATGTTAGGAGCCCCAGATATGGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCATGAACTCTATTACTTTCAAGTACTATTGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608197 Chironominae sp. water mite diet isolate 9799-BHL040517-GBD4953_17908-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAAGAGCCCCAGATATGGCTTTCTCTCGAATAAATAATATAAGTTTTTGACTTCATCCCCATTCAATAAATCTTTTACTGTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608198 Chironominae sp. water mite diet isolate 9802-BHL040517-GBD5780_6408-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATCATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAAAACTTGGACGACCTAGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTTTTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATGTAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608199 Chironominae sp. water mite diet isolate 9803-BHL040517-GBD11991_27729-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTTATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAACTGACTTATTCCCTTAATGTTAGGAGCCCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCCTCATTAACTCTTTTCCTTTCAAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608200 Chironominae sp. water mite diet isolate 9807-BHL040517-GBD21344_11976-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTATGTACTTCTTTATGTATGCTAATTCGAGCAAAACTTGGACGAACTGGTACTTTTATCTGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTGTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608201 Chironominae sp. water mite diet isolate 9809-BHL040517-GBD14846_18842-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGTATGCTTATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGATTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608202 Chironominae sp. water mite diet isolate 9810-BHL040517-GBD29611_16803-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCAGTAACGCGGGGACTTGCAAATTCTAGTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608203 Chironominae sp. water mite diet isolate 9811-BHL040517-GBD26486_20685-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTATGTACTTCTTTAAGTATGCTTATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCATAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGTTCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACGCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608204 Chironominae sp. water mite diet isolate 9812-BHL040517-GBD22824_21310-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATCTACAATGTAATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCTATTTTAATTGGAGGTTTTGGAAATTGACTTTTTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608205 Chironominae sp. water mite diet isolate 9813-BHL040517-GBD7995_20035-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGTATGCTTATTCGAGCAGAATTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAGTTGTCACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTCTACCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608206 Chironominae sp. water mite diet isolate 9815-BHL040517-GBD12662_18306-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCTATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCCGATATGGCTTTCCCCCGAATAAATAACATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTTCTACTATCAAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608207 Chironominae sp. water mite diet isolate 9816-BHL040517-GBD27094_11116-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACGTCCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTATTCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACGTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608208 Chironominae sp. water mite diet isolate 9817-BHL040517-GBD20822_25754-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACAACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTAACAGCACACGCATTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATACCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACCCGTTTACCATCAAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608209 Chironominae sp. water mite diet isolate 9820-BHL040517-GBD3254_14811-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATGCTAATTCGAGCAGAACTTGGACGAGCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATTCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTCTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608210 Chironominae sp. water mite diet isolate 9822-BHL040517-GBD12769_8147-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAGATTGACTAGTTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608211 Chironominae sp. water mite diet isolate 9823-BHL040517-GBD27081_19762-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACGATCTGGTATTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACATTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608212 Chironominae sp. water mite diet isolate 9824-BHL040517-GBD17241_25986-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACAACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGCCACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGCTTTGGAAATTGATTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAACATAAGTTTCTGACTACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608213 Chironominae sp. water mite diet isolate 9826-BHL040517-GBD10863_13833-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATACTTTATTTTTGGAGCTTGATCCGGTATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACTGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTCGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608214 Chironominae sp. water mite diet isolate 9829-BHL040517-GBD24798_12544-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCTAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAGTGTAGTTGTCACAGCACACGCTTTTATAATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608215 Chironominae sp. water mite diet isolate 9830-BHL040517-GBD17939_28823-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTACGTATGCTTATTCGAGCAGAACTTGGGCGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAACAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608216 Chironominae sp. water mite diet isolate 9832-BHL040517-GBD16681_28131-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAAGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTCGGACGTCCTGGTACTTTTATTGGAGATGACCTAATTTATAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTTTTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608217 Chironominae sp. water mite diet isolate 9833-BHL040517-GBD28042_21571-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACAACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAACTGACTTATTCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCCTCATTAACTCTTTTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608218 Chironominae sp. water mite diet isolate 9835-BHL040517-GBD2822_14191-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGTTACTTCTTTAAGTATTCTAATTCGAGCAGAATTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAGTTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTACCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608219 Chironominae sp. water mite diet isolate 9836-BHL040517-GBD21885_12478-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATAGTCACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGCTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAAAATAAGTTTTTGGCTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAGTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608220 Chironominae sp. water mite diet isolate 9838-BHL040517-GBD4877_19163-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATACTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAACAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTTTAATATTAGGAGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTCCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608221 Chironominae sp. water mite diet isolate 9840-BHL040517-GBD5615_22936-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAATAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTCTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCCGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608222 Chironominae sp. water mite diet isolate 9843-BHL040517-GBD26397_20874-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTCGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGTGCCCCAGATATGGCTTTCCCTCGAAAAAATAATATAAGTTTTTGACTTCTGCCCCCTTCATTAACTCTATTACATTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608223 Chironominae sp. water mite diet isolate 9846-BHL040517-GBD5554_7927-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTCTGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCATCATTAACCCTTTTACTTGCAAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608224 Chironominae sp. water mite diet isolate 9847-BHL040517-GBD14121_5917-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGTACTTCTTTAAGAATGCTAATTCGAGCAGAACTAGGACGACCTGGCACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGAATTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTTCTTTCAAGTTCTATTGTAGAAACTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608225 Chironominae sp. water mite diet isolate 9850-BHL040517-GBD3864_9223-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCTTTAAGTATACTAATTCGAGCAGAATTTGGACGACCTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTATTACTTTCAAGTACTATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608226 Chironominae sp. water mite diet isolate 10446-BHL040517-GBD22787_23507-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATTTTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCTATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608227 Chironominae sp. water mite diet isolate 10520-BHL040517-GBD4414_16809-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR765094, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608228 Chironominae sp. water mite diet isolate 10995-BHL101516-GBD22785_27111-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTCGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACGACGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACGCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608229 Chironominae sp. water mite diet isolate 11314-BHL110116-GBD29166_13276-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACCTTAATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTGATTGGAGGCTTTGGAAATTGACTAGTACCTCTTATACTTGGAGCCCCTGATATGGCCTTTCCTCGAATAAATAACATAAGATTCTGGTTACTACCTCCGTCTATAACTTTGCTACTGTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR695491, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608230 Chironominae sp. water mite diet isolate 11384-BHL110116-GBD4879_14674-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGCACTTCCTTAAGTATACTTATTCGAGCAGAGTTAGGACGGCCAGGAACTTTTATTGGAGATGACCAGATTTATAACGTAATTGTAACCGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCGATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGGGCCCCTGATATAGCCTTCCCGCGAATAAATAATATAAGATTTTGACTTTTCCCACCGTCTCTTTCCCTTCGTCTTTCTAGTTCAAATGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR751654, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608231 Chironominae sp. water mite diet isolate 11476-BHL101516-GBD13097_25607-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGCACTTCCTTAAGTATACTTATTCGAGCAGAGTTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTAACCGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCGATTTTAATTGGGGGTTTAGGAAATTGATTAGTACCTTTAATGTTAGGGGCCCCTGATATAGCCTTCCCGCGTATAAATAATATAAGATTTTGACTTCTCCCACCGTCTCTTTCTCTTCTTCTTTCTAGTACAATTGTTGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR751654, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608232 Chironominae sp. water mite diet isolate 11834-BHL101516-GBD16506_6935-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGTACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTGATCGGAGGCTTTGGAAATTGACTATTACCACTTATACTTGGAGCCCCTGATATGGCCTTTCCTCGAATAAATAACATAAGATTCTGGTTACTACCTCCGTCTATTACTTTGCTTCTTTCTAGATCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR765681, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608233 Chironominae sp. water mite diet isolate 12082-BHL040517-GBD25020_21069-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATCCTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCCTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATACCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608234 Chironominae sp. water mite diet isolate 12096-BHL040517-GBD21822_12813-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGCAATTGATTTGTTCCTCTTATATTAGGAGCACCAGATATAGCTTTTCCTCGCATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608235 Chironominae sp. water mite diet isolate 12198-BHL040517-GBD9541_20977-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATACTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTCTTGACTTCTCCCCCCATCCTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608236 Chironominae sp. water mite diet isolate 12206-BHL040517-GBD19335_10507-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTTAGTATATTAATTCGAGCCGAACTTTGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGATTTTGATTACTTCCTCCATCTCTAACTCTTCTTCTTTCAAGTGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608237 Chironominae sp. water mite diet isolate 12216-BHL040517-GBD28072_9561-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGACTTGTTCCTCTTATATTAGGAGCCCCTGATATAGCATTTCCTCGAAAAAACAATATAAGTTTTTGATTACTTCCTCCGTCTCTAACTCTTCTTCTTTCAAGGTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608238 Chironominae sp. water mite diet isolate 12233-BHL040517-GBD26842_19823-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTTATTCGAGCCGAACTTGGACATCCAGGTACCTTTATTGGAGATGACCAATTTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCACTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608239 Chironominae sp. water mite diet isolate 12326-BHL040517-GBD20804_11330-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACAAGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCCTTTACTTTCAAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608240 Chironominae sp. water mite diet isolate 12351-BHL040517-GBD12978_15963-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGATCCGAACTTGGACATCCAGGTACCTTTATTGGAGATGACCATATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATATTAGGAGCCCCTGATATAGCCTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCCCCATCTCTAACTCTTCTTCTTTCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608241 Chironominae sp. water mite diet isolate 12397-BHL040517-GBD13478_4062-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGAACAGGAATGGTAGGAACTTCTTTAACTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTATACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAAAAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608242 Chironominae sp. water mite diet isolate 12475-BHL040517-GBD20499_22477-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACACGCTTTTGTTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCCATTACTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608243 Chironominae sp. water mite diet isolate 12484-BHL040517-GBD24350_13450-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATCAATTCGAGCCAAACTTGGCCATCCAGTTACCTTTATTGGAGATGACCAAATTTATAATGTTATTTTAACTGCTCATGCATTTATTATAATTTTTTTATAGTTATATCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608244 Chironominae sp. water mite diet isolate 12529-BHL040517-GBD17514_8842-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTTTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608245 Chironominae sp. water mite diet isolate 12589-BHL040517-GBD11743_11915-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGGACTTCTTTAAGTATGCTAATTCGAGCTGAACTTGGACGACCTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAGTTGGAGGTTTTGGAAAATGACTTATTCCTTTAATGTTAGGAGCCCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608246 Chironominae sp. water mite diet isolate 12602-BHL040517-GBD25066_22803-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGAACTGATACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTCACAGCACACGCTTTTATAATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAAAATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608247 Chironominae sp. water mite diet isolate 12657-BHL040517-GBD18285_4883-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGCAGAACTAGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTAACTCTTTTTCTTTCAAGTTCTTTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608248 Chironominae sp. water mite diet isolate 12663-BHL040517-GBD26516_9490-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTATTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACAACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTCATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTATTTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTGCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608249 Chironominae sp. water mite diet isolate 12666-BHL040517-GBD26452_10681-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCTTTTAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCGCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608250 Chironominae sp. water mite diet isolate 12685-BHL040517-GBD16764_27054-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATTCTAATTCGAGCAGAACTTGGACAACCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTACTATCAAGTTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608251 Chironominae sp. water mite diet isolate 12716-BHL040517-GBD8260_7542-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACTGCACATACTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTCTAATGTTAGGAGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCACTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608252 Chironominae sp. water mite diet isolate 12723-BHL040517-GBD14937_23240-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCAAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCTATTTTAATTGGAGGGTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCATTAACCCTTTTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608253 Chironominae sp. water mite diet isolate 12753-BHL040517-GBD15019_26265-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTACTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGGTTTTGACTACTTCCCCCTTCATTAACGCTATTACGTTCAATTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608254 Chironominae sp. water mite diet isolate 12772-BHL040517-GBD15792_18037-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCTGAATTAGGACGACCTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTAACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608255 Chironominae sp. water mite diet isolate 12795-BHL040517-GBD27632_22218-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACAACCTGGTACTTTTATTGGAGGTGACCAAATTTACAATGTAATTGTCACAGCACAAGCTTTTATTATAATTTTTTTTATAGTTATGCCAGTTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCACTTCATTAACTCCTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608256 Chironominae sp. water mite diet isolate 12801-BHL040517-GBD19685_28659-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCCTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCCTTTACTTTCAAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608257 Chironominae sp. water mite diet isolate 12802-BHL040517-GBD3782_21248-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTGCTTTAAGTATGCTAATTCGAGCAGAATTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACTGCACACGCTTTTATTATATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACTGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608258 Chironominae sp. water mite diet isolate 12816-BHL040517-GBD20088_25697-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTTTATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTTAGTATGTTAATTCGAGTAGAACTTGGACGACCTGGTACTTTTATTGGATATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAAATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608259 Chironominae sp. water mite diet isolate 12819-BHL040517-GBD5932_23710-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGTTGAACTTGGACGACCTGGTACATTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTATTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608260 Chironominae sp. water mite diet isolate 12857-BHL040517-GBD14591_25352-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTCAAGTATGCTAATTCGAGCAGAACTTAGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCATTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTTCCCCTTCATTAACTCCTTTACTATCAAATTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608261 Chironominae sp. water mite diet isolate 12886-BHL040517-GBD10276_10459-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATTCTAATTCGAGCAGAACTTGGACGAGCTGGTACTTTTATTGGAAATGATCAAATTTACAATGTAATTGTCACCGCACACGCTTTTGTTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGGTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCATTAACTCTTTTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608262 Chironominae sp. water mite diet isolate 12889-BHL040517-GBD28341_19332-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAACTTGATCAGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCTATTTTAATTGGAGGTTTTGGAAATTGACTAATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCATTAACTCTTTTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608263 Chironominae sp. water mite diet isolate 12895-BHL040517-GBD13658_15659-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGTAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCGTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608264 Chironominae sp. water mite diet isolate 12985-BHL040517-GBD13234_11823-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608265 Chironominae sp. water mite diet isolate 13124-BHL040517-GBD11774_15423-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTCGGAGCTTGATCAGGTATAGTAGAAACTTCTTTAAGAATATTAATCCGAACGAAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTCTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608266 Chironominae sp. water mite diet isolate 13213-BHL040517-GBD4240_15667-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTACATTTTATTGTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGACTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608267 Chironominae sp. water mite diet isolate 13305-BHL040517-GBD4910_6478-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608268 Chironominae sp. water mite diet isolate 13497-BHL040517-GBD22258_16915-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTCTACTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608269 Chironominae sp. water mite diet isolate 13504-BHL040517-GBD22521_11514-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGATGATCAAATTTATAACGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTGTTGCCATTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285570, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608270 Chironominae sp. water mite diet isolate 13527-BHL040517-GBD8456_13623-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAAGTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAACGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608271 Chironominae sp. water mite diet isolate 13581-BHL040517-GBD24564_24094-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGCACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTGTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608272 Chironominae sp. water mite diet isolate 13637-BHL040517-GBD29636_15149-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGATTATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCTTTAATACTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCATCTCTAACATTATTACTTTCAAGTAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR765094, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608273 Chironominae sp. water mite diet isolate 13753-BHL040517-GBD18820_13738-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608274 Chironominae sp. water mite diet isolate 13936-BHL040517-GBD16097_19258-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGAAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATGAGATTTTGATTACTTCCCACTGCTTTATCTCTTCTGCGTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608275 Chironominae sp. water mite diet isolate 13961-BHL040517-GBD16222_27298-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACGCCCAGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTTTACCACCCTCTTTAACTCTTTTACTTTCAAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR289362, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608276 Chironominae sp. water mite diet isolate 14003-BHL040517-GBD21075_4662-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCCCTTAATATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTTCCTTCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR286005, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608277 Chironominae sp. water mite diet isolate 14089-BHL040517-GBD25878_6520-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAAAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGCTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608278 Chironominae sp. water mite diet isolate 14119-BHL040517-GBD21495_10896-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAACATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTCTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608279 Chironominae sp. water mite diet isolate 14218-BHL040517-GBD25830_24733-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTATGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAAAAGCTCACTCTTTTATTATAATTTTTTTTATAGTTATACCTATCATAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCTACGAAGAAATAATATGAGATTTTGATTACTTCCACCTTCTTTATCTCTTCTTCAATCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KM960768, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608280 Chironominae sp. water mite diet isolate 14274-BHL040517-GBD12220_4092-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGGACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGTAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608281 Chironominae sp. water mite diet isolate 14286-BHL040517-GBD23444_24327-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGATTATTAGGAACATCACTAAGTATTTTAATTCGAGCAAAACTTGGTAACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATACTAATTGGTGGATCTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTACTATCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608282 Chironominae sp. water mite diet isolate 14305-BHL040517-GBD13960_28989-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCTTTTAGTATATTAATTCGAGCAGAACTAGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCATGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR654792, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608283 Chironominae sp. water mite diet isolate 14368-BHL040517-GBD6621_16481-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCCTGATCTGGAATAGTAGGAACTTCACTTAGTATATTAATTCGAGCAGAACTTGGTCATCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGACTACTTCCCCCTTCTTTAACTCTTTTTCTTTCTAGCACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR289910, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608284 Chironominae sp. water mite diet isolate 14377-BHL040517-GBD13117_25134-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCCTTAATATTGGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTGTATCTCGTCGTCGGTCTAGCGCAATTGTAGAAAAGGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608285 Chironominae sp. water mite diet isolate 14381-BHL040517-GBD27576_11047-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCACTTAGTATATTAATTCGAGCAGAATTTGGACATCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR289910, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608286 Chironominae sp. water mite diet isolate 14387-BHL040517-GBD20426_24555-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCATTAAGAATATTTATTCGAGCGGAATTAGGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCCTACTTTATTACTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608287 Chironominae sp. water mite diet isolate 14394-BHL040517-GBD18411_8139-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACTTTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCATTTAGAATATTTATTCGAGCAGAACTTGGTCACCCTGTAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTTCTGTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR159655, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608288 Chironominae sp. water mite diet isolate 14415-BHL040517-GBD25056_25711-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGATCTGGAATAGTAGGAACATCATTTAGTATATTAATTCGAGCAGAATTTGGTCATCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR289910, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608289 Chironominae sp. water mite diet isolate 14426-BHL040517-GBD27047_20815-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTCGGAGCTTGATCTGGAGTAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTAACTCCTCTTCTATCTAGCACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KM988908, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608290 Chironominae sp. water mite diet isolate 14432-BHL040517-GBD13583_9911-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCTCTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCCTTTCCACGAATAAATAATATGAGATTTTGATTACTACCACCATCTTTAACTCTACTTCTTTCAAGCACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM960768, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608291 Chironominae sp. water mite diet isolate 14436-BHL040517-GBD22504_4342-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACTTTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCATTAAGTATATTAATTCGAGCAGAACTAGGACACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR174905, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608292 Chironominae sp. water mite diet isolate 14443-BHL040517-GBD6048_23648-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCTTTTAGTATTTTAATTCGAGCAGAATTAGGTCATCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAGTTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR289910, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608293 Chironominae sp. water mite diet isolate 14455-BHL040517-GBD5631_13301-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATGGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACATCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608294 Chironominae sp. water mite diet isolate 14475-BHL040517-GBD21993_19310-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCATTTAGTATATTAATTCGAGCAGAACTCGGTCACCCTGGATCTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCTTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTCCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR642580, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608295 Chironominae sp. water mite diet isolate 14486-BHL040517-GBD24570_9355-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAGCTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCACTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTGATTACGTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608296 Chironominae sp. water mite diet isolate 14499-BHL040517-GBD19543_13980-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTCCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTTGTGATGATCAAATTTACAATGTTATTGTAGCAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCACCTTCTTTAACTCTACTTCTTTCTAGCACAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608297 Chironominae sp. water mite diet isolate 14516-BHL040517-GBD7994_21892-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACCTCACTTAGTCTATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACGTCCCCCTACTTTATCACATCTTCTATCTAGCGCAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608298 Chironominae sp. water mite diet isolate 14527-BHL040517-GBD28918_16376-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCATTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTAACACTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KM988908, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608299 Chironominae sp. water mite diet isolate 14549-BHL040517-GBD16416_26351-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCCCTAAGTATATTAATTCGAGCAGAACTTGGGCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAACATAAGATTTTGATTACTTCCCCCTTCTTTATCCCTTCTTCTTTCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR286005, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608300 Chironominae sp. water mite diet isolate 14733-BHL040517-GBD13574_12049-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAGCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTCTTATTACAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACCTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608301 Chironominae sp. water mite diet isolate 14815-BHL040517-GBD4663_18540-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608302 Chironominae sp. water mite diet isolate 15112-BHL040517-GBD25524_10618-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACGCCCAGGTACCTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTTATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGACTATTACCACCCTCTTTAACTCGTTTACTTTCAAGATCAATTGTAGGAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR289362, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608303 Chironomus crassicaudatus water mite diet isolate 1592-BHL110116-GBD23792_22511-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTTGTCCCTTTAATAGTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTATAACTCTTCTAATTTCTAGTGCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608304 Chironomus crassicaudatus water mite diet isolate 2805-BHL032417-GBD24127_18911-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTAATGACCAAATTTATATTGTAGTAGTTACAGCTCACGCATTTTTTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCACCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608305 Chironomus crassicaudatus water mite diet isolate 2873-BHL032417-GBD10302_13606-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAAATATGGCCTTCCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCATCTTTAACTCTTCTTCTTTCTAGTACATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608306 Chironomus crassicaudatus water mite diet isolate 3324-BHL032417-GBD4225_22492-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTATCTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608307 Chironomus crassicaudatus water mite diet isolate 4042-BHL032417-GBD7176_23274-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTATTAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATTTTGTAGTTACATCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATATATAATATAAGTTTTTGAGTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608308 Chironomus crassicaudatus water mite diet isolate 4130-BHL032417-GBD28124_15800-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGAATTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608309 Chironomus crassicaudatus water mite diet isolate 5086-BHL032417-GBD10004_10911-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCGCGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCATTCCCTCGAATAAATAATATAAGTTTTTGAATTCTCCCCCCACCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608310 Chironomus crassicaudatus water mite diet isolate 5087-BHL032417-GBD28111_20047-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACACATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608311 Chironomus crassicaudatus water mite diet isolate 5178-BHL032417-GBD20586_12221-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCCTTTAGAATATTAATTCGAGCTGAATTAGGACGACCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTAACAGCTCACGCATTTATTATAATTTTTTTAATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608312 Chironomus crassicaudatus water mite diet isolate 5205-BHL032417-GBD13709_28507-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGATTTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTTATATTTGTACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGAATTCTCCCCCCATCTTTAACTCTACTACTATCTAGTTCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608313 Chironomus crassicaudatus water mite diet isolate 5269-BHL032417-GBD18769_11456-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAATAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATGGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCGCGAATAAATAATATAAGATTCTGACTACTCCCCCCATCTTTAACCCTTCTTCTATCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608314 Chironomus crassicaudatus water mite diet isolate 5274-BHL032417-GBD23090_22885-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTTATTCGAGCAGAATTAGGACGTTCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAGTAGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCCCTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608315 Chironomus crassicaudatus water mite diet isolate 5358-BHL032417-GBD24962_8102-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATACATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCTTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAACTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTCTGAATTCTACCCCCCTCTTTAACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608316 Chironomus crassicaudatus water mite diet isolate 5379-BHL032417-GBD16124_23548-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAAAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATATCAATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAACATAAGTTTTTGACTACTCCCCCCATCTTTAACACTACTACTATCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608317 Chironomus crassicaudatus water mite diet isolate 5526-BHL032417-GBD18104_28403-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTTTATATCTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATATAGTAGTTACAGCTCATGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTAGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGATTTTGAATTCTACCCCCATCTTTAACTCTTCTACTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608318 Chironomus crassicaudatus water mite diet isolate 5535-BHL032417-GBD13469_26145-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGCATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGAATACTCCCCCCATCGCTAACACTTCATCAATCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608319 Chironomus crassicaudatus water mite diet isolate 5539-BHL032417-GBD26727_6998-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCTTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATAGTTACAGCTCATGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGATTTTGAATACTCCCCCCTTCTTTAACTCTTCTTCTATCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608320 Chironomus crassicaudatus water mite diet isolate 5551-BHL032417-GBD27956_12239-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCTTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTAGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTTCCCCGAATAAATAATATAAGTTTTGGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTACATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608321 Chironomus crassicaudatus water mite diet isolate 5562-BHL032417-GBD14271_3454-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCGATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTCTTTCTTGTTCATTTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608322 Chironomus crassicaudatus water mite diet isolate 5742-BHL032417-GBD14243_27054-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCCTCTTCTTCTTTCTAGTTCATTTGTAGAAGATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608323 Chironomus crassicaudatus water mite diet isolate 5810-BHL032417-GBD4346_21039-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACATCCTGGATCTTTTATTGGTGATGATCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTACACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCTATCTTTAACTCTTCTTCTATCTAATTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608324 Chironomus crassicaudatus water mite diet isolate 5815-BHL032417-GBD10995_13410-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTCGATCAGGAATAGTAGGAACTTCCTTTAGAATATTAATTCGAACAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCATATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGATTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATAAGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCTATCTTTAACTCTTCTTCTTTCTAATTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608325 Chironomus crassicaudatus water mite diet isolate 5817-BHL032417-GBD25225_19613-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCATTAGAATATTAATTCGAGTAGAATTAAGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTGCAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTAGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCTATCTTTAACTCTTCTTCTTTCTAATGCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608326 Chironomus crassicaudatus water mite diet isolate 5835-BHL032417-GBD16442_24849-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGGATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCCTCCCTCGAATAAATAATATAAGATTTTGACTATTCCCCCTATCTTTAACTCTTCTTCTTTCTAATACATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608327 Chironomus crassicaudatus water mite diet isolate 5851-BHL032417-GBD16844_17204-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCTTTAGTATATCAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTACCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCGATCTTTAACTCTTCTTCTTTCTAATTCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608328 Chironomus crassicaudatus water mite diet isolate 5873-BHL032417-GBD18088_26014-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTATGAACTTCCCTTAGAATATTAATTCGAGCGGAATTAGGACGTCCCGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTACTCCCCCTATCTTTAACTCTACTACTGTCTAATTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608329 Chironomus crassicaudatus water mite diet isolate 5876-BHL032417-GBD29495_15398-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAACTAGGACGTCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATAGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTATCTAATTCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608330 Chironomus crassicaudatus water mite diet isolate 5931-BHL032417-GBD23268_10820-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTCTTTTTGGTGCTTGATCAGGAATAGTATGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATATAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCTATCTTTAACTCTTCTTCTTTCTAATTCATTTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608331 Chironomus crassicaudatus water mite diet isolate 5966-BHL032417-GBD24240_7060-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTCCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCGCCCCCTATCTTTAACTCTTCATCTATCTAATGCATTTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608332 Chironomus crassicaudatus water mite diet isolate 5971-BHL032417-GBD11595_8817-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAATTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAAATGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCTCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCTATCTTTAACTCTTCTTCTTTCTAATTCATTTATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608333 Chironomus crassicaudatus water mite diet isolate 5978-BHL032417-GBD22499_22146-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATAAAAATTTTAATTGGAGGTTTCGGAAATTGTCTTGTCCCTTTATTATTA	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608334 Chironomus crassicaudatus water mite diet isolate 6201-BHL032417-GBD21265_23989-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTATAACTCTTTTTCATACTAGTTCATTTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608335 Chironomus crassicaudatus water mite diet isolate 6733-BHL032417-GBD11260_16643-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATATATAATATAAGTTTTTGAGTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608336 Chironomus crassicaudatus water mite diet isolate 7058-BHL032417-GBD11245_16653-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATATATAATATAAGTTTTTGAGTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608337 Chironomus crassicaudatus water mite diet isolate 8404-BHL101416-GBD24728_12251-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTTGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608338 Chironomus crassicaudatus water mite diet isolate 8538-BHL101416-GBD8703_12508-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCCTTTATTATAATTTTTTTTATAGTTATACCAATTTTAACTGGAGGATTTGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608339 Chironomus crassicaudatus water mite diet isolate 8539-BHL101416-GBD13039_25518-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTATGACGTCCTGGATCTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTGTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCATCTTTAACTCTATTTCTTTCTAGTGCAGTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608340 Chironomus crassicaudatus water mite diet isolate 8631-BHL101416-GBD13898_5499-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACTTCCTGTAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGGCACTTTAATATTAGGAGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTCGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608341 Chironomus crassicaudatus water mite diet isolate 8739-BHL101416-GBD25683_10790-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTTTATATTTTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAAAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTTGTTACAGCTCATGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGTCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTACCCCCATCTTTAACTCTTTTTCTTTCTAGTTCATCTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608342 Chironomus crassicaudatus water mite diet isolate 8750-BHL101416-GBD2395_17428-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCTCTTAGAATATTAATTCGAGCAAAATTAGGACGTCCTGGCACTTTTATTGGTGATGACCAAATTTATAATGTAGTTGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATCGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCATTAACTCTTTTTCTATCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608343 Chironomus crassicaudatus water mite diet isolate 8783-BHL101416-GBD24346_16674-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTTGTTGCAGCTCACGCATTTATTATAACTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCCGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608344 Chironomus crassicaudatus water mite diet isolate 8789-BHL101416-GBD26008_9191-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGAACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCTTTTAATATTAGGAGCTCCAGATATAGCCTTCCCTCGAATAAATAACATAAGTTTTTGACTACTTCCCCCATCTTTAACTCTTTTTCTATCTAGTACATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608345 Chironomus crassicaudatus water mite diet isolate 8793-BHL101416-GBD9993_11049-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCTCTTAGAATATTAATTCGAGTAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATAGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTACTCCCCCCATCTTTAACACTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608346 Chironomus crassicaudatus water mite diet isolate 8834-BHL101416-GBD14483_4183-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGGACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATGTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTCCTAGTTCATCTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608347 Chironomus crassicaudatus water mite diet isolate 8841-BHL101416-GBD17109_15296-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTAGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCAACCCCTATCTTTAACTCTTCGTCGTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608348 Chironomus crassicaudatus water mite diet isolate 8864-BHL101416-GBD23299_6729-Lq60 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAAAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCCACTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608349 Chironomus crassicaudatus water mite diet isolate 9708-BHL032417-GBD28261_14111-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGATTTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGACATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACACCTCTTCTTTCTAGTTCATGTGTAGAAAATGGAGCCGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608350 Chironomus crassicaudatus water mite diet isolate 9901-BHL040517-GBD13127_7821-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608351 Chironomus crassicaudatus water mite diet isolate 10011-BHL040517-GBD21389_7326-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCGCTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608352 Chironomus crassicaudatus water mite diet isolate 12043-BHL040517-GBD24728_12251-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTTGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608353 Chironomus crassicaudatus water mite diet isolate 12177-BHL040517-GBD8703_12508-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCCTTTATTATAATTTTTTTATAGTTATACCAATTTTAACTGGAGGATTTGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608354 Chironomus crassicaudatus water mite diet isolate 12178-BHL040517-GBD13039_25518-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTATGACGTCCTGGATCTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTGTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCATCTTTAACTCTATTTCTTTCTAGTGCAGTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608355 Chironomus crassicaudatus water mite diet isolate 12270-BHL040517-GBD13898_5499-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACTTCCTGTAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGGCACTTTAATATTAGGAGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTCGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608356 Chironomus crassicaudatus water mite diet isolate 12378-BHL040517-GBD25683_10790-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTTTATATTTTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAAAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTTGTTACAGCTCATGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGTCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTACCCCCATCTTTAACTCTTTTTCTTTCTAGTTCATCTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608357 Chironomus crassicaudatus water mite diet isolate 12389-BHL040517-GBD2395_17428-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCTCTTAGAATATTAATTCGAGCAAAATTAGGACGTCCTGGCACTTTTATTGGTGATGACCAAATTTATAATGTAGTTGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATCGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCATTAACTCTTTTTCTATCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608358 Chironomus crassicaudatus water mite diet isolate 12422-BHL040517-GBD24346_16674-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTTGTTGCAGCTCACGCATTTATTATAACTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCCGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608359 Chironomus crassicaudatus water mite diet isolate 12428-BHL040517-GBD26008_9191-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGAACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCTTTTAATATTAGGAGCTCCAGATATAGCCTTCCCTCGAATAAATAACATAAGTTTTTGACTACTTCCCCCATCTTTAACTCTTTTTCTATCTAGTACATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608360 Chironomus crassicaudatus water mite diet isolate 12432-BHL040517-GBD9993_11049-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCTCTTAGAATATTAATTCGAGTAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATAGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTACTCCCCCCATCTTTAACACTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608361 Chironomus crassicaudatus water mite diet isolate 12473-BHL040517-GBD14483_4183-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGGACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATGTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTCCTAGTTCATCTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608362 Chironomus crassicaudatus water mite diet isolate 12480-BHL040517-GBD17109_15296-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTAGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCAACCCCTATCTTTAACTCTTCGTCGTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608363 Chironomus crassicaudatus water mite diet isolate 12569-BHL040517-GBD10936_3481-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCATTCCCTCGAATAAATAATATAAGTTTTTGAATTCTCCCCCCATCTTTAACTCTTCTACTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608364 Chironomus entis water mite diet isolate 764-BHL040916-GBD13431_6694-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTACTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTTACATTACTCCTATCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.1% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608365 Chironomus entis water mite diet isolate 912-BHL100916-GBD9505_14327-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGATGTAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTCACATTACTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.7% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608366 Chironomus entis water mite diet isolate 1782-BHL110116-GBD10195_16002-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTATTTTAAATATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTACTTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTTACATTACTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608367 Chironomus entis water mite diet isolate 2703-BHL032417-GBD17216_13817-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGATATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTTACATTATTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608368 Chironomus entis water mite diet isolate 5944-BHL032417-GBD25737_23714-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGGTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGATATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTATTTCCCCCATCACTTACATTATTCCTATCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.1% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608369 Chironomus entis water mite diet isolate 7585-BHL040517-GBD12912_14694-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGTTAGGGACTTCTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGCTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACATGTACCTTTAATACTAGGGGCCCCTGATTTAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTTACATTACTCCATTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608370 Chironomus entis water mite diet isolate 13132-BHL040517-GBD6406_23834-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTACTTTAAGTATGCATATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTTACATTACTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.1% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608371 Chironomus entis water mite diet isolate 13776-BHL040517-GBD16214_2821-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTACTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTTTTGGCGACTACCATATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAACTTGACTTGTACCTTTAATACTAGGGGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTTACATTACTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608372 Chironomus entis water mite diet isolate 14122-BHL040517-GBD16153_9238-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTACTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTTACATTACTCCGTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.1% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608373 Chironomus entis water mite diet isolate 14543-BHL040517-GBD11440_24096-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTACTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGATCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGACCCTGACATAGCTTTCCCCC	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608374 Chironomus maturus water mite diet isolate 700-BHL072216-GBD15400_5979-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTCTTAGTATGCTTATTCGAGCAAAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTAACTGCCCACGCATTTATTATAATTTTTTTCATAGTTATACCAATTCTAATTGGTGGTTTTAGTCATTGACTTGTACCCTTAATATTAGGAGCCCCAGATATGGCTTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTTACTCTTTTACTTCCTAGTTCATTCGTAGCAAATGCAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR665396, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608375 Chironomus maturus water mite diet isolate 710-BHL072216-GBD6586_24001-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTTTACATTATTTCTGGTGCTTGATCAGGAATGGTAGGGACTTCTCTTAGTATGCTTATTCGAGCAGAATTAGGACGTCCTGGAGCTTTTATTGGTGATGACCAAATTTATAATGTAGTTGTAACTGCCCACGCATTTATTATAATTTTTTTCATAGTTATACCAATTCTAATTGGTGGATCTGGTAATTGACTTGTACCCTTAATATTAGGAGCCCCAGATATGGCTTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTAACTCTATTACTTCCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR665396, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608376 Chironomus maturus water mite diet isolate 711-BHL072216-GBD6205_12634-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGACCTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGCCTTCTCTTGGTATGCTTATTCGAGCAGAATTAGGCTGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTAACTGCCCACGCATTTATTATAATTTTTTTCATAGTTATACCAATTCTAATTGGTGGTTCTGGTAATTGACTTGTACCCTTAATATTAGGAGCCCCAGATATGGCTTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTTACTCTTTTACTTCCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR665396, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608377 Chironomus maturus water mite diet isolate 712-BHL072216-GBD27793_12172-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTTTACATTATTTTTGGTGCTTGATCAGGCATGGTAGGGACTTCTCTTAGTATGCTTATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTAACTGCCCACGCATTTATTATAATTTTTTTCATAGTTATACCAATTCTAATTGGTGGTTCTGGTAATTGACTTGTACCCTTAATATTAGGAGCCCCAGATATGGCTTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTTACCAATTTACTACCTAGTTCATTCGTAGAAAGTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR665396, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608378 Chironomus maturus water mite diet isolate 713-BHL072216-GBD9981_17130-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTTTATTTTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTCTTAGTATGCTTATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTTGTAACTGCCCACGCATTTATTATAATTTTTTTCATAGTTATACCAATTCTAATTGGTGGTTTTGGTAATTGACTTGTACCCTTAATATTAGGAGCCCCAGATATAGCTTTCCCCCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCTCTAACTCTTTTACTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR665396, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608379 Chironomus maturus water mite diet isolate 718-BHL072216-GBD12834_14749-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTCTTAGTATGCTTATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTTGTAACTGCCCACGCATTTATTATAATTTTTTTCATAGTTATACCAATTCTAATTGGTGGTTTTGGAAATTGACTTGTACCCTTAATATTAGGAGCCCCAGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGACTGCTTCCCCCTTCACTTACTCTATTACTATCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR665396, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608380 Chironomus maturus water mite diet isolate 732-BHL072216-GBD22405_11292-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTTTACATTATTTTTGGTGCTTGATCAGGAATAGTAGGGACTTCTCTTAGTATGCTTATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTAACTGCCCACGCATTTATTATAATTTTTTTCATAGTTATACCAATTCTAATTGGTGGTTCTGGTAATTGACTTGTACCCTTAATATTAGGAGCCCCAGACATAGCTTTCCCCCGAATGAATAATATAAGTTTTTGACCTCTACCCCCTTCTCTTACTCTTTTACTTCCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR665396, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608381 Chironomus maturus water mite diet isolate 738-BHL072216-GBD23198_6213-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTCTTAGTATGCTTATTTGAGCAGAATTAGGACGTACTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTAACTGCTCACGCATTTATTATAATTTTTTTCATAGTTATACCAATTCTAATTGGTGGTTTTGGTAATTGACTTGTACCCTTAATATTAGGAGCCCCAGATATGGCTTTCCCCCGAATAAATAATATAAGTTTTTGACTACTACCCCCTTCTCTTACCCTATTACTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR665396, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608382 Chironomus maturus water mite diet isolate 739-BHL072216-GBD7309_17518-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTTTACTTTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTCTTAGTATGCTTCTTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTCGTAGTAACTGCCCACGCATTTATTATAATTTTTTTCATAGTTATACCAATTCTAATTGGTGGGTCTGGTAATTGACTTGTACCCTTAATATTAGGAGCCCCAGATATGGCTTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTTACACTTTTACTTCCTAGTGCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR665396, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608383 Chironomus riparius water mite diet isolate 441-BHL040517-GBD11998_10564-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGTTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608384 Chironomus riparius water mite diet isolate 564-BHL040517-GBD17121_28909-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAGCTTTATACATTATTTTTGGGGATTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTTCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCTCTCTTACTCTTCTTCTTCTTTCTAGTTTTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608385 Chironomus riparius water mite diet isolate 716-BHL072216-GBD23246_9801-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATATTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCTCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608386 Chironomus riparius water mite diet isolate 733-BHL072216-GBD21825_5091-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGTATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGTACATGCTTTTATTATAATTTTTTTCATAGTTATACCATTTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTATCCCCCTCTCCTACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608387 Chironomus riparius water mite diet isolate 736-BHL072216-GBD18100_4759-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCTGAACTTTCATTGAAGATGACCATATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTCCTGACTTTTTCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608388 Chironomus riparius water mite diet isolate 750-BHL040916-GBD26210_8959-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGATCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACACTTCTTCTTTCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608389 Chironomus riparius water mite diet isolate 761-BHL040916-GBD20885_21155-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCCTCTTCTTTCTAGAGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608390 Chironomus riparius water mite diet isolate 781-BHL040916-GBD20226_18917-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCATTTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAAAAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCCTTCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608391 Chironomus riparius water mite diet isolate 787-BHL040916-GBD29201_16226-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTAATTGGAGATGACCAAGTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCGTAGTTATACCTATTTTAATTGTAGGATTCGGAAACTGAGTTGTCCCCCTAATACTTGGAGTACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608392 Chironomus riparius water mite diet isolate 790-BHL040916-GBD2770_19082-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCAAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATACTTTTATTATAATCTTTTTCATAGTTATACCAATTTTAATCGGAGGTTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAGTAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608393 Chironomus riparius water mite diet isolate 799-BHL100916-GBD27624_11175-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATGCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCAACTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608394 Chironomus riparius water mite diet isolate 1123-BHL110116-GBD7421_15303-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCGCTCTTACGCTTCTTCTTTCTAGGTCTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608395 Chironomus riparius water mite diet isolate 1257-BHL110116-GBD8773_20274-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTGCCCCCCTCTCTTACTCTTCTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608396 Chironomus riparius water mite diet isolate 1505-BHL110116-GBD28976_19213-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACATTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608397 Chironomus riparius water mite diet isolate 1611-BHL110116-GBD21951_8756-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTGTTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAACCTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCGTACGCTGCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608398 Chironomus riparius water mite diet isolate 1629-BHL110116-GBD24480_6841-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATAATTGGAGCACCTGACAGAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTAACCCCCTCACTAACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608399 Chironomus riparius water mite diet isolate 1667-BHL110116-GBD22667_9496-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGATCTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTTGTCCCCCTAATATTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCACTTACTCTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608400 Chironomus riparius water mite diet isolate 1670-BHL110116-GBD19253_27241-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTCTACCCCCCTCTCTAACCCTTCTTCTATCTAGTACATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608401 Chironomus riparius water mite diet isolate 1722-BHL110116-GBD18803_16228-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTTGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTATGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608402 Chironomus riparius water mite diet isolate 1744-BHL110116-GBD28668_18688-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACCTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGCTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCACTCTTACTCTACTACTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608403 Chironomus riparius water mite diet isolate 1753-BHL110116-GBD2257_12347-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGTAGAATTAGGACGACCCGGAACATTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608404 Chironomus riparius water mite diet isolate 1758-BHL110116-GBD26242_8960-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608405 Chironomus riparius water mite diet isolate 1803-BHL101516-GBD21458_22961-Ldc86 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTATTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGCTTTAGGACGACCCGGAACTTTCATTGGAGATGACCAATTTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTGACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608406 Chironomus riparius water mite diet isolate 1808-BHL101516-GBD18620_27606-Ldc86 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGCATGCTTATTCGAACAGAATTAGGACGACCCGGAACTTTCATTGGGGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTAATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAGTAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTACTTTCTAGTTCTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608407 Chironomus riparius water mite diet isolate 1811-BHL101516-GBD15052_7620-Ldc86 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTAATCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGAATCTGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGGCTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608408 Chironomus riparius water mite diet isolate 1865-BHL072216-GBD26124_14448-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACACTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGCCCCGGATCTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTACTACTATCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608409 Chironomus riparius water mite diet isolate 1886-BHL022317-GBD27390_9691-Ldc90 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGTAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAGCTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAACAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACACTTCTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608410 Chironomus riparius water mite diet isolate 1888-BHL022317-GBD24951_22649-Ldc90 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGAGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGTCCCGGAACATTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCGCCCTAATATTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608411 Chironomus riparius water mite diet isolate 1890-BHL022317-GBD2171_17651-Ldc90 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAGTTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACGTAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCGTACTCTTCTTCTTTCTAGAACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608412 Chironomus riparius water mite diet isolate 1891-BHL022317-GBD25443_24890-Ldc90 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTTTACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTTTTACCCCCATCTCTTACTCTACTACTTTCTAGTTCTTTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608413 Chironomus riparius water mite diet isolate 2100-BHL072216-GBD4569_9444-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608414 Chironomus riparius water mite diet isolate 2702-BHL032417-GBD4718_10965-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGACTTGATTCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAACTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTGTAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCATTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608415 Chironomus riparius water mite diet isolate 2708-BHL032417-GBD11985_18381-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTATTACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.8% identical to accession ID KR756187, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608416 Chironomus riparius water mite diet isolate 2854-BHL032417-GBD23738_6942-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGATCCGGAACCTTCATTGGAGATGGCCAAATTTATAATGTTGTAGTTCCTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATCGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACGCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608417 Chironomus riparius water mite diet isolate 2894-BHL032417-GBD11144_4764-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCTTTATTACTTGGAGCCCCTGACATGGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTATTACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608418 Chironomus riparius water mite diet isolate 2908-BHL032417-GBD23695_22956-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTATTGGGGCTTGATCCGGAATAGTGGCAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAGTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAACACCTTACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCACTCTTACTCTTCTTCGTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608419 Chironomus riparius water mite diet isolate 2909-BHL032417-GBD25633_18405-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATACGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACCTTCATTGGAGATGGCCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATTGTTATATCAATTTTAATTGGAGGGTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGTATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTCCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608420 Chironomus riparius water mite diet isolate 2924-BHL032417-GBD9171_18731-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGAGCCTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCTTATTACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608421 Chironomus riparius water mite diet isolate 3001-BHL032417-GBD21145_4077-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATCCTTCTTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTCGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGACACTGACTTGTCCCCTTATTACTTGGATCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608422 Chironomus riparius water mite diet isolate 3070-BHL032417-GBD18345_4227-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTGTATACATTATTATTGGGGCTTGATCCGGAAAAGTGGAAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGACGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTGGGAAACTGACTTGTCCCCCTAATACTTGGGACACCATACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608423 Chironomus riparius water mite diet isolate 3075-BHL032417-GBD7835_25305-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAAATTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGGCCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCATTTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGAAGCAACTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608424 Chironomus riparius water mite diet isolate 3080-BHL032417-GBD13168_27048-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCCGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTTTCCCCTTATTACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTACTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608425 Chironomus riparius water mite diet isolate 3081-BHL032417-GBD27532_13449-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACCTCCATTGGAGATGGCCAAATTTATAATGTTGTAGTTACCGCACATGCTTCTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGGCTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608426 Chironomus riparius water mite diet isolate 3154-BHL032417-GBD6646_17794-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAGTAGTGGGAACTTCATTAAGAATGCTAATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATTACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTATTATTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAAAGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608427 Chironomus riparius water mite diet isolate 3155-BHL032417-GBD16675_14673-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGAAGAATTAGGACGTCCCGGAACTTTCATTGGAGATGGCCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608428 Chironomus riparius water mite diet isolate 3178-BHL032417-GBD7729_7009-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACCTTCATTGGAGATGGCCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTAGCCCCCTCTCTTACCCTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608429 Chironomus riparius water mite diet isolate 3198-BHL032417-GBD7939_12482-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGACTTGATCCGGAATAGGGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCAGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTATTACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTGACCCCCCTCTCTTACTCGTCTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608430 Chironomus riparius water mite diet isolate 3213-BHL032417-GBD4536_9371-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTTGAGCAGAATTAGGACGATCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTCTAATTGGAGGATTAGGAAACTGACTTGTCCCCCTAATACTTGGAACACCTTACATAGCTTTTCCTCGAATAAATATTATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608431 Chironomus riparius water mite diet isolate 3270-BHL032417-GBD15435_26354-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGACTTGATCCGGAATAGTGGTAACTTCATTAAGAATGCTTATTCGAGCAGAACTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTATAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTATTACTTGGAGTACCTGAGATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608432 Chironomus riparius water mite diet isolate 3321-BHL032417-GBD27675_10957-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTATGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGGCCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGCCCCCCTAATACTTGTAGCACCTGACATAGCTTGTCCTCGAATAAATAATATAAGCTTCTGATTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608433 Chironomus riparius water mite diet isolate 3339-BHL032417-GBD8903_13935-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGTAGAATTAGGACGACCCGGAACTTTCATTGGAGATGGTCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTTGTCCCCCTAATACTTGGAGCTCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608434 Chironomus riparius water mite diet isolate 3346-BHL032417-GBD14805_28357-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAGATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACATGTCCCCTTATTACTTGGAGCACCTGACATAGCGTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTACTTTCGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608435 Chironomus riparius water mite diet isolate 3350-BHL032417-GBD14609_9661-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCTGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACGTGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGTATTCGGAAACTGACTTGTCCCCTTATCACTTGGAGTACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCCCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608436 Chironomus riparius water mite diet isolate 3361-BHL032417-GBD19432_27374-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGGCCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTCTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCGCTCTTACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608437 Chironomus riparius water mite diet isolate 3364-BHL032417-GBD17707_2389-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGTAACGTTCATTGGAGATGACCATATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAAGATTAGGAAACTGACTTGTCCCCTTATTACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATGATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608438 Chironomus riparius water mite diet isolate 3375-BHL032417-GBD21519_18930-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTAGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGATGGCCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTTCCCCTAATACTTGGAGCACCAGACATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608439 Chironomus riparius water mite diet isolate 3396-BHL032417-GBD22930_14233-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAGGAATGCTTATTCGAGCAAACTTAGGACGACCCGGAACTTTCAGTGGAGATGGCCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCCCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608440 Chironomus riparius water mite diet isolate 3436-BHL032417-GBD2475_15130-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACCAGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTATCCCCTTATTACTTGGAGCACCTGAAATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGAATTTTACCCTCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608441 Chironomus riparius water mite diet isolate 3494-BHL032417-GBD16118_5913-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATGTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTGATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGATTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAATTGGAGGATTCGGAAACTGACTTGTTCACCTAATACTTGGAGCACCTGACATAGCTTTTCCTAGAAAAAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608442 Chironomus riparius water mite diet isolate 3611-BHL032417-GBD4174_21143-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATGTTTGGAGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTCGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGACTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTAGAAAAAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTATACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608443 Chironomus riparius water mite diet isolate 3625-BHL032417-GBD6476_15977-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACCTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608444 Chironomus riparius water mite diet isolate 3708-BHL032417-GBD20379_14650-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATGTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAGTTTATAATGTTGTAGTTACTACACATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTAGAAAAAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTAATCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608445 Chironomus riparius water mite diet isolate 3711-BHL032417-GBD26466_7558-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATGTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTCAGCATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTGCCTAGAAAAAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCGTCTTTCTAGGTCTTTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608446 Chironomus riparius water mite diet isolate 3760-BHL032417-GBD9780_20303-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCTTATACATTATGTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTAGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608447 Chironomus riparius water mite diet isolate 4005-BHL032417-GBD22113_22260-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATGTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCTCTAATACTTAGAGCACCTGACATAGCTTTTCCTAGAAAAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608448 Chironomus riparius water mite diet isolate 4344-BHL032417-GBD18528_19759-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTTACTCTTCTTCTTTCTAGAAGATCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608449 Chironomus riparius water mite diet isolate 4931-BHL032417-GBD29239_18366-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTCTGGGGCTTCATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608450 Chironomus riparius water mite diet isolate 5111-BHL032417-GBD10835_4719-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGTTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTGGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCACGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608451 Chironomus riparius water mite diet isolate 5165-BHL032417-GBD3549_17817-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGGGGCTTCATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGATCTTTCATTGGAGATGACCAAATTTATAATGTTATAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608452 Chironomus riparius water mite diet isolate 5190-BHL032417-GBD2554_11779-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCATGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCTCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACACTTCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608453 Chironomus riparius water mite diet isolate 5200-BHL032417-GBD10684_17243-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCAAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTACAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTGCTAGTGCTGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608454 Chironomus riparius water mite diet isolate 5223-BHL032417-GBD4930_9109-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCTTCTCTTACTCTACTTCTATCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608455 Chironomus riparius water mite diet isolate 5306-BHL032417-GBD9935_4843-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTTTACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGGTTTTGACCTTTACCCCCCTCTCTTACTCTGCGTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608456 Chironomus riparius water mite diet isolate 5331-BHL032417-GBD21188_10504-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATGTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTCCATTGGAGATGACCAAATTTATAATGTTGTAGTTATTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATGGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAACTTTTCCTAGAAAAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCGTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608457 Chironomus riparius water mite diet isolate 5492-BHL032417-GBD9411_22884-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTTTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTAACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCGCTTACTCTTCTTCTATCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608458 Chironomus riparius water mite diet isolate 5542-BHL032417-GBD5544_22353-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTCATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCAGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACTTAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTAACCCCCTCTCTTACTCTTCTGCTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608459 Chironomus riparius water mite diet isolate 5654-BHL032417-GBD18015_6053-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCGTATTCGAGCAGAATTAGGACGACCCTTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGGTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCACTTTTAATGGGAGGATTGGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608460 Chironomus riparius water mite diet isolate 5700-BHL032417-GBD27273_19215-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTATAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAAATTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCCCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTACATCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608461 Chironomus riparius water mite diet isolate 5701-BHL032417-GBD15687_27376-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCTCTAATATTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608462 Chironomus riparius water mite diet isolate 5714-BHL032417-GBD15927_18222-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTCGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTATTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCATCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTGCTTCTTTCTTGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608463 Chironomus riparius water mite diet isolate 5947-BHL032417-GBD14147_5721-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGATTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACTACCCTGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGGTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATATTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCTTCTCTTACTCTTCTTCTTTCTAGTTCTATCGTAGAAACTGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608464 Chironomus riparius water mite diet isolate 6103-BHL032417-GBD6620_10928-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATATTTATACCAATTTTAATTGGAGGATTCGGAAGCTGACTTGTCCCCCTAATACTTAGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608465 Chironomus riparius water mite diet isolate 6116-BHL032417-GBD12799_4072-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTTAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGCTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCGTCTTTCTAGATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608466 Chironomus riparius water mite diet isolate 6122-BHL032417-GBD19614_3256-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACACTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCGTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCATTAACACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCGTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608467 Chironomus riparius water mite diet isolate 6217-BHL032417-GBD8023_4788-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGTTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAACAGAATTAGGACGACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCGTAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTAGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608468 Chironomus riparius water mite diet isolate 6768-BHL032417-GBD27578_9598-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTTCCCCTAATATTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCCTCTTTCTAGTTCTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608469 Chironomus riparius water mite diet isolate 6796-BHL032417-GBD25603_6041-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGAAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAGATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATTGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCGCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACCTCTTTCTAGTTCTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608470 Chironomus riparius water mite diet isolate 6829-BHL032417-GBD18193_27588-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTGGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTTCCTCTTTCAAGTTTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608471 Chironomus riparius water mite diet isolate 6881-BHL032417-GBD17827_27948-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTCACTGCACATGCTTTTATTATAATTTTTTTCATAGCTATACCAATTTTAATTAGAGGATTCGGAAACTGACTTGTCCCCCTAATACTCGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTTCCTCTTTCTAGTTCTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608472 Chironomus riparius water mite diet isolate 6935-BHL032417-GBD15724_9864-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTCTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608473 Chironomus riparius water mite diet isolate 7031-BHL032417-GBD7756_19409-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTGATACTTGGAGCCCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTATCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608474 Chironomus riparius water mite diet isolate 7063-BHL032417-GBD23407_7234-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACACTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAAATGACCAAATTTATAATGTTGTAGTTACTGCACATCCTTTTATTATAATTTTTTTCATAGTTATATCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCTCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTCTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608475 Chironomus riparius water mite diet isolate 7071-BHL032417-GBD20875_8792-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGTCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTATCTTAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608476 Chironomus riparius water mite diet isolate 7096-BHL032417-GBD10017_21554-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCATGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTGATTGGAGATGACCAAGTTTATAATGTTGTAGTTACTACACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATCCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608477 Chironomus riparius water mite diet isolate 7097-BHL032417-GBD14239_14378-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGTGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCTTTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTAAAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTGCTGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608478 Chironomus riparius water mite diet isolate 7110-BHL032417-GBD28279_21065-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGCACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTTTTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTACTTCTTGCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608479 Chironomus riparius water mite diet isolate 7115-BHL032417-GBD16344_2077-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGACTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCAAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGATTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608480 Chironomus riparius water mite diet isolate 7119-BHL032417-GBD12786_11156-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCCTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAATTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTACACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCTCTCTCTTACTCTACATCATTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608481 Chironomus riparius water mite diet isolate 7122-BHL032417-GBD17207_20627-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTTGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATAACCAAATTTATAATGTTGTAGTTACTGATCATCCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608482 Chironomus riparius water mite diet isolate 7125-BHL032417-GBD20447_2326-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGAGCTTGATCCGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTCTCTGACTTTTACCCCCCTCACTTACTCTTCTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608483 Chironomus riparius water mite diet isolate 7134-BHL032417-GBD27177_9037-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGTAGAATTAGGGCGACCCGGATCTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGAATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608484 Chironomus riparius water mite diet isolate 7135-BHL032417-GBD2907_13711-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGTTTGATCCGGAATAGTGTGAACTTCCTTAAGAATGCTTATTTGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGTACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACCCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608485 Chironomus riparius water mite diet isolate 7140-BHL032417-GBD24029_23410-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGATCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCCAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTATCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608486 Chironomus riparius water mite diet isolate 7142-BHL032417-GBD6783_8348-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTGAGAATGCTTATTCGAGCAGAATTAGGATGACCCGGAACTTTCATTGGAGATGACCAAATATATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTTCCCTCTCTTACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608487 Chironomus riparius water mite diet isolate 7150-BHL032417-GBD28828_20019-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGTTACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCACGAATAAATAATATAAGTTTCCGACTTTTAGCCCCCTCTCTTACTCTACTTCTGTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608488 Chironomus riparius water mite diet isolate 7165-BHL032417-GBD16302_24267-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATGGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCGCTCATACTCGTCTTCATTCGAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608489 Chironomus riparius water mite diet isolate 7186-BHL032417-GBD24926_6768-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTATTGTTACTGCACATGCTTTTATTATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTCCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608490 Chironomus riparius water mite diet isolate 7187-BHL032417-GBD26012_23633-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTTCCCCTAATACTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTTCCCCCCTCTCTAACTCTTCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608491 Chironomus riparius water mite diet isolate 7195-BHL032417-GBD15403_11986-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGAGAACTTCATTAAGAATGCATATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATAACCAAATTTATAATATTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAAGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTCTCCTCGAATAAACAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608492 Chironomus riparius water mite diet isolate 7201-BHL032417-GBD7734_19425-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTTTACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCCGAATTAGGACGACCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATAATTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608493 Chironomus riparius water mite diet isolate 7216-BHL032417-GBD26452_21004-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCTGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTAACTCTTCTTCTTGCTAGGACGTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608494 Chironomus riparius water mite diet isolate 7217-BHL032417-GBD13801_3686-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTGTATACATTATTTTTGGGGCTGGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACTACCCGTAACTTTCATTGGAGATGACCATATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTAGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAACTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608495 Chironomus riparius water mite diet isolate 7234-BHL032417-GBD6488_16443-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAATTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTAGGAGCTCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTTACCCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608496 Chironomus riparius water mite diet isolate 7242-BHL032417-GBD14088_2951-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACCGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGGCTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATAGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608497 Chironomus riparius water mite diet isolate 7245-BHL032417-GBD20588_9480-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCGGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCTCCTAATACTTGGAGCACCTGACATAACATTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCAGCCTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608498 Chironomus riparius water mite diet isolate 7248-BHL032417-GBD13420_26950-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGACTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCAAGCAGAATTAGGACTACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCCGACTTTTACCCCCCTCTCTTACCCTGCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608499 Chironomus riparius water mite diet isolate 7250-BHL032417-GBD16151_4661-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATATTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGATTACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTAGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608500 Chironomus riparius water mite diet isolate 7265-BHL032417-GBD2552_15068-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCCCTTTATACATTATTTTTGGGGCTTACTCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAGAATTCGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGGTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608501 Chironomus riparius water mite diet isolate 7267-BHL032417-GBD4297_14552-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTACAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGATCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTGTACCCCCCTCTCTTACACTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608502 Chironomus riparius water mite diet isolate 7270-BHL032417-GBD25627_22932-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGATACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGAAACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTGTACTCCCCACTCTAACTCTTCATCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608503 Chironomus riparius water mite diet isolate 7295-BHL032417-GBD18399_25230-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACTTTATTTTTGGGGCTTGATCCGTAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATCTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGTCATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608504 Chironomus riparius water mite diet isolate 7301-BHL032417-GBD26654_22292-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTAATTTGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCATCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608505 Chironomus riparius water mite diet isolate 7307-BHL032417-GBD26589_12524-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGCCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGACTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCGCGAATAAATAATATAAGTTTCCGACTATTACCCCCCTCACTAACTCTTCTTCTATCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608506 Chironomus riparius water mite diet isolate 7310-BHL032417-GBD14451_3672-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGACTAGTGGGAACTTCATTAAGAATGCTGATTCGAGCAGAATTAGGACGACCCTCAACTTTCATTGGAGATGACCAAATTTATAATGTTTTAGTTACTGCACATGCTTTTATTATAATTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGAATTGTCACCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608507 Chironomus riparius water mite diet isolate 7319-BHL032417-GBD11310_6995-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACACTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCCGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTATAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGAATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGAAATAGCTTTTCCACGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608508 Chironomus riparius water mite diet isolate 7323-BHL032417-GBD5570_17465-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGACTTAGGAAGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGATGTAGTTACTGCACATGCTTTTATTATAATCTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGTAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTGACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608509 Chironomus riparius water mite diet isolate 7333-BHL032417-GBD19367_6523-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTGTCCTCGAAGAAATAATATAAGTTTCTGACTTTTACGCCCCTCGCTTACTCGTCTTCTGTCTAGTTATTGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608510 Chironomus riparius water mite diet isolate 7340-BHL032417-GBD23880_24591-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTTGAGCAAAATTTGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCACTAACACTTCTTCTTTCTAGTTCTTGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608511 Chironomus riparius water mite diet isolate 7344-BHL032417-GBD20091_8483-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCATTTATTATAATTTTTTTCATAGTTATACCGATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGTGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTATTACCCCCCTCACTTACCCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608512 Chironomus riparius water mite diet isolate 7348-BHL032417-GBD20233_10981-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATTCTTATTCGGGCAGAATTAGGACAACCCGGAACTTTCATTGGTGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCACGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608513 Chironomus riparius water mite diet isolate 7349-BHL032417-GBD23482_26099-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTCGGGGCTTGATCCGGAATAGTGGTAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGAAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTTCTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608514 Chironomus riparius water mite diet isolate 7361-BHL032417-GBD19291_11928-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTCGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACACATCTTCAATCTAGTGCTTGCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608515 Chironomus riparius water mite diet isolate 7363-BHL032417-GBD29455_17807-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGAAGGATTCGGAAACTGACTTGTCACCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTC	Using NCBI BLASTN in June 2018, this sequence was 98.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608516 Chironomus riparius water mite diet isolate 7366-BHL032417-GBD18184_4548-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCTGAACTTTCATTGGAGATGACCAAATTTATAATGGTGTAGGTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTAGACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGCGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608517 Chironomus riparius water mite diet isolate 7368-BHL032417-GBD19480_16330-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCTCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGGCTTTTACCCCCTTCTCTAACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608518 Chironomus riparius water mite diet isolate 7375-BHL032417-GBD12872_6454-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCTGGAATAGTGGGCACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACGCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCATCTCTTACTCTTCTTCTATCTAGTGCGTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608519 Chironomus riparius water mite diet isolate 7386-BHL032417-GBD8057_4988-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGGATGTTTATTCGAGCAGAATTAGGACGACCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCACTTACTCTACTATTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608520 Chironomus riparius water mite diet isolate 7387-BHL032417-GBD23541_4269-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCATATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTGCCTCGAATAAATAATATAAGTTTCTGACTTTGACTCCCCGCTCTTACTCTACTGCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608521 Chironomus riparius water mite diet isolate 7394-BHL032417-GBD25736_10848-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGATTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCTGGAACGTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTGGGAGTACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608522 Chironomus riparius water mite diet isolate 7399-BHL032417-GBD14668_24153-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGTAAAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATATTTTTTTTCATAGTTATACCAATTTTAGTTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608523 Chironomus riparius water mite diet isolate 7403-BHL032417-GBD28319_19513-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTTGAGCAGAATTAGGACGACCCTGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTATTGCACATACTTTTATTATAATTTTTTTCATAGTTATCCCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608524 Chironomus riparius water mite diet isolate 7411-BHL032417-GBD16401_16862-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGAGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTAATTCGAGCAAAAGTAGGACGTCCCGGAACTTTCATTGGTGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608525 Chironomus riparius water mite diet isolate 7413-BHL032417-GBD19891_6440-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTTCCCCTAATACTTGGAGCCCCTGACATAGCATTTCCACGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTTCTTCTTTCTAGTTCTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608526 Chironomus riparius water mite diet isolate 7414-BHL032417-GBD12590_22947-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGTAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTACACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGGTTTTCCTCGAATAAATAATATAAGATTCCGACTTTTACCCCCCTATCTAACTCTACTTCTTTCAAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608527 Chironomus riparius water mite diet isolate 7423-BHL032417-GBD19826_6287-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTACACATTATTTTTGGGGCTTGATCCGGAATAGCGGGAACTTCATTAAGAATGGATATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTTCACGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCCTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608528 Chironomus riparius water mite diet isolate 7426-BHL032417-GBD24519_10700-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGTTTCGGAAACTGACTTGTACCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCACCCTCTCTTACTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608529 Chironomus riparius water mite diet isolate 7433-BHL032417-GBD13450_3356-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTAGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGGTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTGGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTTGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAGATGGTGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608530 Chironomus riparius water mite diet isolate 7439-BHL032417-GBD28838_15508-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACGTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACCGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCTCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCACTCTTACTCTTCTTCATTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608531 Chironomus riparius water mite diet isolate 7444-BHL032417-GBD17351_8355-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACCTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAACATAAGTGTCCGACTTTTACCCCCCTCGCTTACTCTGCTTCTTGCGAGTTCTTGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608532 Chironomus riparius water mite diet isolate 7447-BHL032417-GBD28119_11016-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATACTCTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCTGGTACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608533 Chironomus riparius water mite diet isolate 7448-BHL032417-GBD26930_12334-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCGCTTACTCTACTTCTTTCTAGTTCTTGCGTATATAATGGCGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608534 Chironomus riparius water mite diet isolate 7450-BHL032417-GBD16625_18527-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACCTTATTGTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAAATTTCCTTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608535 Chironomus riparius water mite diet isolate 7461-BHL032417-GBD17064_2608-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGGTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTGGGAGCACCCGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608536 Chironomus riparius water mite diet isolate 7465-BHL032417-GBD9521_5197-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTACACAAGCTTTTACTATAATTTTTTTCATAGTTATACCAATTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCATCTGACATGGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608537 Chironomus riparius water mite diet isolate 7476-BHL032417-GBD24920_5182-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCCTACACATCTTCTAGCTAGTTCTTTAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608538 Chironomus riparius water mite diet isolate 7480-BHL032417-GBD14695_3362-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACACTTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTAGGAAACAGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGCGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608539 Chironomus riparius water mite diet isolate 7481-BHL032417-GBD20480_25500-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAGCTTTATACATTATTTTTGGGGCTTGATCCGGTATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTATTCATAGTTATACCAATTTTAATTGGAGGTTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608540 Chironomus riparius water mite diet isolate 7487-BHL032417-GBD16890_2757-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGAGCCGGAATAGTGGGAACTGCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACATTCATTGGAGATGACCAAATTTATAATGGTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTGGGAAACTGACTTGTCCCCCTAATACTTGGAGCAGCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608541 Chironomus riparius water mite diet isolate 7491-BHL032417-GBD23891_22549-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCCTTTATTATAATTTTTTTCATAGTTATACCAATTTTAAATGGAGGATTCGGAAACTGACTTGTTCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608542 Chironomus riparius water mite diet isolate 7494-BHL032417-GBD3676_9575-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGCGATGACCAAATTTATAATGGTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAATTGGAGGATTCGGAAATTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGGTTCTGACTTTTACTCCCCTCTCTTACTCTGCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAA	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608543 Chironomus riparius water mite diet isolate 7495-BHL032417-GBD7164_8981-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCAAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATAACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCAAAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCACCCTCTCTTACTCTTATTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608544 Chironomus riparius water mite diet isolate 7496-BHL032417-GBD9837_8774-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGAGAACTTCATTAATAATGCTTATTCGAGCAGAATTATGACGACCCGGAACTTTCACTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608545 Chironomus riparius water mite diet isolate 7506-BHL032417-GBD2947_13773-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATTCGAGCAGATTTAGGACGACCCTGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATGCTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCACTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608546 Chironomus riparius water mite diet isolate 7518-BHL040517-GBD15808_26855-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATATTGTAGTTACTCCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTAACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608547 Chironomus riparius water mite diet isolate 7537-BHL040517-GBD24837_10430-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGTTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGTTTTTATTATAATTTTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCATAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTCACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608548 Chironomus riparius water mite diet isolate 7571-BHL040517-GBD24913_6179-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGACTGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGGGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTAATATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCTCTCTTACTCTACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608549 Chironomus riparius water mite diet isolate 7590-BHL040517-GBD23564_3915-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCCTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTCGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608550 Chironomus riparius water mite diet isolate 7611-BHL040517-GBD14495_3955-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCATATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGCGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608551 Chironomus riparius water mite diet isolate 7615-BHL040517-GBD17193_10201-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTGTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTATCTGACTTATATCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAA	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608552 Chironomus riparius water mite diet isolate 7628-BHL040517-GBD5625_7502-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAATAACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTTATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608553 Chironomus riparius water mite diet isolate 7658-BHL040517-GBD15674_11175-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTAGGAGCACCTGACATAGCTTTTCCTCGAATAAGTAATATAAGTTTCTGACTTTTATCCCCCTCTCTTACTCTTCTTCTATCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608554 Chironomus riparius water mite diet isolate 7686-BHL040517-GBD17289_11072-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATATTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTGTTACACCCCTCTCTTACTCTACTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608555 Chironomus riparius water mite diet isolate 7693-BHL040517-GBD16466_11315-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCCTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCCGACTTTTACCCCCCTCTCTTACACTACTTCTTTCCAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608556 Chironomus riparius water mite diet isolate 7705-BHL040517-GBD23809_18714-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACATCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCCTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608557 Chironomus riparius water mite diet isolate 7718-BHL040517-GBD25454_18820-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTAGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACATGGAGCACCTCACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTAACTCTACTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608558 Chironomus riparius water mite diet isolate 7732-BHL040517-GBD15965_5823-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTAATTCGAGCAGAATTAGGACGACCCTGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTGGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTTCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGCGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608559 Chironomus riparius water mite diet isolate 7733-BHL040517-GBD8728_3692-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGACCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATGTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCCCCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608560 Chironomus riparius water mite diet isolate 7741-BHL040517-GBD23212_23720-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCCTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTATTATTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608561 Chironomus riparius water mite diet isolate 7745-BHL040517-GBD12181_10400-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATCTCTGGGGCTTGATCCGGGATAGTGGGAACTTCATTAAGAATGCCTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGGGATGACCAAATTTATAATGATGTAGTTACTGCACATGCTTTTAATATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608562 Chironomus riparius water mite diet isolate 7753-BHL040517-GBD19613_27020-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATATCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCACACTAATACTTGGAGCACCTGGCATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCCTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608563 Chironomus riparius water mite diet isolate 7755-BHL040517-GBD24307_12084-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACACGCATTTATTATAATTTTTTCCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608564 Chironomus riparius water mite diet isolate 7763-BHL040517-GBD27056_9080-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGTGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGACTTAGGACGATCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAGACTGACTTGTCCCACTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCCTACTCTTCCTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608565 Chironomus riparius water mite diet isolate 7764-BHL040517-GBD21126_14786-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACTTTATTTTTAGGGCTTGATCCGGAACAGTGGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTCCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608566 Chironomus riparius water mite diet isolate 7767-BHL040517-GBD26230_20269-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGATTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTTAACCTACTACTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608567 Chironomus riparius water mite diet isolate 7768-BHL040517-GBD15691_9176-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACACTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCCTTAAGAATGCTTATTCGAGCTGAATTGGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTGCTTCTTTCTAGTTCTTGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608568 Chironomus riparius water mite diet isolate 7782-BHL040517-GBD23323_21432-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGAACCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTATTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCACTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTATCTAGCTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608569 Chironomus riparius water mite diet isolate 7786-BHL040517-GBD13626_20269-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTAGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATAGCAATTTTAATTGGAGGATTTGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608570 Chironomus riparius water mite diet isolate 7790-BHL040517-GBD22118_3676-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTAGAGCAGAATTAGGACAACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTATTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608571 Chironomus riparius water mite diet isolate 7794-BHL040517-GBD8865_5444-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTGTTGCCCCCCTCTCTAACTCTTCTACTATCTAGTGCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608572 Chironomus riparius water mite diet isolate 7797-BHL040517-GBD22278_7426-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAAATAGGACGACCCGGAACATTCAATGGAGATGACCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATGATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608573 Chironomus riparius water mite diet isolate 7810-BHL040517-GBD12738_24772-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCCGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTAGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608574 Chironomus riparius water mite diet isolate 7814-BHL040517-GBD5731_17328-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGATCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAGTAATTACTGCACATGCTTTTATTATAATTTTTTTCACAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACACTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608575 Chironomus riparius water mite diet isolate 7815-BHL040517-GBD16386_17925-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGTCCGAATTTATAATGTTGTAGTTACTGTAGATGCTTTTATTATAATTTTTTTCATAGTTATATCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTATTACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTGCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608576 Chironomus riparius water mite diet isolate 7821-BHL040517-GBD8073_11772-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCGATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCCCCTGACATAGCTTTTCCCCGAAAAAAATAAAATAAGTTTCTGAACTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608577 Chironomus riparius water mite diet isolate 7826-BHL040517-GBD20354_12627-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACGCGGAATTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTCACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTTACTCTTCTTCTGTCTAGTACGTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608578 Chironomus riparius water mite diet isolate 7827-BHL040517-GBD24541_7640-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCTTATACATTATTTTTGGGGCTTGATCGGGAATAATGGGAACTTCTTTAAGAATGCTTATTCGCGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGAGTTGTCCCACTAATACTTGGAGCACCTGACATGGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608579 Chironomus riparius water mite diet isolate 7829-BHL040517-GBD26013_9481-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCATGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCTGAATTATGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGCTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCTCCCTCTCTTACTCCACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608580 Chironomus riparius water mite diet isolate 7834-BHL040517-GBD24663_5515-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTATGACTACCCGGAACTTTCCTTGGAGATGACCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCGAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCGCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608581 Chironomus riparius water mite diet isolate 7842-BHL040517-GBD3503_11233-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCCGGAACAGTGGGAACTTCATTAAGTATGCTTATTAGAGCAGAATTAGGACGACCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATGCTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608582 Chironomus riparius water mite diet isolate 7849-BHL040517-GBD18470_23159-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAATTTCATTATGAATGCTTATTCGAGCAGACTTATGACGACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCCTCTTCTTTCTAGTTCTTTCGTAGAGAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608583 Chironomus riparius water mite diet isolate 7850-BHL040517-GBD21681_8321-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTGTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATGCTTATTCGAGCAGAAATAGGACGACCCGGAACTTTCATTGGTGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608584 Chironomus riparius water mite diet isolate 7858-BHL040517-GBD17977_16671-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTCGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTAGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAATTTTATAAAGGTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608585 Chironomus riparius water mite diet isolate 7859-BHL040517-GBD6281_6231-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTGTTGGGGCTTGCTCCGGAATAGTGTGAACTTCCTTAAGAATGCTTATTCGAGCAGCATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCGCTCTTACTCGTCTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608586 Chironomus riparius water mite diet isolate 7868-BHL040517-GBD27928_21825-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTAATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTGTTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTAGTCCCCCTAATACTTGGAGCCCCTGACATAACTTTTCCCCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608587 Chironomus riparius water mite diet isolate 7869-BHL040517-GBD13212_9520-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTGTTGGGGCTTGATCCGGTATAGTGGGTACTTCATTAAGAATGTTTATTCGAGCAGAATTCGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608588 Chironomus riparius water mite diet isolate 7876-BHL040517-GBD7380_13643-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAGTTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCTCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATGAATAATATAAGTTTCTGACTTTTCCCCCCCTCTCTTACTCTGCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608589 Chironomus riparius water mite diet isolate 7878-BHL040517-GBD27014_12627-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGTGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACCACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTCGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACCTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTACTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608590 Chironomus riparius water mite diet isolate 7883-BHL040517-GBD28434_12659-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTAGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATATTTGGTGCACCCGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACGCTTCTTCTTTCTAGTTCTTTCGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608591 Chironomus riparius water mite diet isolate 7888-BHL040517-GBD24443_19188-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGTGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATTTTTATTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTTTCACCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608592 Chironomus riparius water mite diet isolate 7891-BHL040517-GBD18609_19301-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCATTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608593 Chironomus riparius water mite diet isolate 7894-BHL040517-GBD5181_18421-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTATGATGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTATTTCTAGTGCTTTCGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608594 Chironomus riparius water mite diet isolate 7901-BHL040517-GBD26575_10586-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGCATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCACTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACGCTTCTTCTTTCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608595 Chironomus riparius water mite diet isolate 7904-BHL040517-GBD5695_12805-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGGATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCCTTTATTATAATCTTTTTCATAGTTATACCAATTTTAATCGGAGGTTTCGGAAACTGACTTGTCCCCCTAATACTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608596 Chironomus riparius water mite diet isolate 7907-BHL040517-GBD18979_13244-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGTATAGTGGGAGCTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGTCCCGGAACTTTCATTGGTGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTATTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608597 Chironomus riparius water mite diet isolate 7911-BHL040517-GBD29097_14567-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCCTTAAGAATGCTTATTCGAGCAGAATTAGGATGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTGTACCCCCCTCTCTAACTCTTCTGCTTTCTAGTACTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608598 Chironomus riparius water mite diet isolate 7917-BHL040517-GBD4776_11879-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCCTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAGTGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGGAGCTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCCTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608599 Chironomus riparius water mite diet isolate 7920-BHL040517-GBD10542_12005-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTTTACATTATTGTTGGGGCTTGACCCGGAATATTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACACTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608600 Chironomus riparius water mite diet isolate 7926-BHL040517-GBD4697_21914-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTAGAGCAGAATTAGGATGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTCTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTGACCCCCCTCTCCTACTCTTCTTCATTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608601 Chironomus riparius water mite diet isolate 7929-BHL040517-GBD10832_4835-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGAACCGGAGTAGTGGGAACTTCATTAAGAATGCTTGTTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTCTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATGTAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608602 Chironomus riparius water mite diet isolate 7935-BHL040517-GBD26469_22569-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGAGCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGGTTCGGAAACTGACTTGTCCCCCAAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTACTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608603 Chironomus riparius water mite diet isolate 7950-BHL040517-GBD26614_14145-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTCACATAGCTTTTCCTCAAGTAAATAATATAAGTTTCTGACTGTTACCCCCCTCACTTACTCTACTGCTATCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608604 Chironomus riparius water mite diet isolate 7954-BHL040517-GBD10686_9722-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGAGCTTGATCCGGAATAGTAGGAACTTCATTAAGAATTCTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACTAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAA	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608605 Chironomus riparius water mite diet isolate 7956-BHL040517-GBD29561_16638-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCGCTGAC	Using NCBI BLASTN in June 2018, this sequence was 99.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608606 Chironomus riparius water mite diet isolate 7958-BHL040517-GBD16702_13590-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACAACCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTAGTTCCACTAATACTCGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608607 Chironomus riparius water mite diet isolate 7962-BHL040517-GBD24406_21633-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTCTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGAATTCGGAAACTGACTTGTCCCCCTAATAGTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608608 Chironomus riparius water mite diet isolate 7963-BHL040517-GBD26377_23134-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTTGGAACTTCCTTAAGACTGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGGGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTAATATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCGGACTTTTACCTCCCTATCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608609 Chironomus riparius water mite diet isolate 7969-BHL040517-GBD7533_22035-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGAGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACATGTCCCACTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCATCTCTTACTCTACTTCTTTCAAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608610 Chironomus riparius water mite diet isolate 7970-BHL040517-GBD21191_18937-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGTACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGGGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATCTTTTTCATAGTTATACCAATTTTAATCGGAGGCTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTGCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608611 Chironomus riparius water mite diet isolate 7980-BHL040517-GBD26265_10673-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGATCTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTAGAGCAGAATTAGGACGACCCGGAACTTTCATTGAAGATGACCATATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACACTTCTTCTATCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608612 Chironomus riparius water mite diet isolate 7982-BHL040517-GBD18493_12231-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTATTGCACATGCTTTTATTATAATCTTTTTCATACTTATACCAGTTTTAATCGGAGGTTTCGGAAACTGACTTGTCCCCCTAATACGTGGAGTACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608613 Chironomus riparius water mite diet isolate 7983-BHL040517-GBD23662_6057-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGATCAGAATTATGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTCACATAGCTTTGCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCGACTTCTTTCTAGTGCTTGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608614 Chironomus riparius water mite diet isolate 7993-BHL040517-GBD23383_17428-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGATCTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTTTCCCCCTAATACTTGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCCTCTTCTTCCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608615 Chironomus riparius water mite diet isolate 8000-BHL040517-GBD4038_15741-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTCATTACTGCCCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTTTCCCCCTAATACTTGGAGCACCTGGCATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608616 Chironomus riparius water mite diet isolate 8001-BHL040517-GBD16494_10712-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGGGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCCCTTACCCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608617 Chironomus riparius water mite diet isolate 8004-BHL040517-GBD18806_19876-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGACCTTCATTAATACTGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTATTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTATCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608618 Chironomus riparius water mite diet isolate 8020-BHL040517-GBD16242_4091-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTTGAGGATTGGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTTCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTCCTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608619 Chironomus riparius water mite diet isolate 8021-BHL040517-GBD16780_20766-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACGTTTACCCCCCTCTCGCACGCTGCTTCGTTCTAGTGCTTTCGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608620 Chironomus riparius water mite diet isolate 8022-BHL040517-GBD18982_2707-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTGGTCCCCCTAATATTTGGAGCTCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608621 Chironomus riparius water mite diet isolate 8023-BHL040517-GBD19963_4164-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATTCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCGTCGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCCCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608622 Chironomus riparius water mite diet isolate 8036-BHL040517-GBD23049_23859-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTTGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTAACCCTTCTTCTATCTAGTTCTTTCCTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608623 Chironomus riparius water mite diet isolate 8037-BHL040517-GBD16458_26614-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTAGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACTAATTTTAATTGGAGGAATGGGAAACTGACTTGTCCCCCTAATACTTGGTGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608624 Chironomus riparius water mite diet isolate 8041-BHL040517-GBD24863_7668-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGTGGCTTGATCCGGAATAGGGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACTCGTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACGTGTCCCCCTAATACTTGGAGCAACTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608625 Chironomus riparius water mite diet isolate 8043-BHL040517-GBD24456_18308-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGACTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGGCCAAATTTATAATGTCGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGAAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTAGCCTCCTCTCTTACTCTTCGTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608626 Chironomus riparius water mite diet isolate 8049-BHL040517-GBD22668_14030-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCCTGATGCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACGAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAACTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608627 Chironomus riparius water mite diet isolate 8050-BHL040517-GBD29216_11734-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTAATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTGGTCCCCCTAATACTTGGATCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGTCCTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608628 Chironomus riparius water mite diet isolate 8051-BHL040517-GBD8330_11942-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTGTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCCCCTGACATACCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACGCTACTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608629 Chironomus riparius water mite diet isolate 8054-BHL040517-GBD25759_8617-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGAGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTACCCCTAATACTAGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACCATTACCCCCCTCTCTTACCCCTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608630 Chironomus riparius water mite diet isolate 8055-BHL040517-GBD12172_9289-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTAGAGCAGAATTAGGACGACCCGGAACTTTCATTGTAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTAATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCTCCTGACACAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608631 Chironomus riparius water mite diet isolate 8064-BHL040517-GBD12330_16107-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTTATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGTAGGAGATCAAATTTATAATGCTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACATGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608632 Chironomus riparius water mite diet isolate 8066-BHL040517-GBD24791_21763-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATGCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATATTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAAAAAAAGTATCTGACTTTTACCCCCCTCTCTAACTCTACTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608633 Chironomus riparius water mite diet isolate 8067-BHL040517-GBD15191_24779-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGAACAGGGACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTTCTTCTATCTAGTGCGTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608634 Chironomus riparius water mite diet isolate 8069-BHL040517-GBD27532_20061-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTATGAATGCTTATTCGAGTAGAATTAGGACGACCCGGAACTTTCAATGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACACAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCACTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608635 Chironomus riparius water mite diet isolate 8070-BHL040517-GBD26136_17762-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGGGGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATGCTGATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATGGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACGCGTCTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608636 Chironomus riparius water mite diet isolate 8072-BHL040517-GBD21839_10271-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGTGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTTGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTAACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608637 Chironomus riparius water mite diet isolate 8075-BHL040517-GBD22501_20610-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGTCTTGTCCCTCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTGACTCTTCTTCCTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608638 Chironomus riparius water mite diet isolate 8089-BHL040517-GBD10566_27971-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGGACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTGGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCCCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCACTTACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608639 Chironomus riparius water mite diet isolate 8095-BHL040517-GBD11261_6326-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAACGTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCCGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCCTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608640 Chironomus riparius water mite diet isolate 8102-BHL040517-GBD14960_15044-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGACTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTAGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCGAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCGATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATGTAAGTTTCTGACTTTTACGCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608641 Chironomus riparius water mite diet isolate 8103-BHL040517-GBD21818_18277-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGACTTTATACTTTATTTTTGGGGCTTGATCCGGAATATTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGGCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATCGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCCTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608642 Chironomus riparius water mite diet isolate 8109-BHL040517-GBD16091_27106-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAACAGTGGGAACTTCATTAATAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTATAGTTACTGCTCATGCCTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTACTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACGCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608643 Chironomus riparius water mite diet isolate 8114-BHL040517-GBD16743_25808-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAACAGAGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATCATTTTTTTCATCGTTATACCAATTTTAATTGGAGTATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAACAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608644 Chironomus riparius water mite diet isolate 8116-BHL040517-GBD7853_10626-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGAAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAGTTGGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGTTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTTATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608645 Chironomus riparius water mite diet isolate 8117-BHL040517-GBD28241_15211-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACGTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTCTAATTGGAGGATTCGGAAACTGACTTGTCCCTCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTATTACCCCCCTCTCTAACCCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608646 Chironomus riparius water mite diet isolate 8118-BHL040517-GBD5091_10806-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATGGGAACTTTGTACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTAGAGCAAAATTAGGACGACCCGGAACTTTCATTGAAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608647 Chironomus riparius water mite diet isolate 8120-BHL040517-GBD7562_15809-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATACGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCCGAATTAGGACGACCCGAAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCACTAATATTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCATTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608648 Chironomus riparius water mite diet isolate 8128-BHL040517-GBD3404_20311-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGATGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTACTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGTTTCGGAAACTGACTAGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608649 Chironomus riparius water mite diet isolate 8132-BHL040517-GBD19500_27429-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATGAGGAATAGTGGGAACTTCATTAAGGATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCCCATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTGTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608650 Chironomus riparius water mite diet isolate 8138-BHL040517-GBD10301_7502-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGTAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATTCTTGGATCACCTGAAATAGCTTTTCCCCCAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608651 Chironomus riparius water mite diet isolate 8144-BHL040517-GBD4184_12348-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACCTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTCGGACGACCCGGGACTTTCATTGGAGATGACCAAATTTATAATGCTGTAATTACTGCCCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTATCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608652 Chironomus riparius water mite diet isolate 8147-BHL040517-GBD26982_11137-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGACTTGATCCGGAATAGTGGTAACTTCATTAAGTATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATAGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTATCACCCTAATACTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608653 Chironomus riparius water mite diet isolate 8154-BHL040517-GBD25146_7682-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGAACCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCACCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGCAAAAATAATATAAGGTTCTGACTTTTACCCCCCACTCTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608654 Chironomus riparius water mite diet isolate 8159-BHL040517-GBD16414_18267-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCCTTTACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTAACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCAAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCCTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608655 Chironomus riparius water mite diet isolate 8162-BHL040517-GBD29391_17187-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTTATTAAGAATGCTTATTCGAGCAGAATTCGGACGACCCGGTACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGTTTCGGAAACTGACATGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608656 Chironomus riparius water mite diet isolate 8163-BHL040517-GBD22686_3444-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGACCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTAGAGCAGAATTAGGACGTCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608657 Chironomus riparius water mite diet isolate 8164-BHL040517-GBD17772_19763-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCTCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTGACCCCCCGAACATACTCTTCGTCGTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608658 Chironomus riparius water mite diet isolate 8172-BHL040517-GBD14159_24560-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCCTTGGAGATGTCCAAATTTATAATGTGGTAGTTCCTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCTCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608659 Chironomus riparius water mite diet isolate 8179-BHL040517-GBD6795_24698-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTGTCGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGGGGATTGGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608660 Chironomus riparius water mite diet isolate 8183-BHL040517-GBD22825_14420-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAACAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTACTATAATTTTTTTCATAGTGATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608661 Chironomus riparius water mite diet isolate 8186-BHL040517-GBD6712_6572-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGTCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACTCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCTCCCTAATTCTTGGAGCACCTGACATAGCCTTTCCTTGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCCTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACGGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608662 Chironomus riparius water mite diet isolate 8187-BHL040517-GBD24439_18477-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAACAGTGGGAAGTTCATTAAGAATGCTTATTCGAGCAGAAGTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTCTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTAACCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608663 Chironomus riparius water mite diet isolate 8188-BHL040517-GBD16537_10259-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTGTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGTAGAATTAGGACGACCCGGAACTTTCATTAGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTAGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGTTTTTCCCCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACACTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608664 Chironomus riparius water mite diet isolate 8189-BHL040517-GBD14010_2019-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGACCTTTATACATTATTTTTGGGGCTTGCTCCGGAATAGTGGGACCTTCCTTAGGTATGCTTATTCGGGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608665 Chironomus riparius water mite diet isolate 8195-BHL040517-GBD14794_2897-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGACTTTATACATTATTTTTGGGGCTTGAGCCGGAATAGTGGGAACTGCATTAAGAATGCTAATTCGAGCAGAATTAGGACGACCCTGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATATTTTTCATAGTTATACCAATTTTAATGGGAGGTTTAGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608666 Chironomus riparius water mite diet isolate 8196-BHL040517-GBD7883_3737-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACCTTATTTTTGGGGCTTGATCCGGAATAGTGGGACCTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGATCTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATCTTTTTCATAGTTATACCAATTTTAATCGGAGGTTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTAGTAGAAAATGGAGTTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608667 Chironomus riparius water mite diet isolate 8202-BHL040517-GBD27806_15651-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGACCTTTGTACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACAGGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTGTCCGACTTTTACCCCCCACGCTTACTCAGCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608668 Chironomus riparius water mite diet isolate 8204-BHL040517-GBD13440_15636-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAGCTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATGATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGGCATAGCCTTTCCCCGAATAAATAATATAAGTTTCTTACTTTTACCCACCTCTCATACTCCTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608669 Chironomus riparius water mite diet isolate 8206-BHL040517-GBD3740_10829-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAAAATTAGGACGTCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGAGTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCGTACTCTTCCTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608670 Chironomus riparius water mite diet isolate 8209-BHL040517-GBD5859_17253-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGTCCAAATTTATAATGTTGTAGTTACTGCAGATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTTGTCCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608671 Chironomus riparius water mite diet isolate 8213-BHL040517-GBD23609_18472-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTCAAAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTAGTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCCCCTAATACTTGGAGCCCCCGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608672 Chironomus riparius water mite diet isolate 8215-BHL040517-GBD6785_16265-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTGTTGGGGCTTGATCCGGAATAGTGGTAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGAGCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCACCTAATATTTGAAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTGCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608673 Chironomus riparius water mite diet isolate 8221-BHL040517-GBD11782_7517-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGATCTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAGCTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTCATAGGTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATATTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608674 Chironomus riparius water mite diet isolate 8235-BHL040517-GBD15947_11567-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATTCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTACCCCTAATACTTGGAGCACCTCGCATTGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608675 Chironomus riparius water mite diet isolate 8242-BHL040517-GBD20566_3160-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTCTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAGCTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTCACATAGCTTTTCCTCAAATAAATAATATAAGTTTCTGACTTTTACCCCACTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608676 Chironomus riparius water mite diet isolate 8246-BHL040517-GBD2879_16224-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTGTTGGGGCTTGATCCGGAATAGTAGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTATTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608677 Chironomus riparius water mite diet isolate 8247-BHL040517-GBD9826_4803-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGAGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTTTAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCCGAAACTGACTTGTCCCCCTAATACTTGGAGCAACTGACATAGCTTTTCCTCGAATGAATAATATAAGTTTCTGGCCTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608678 Chironomus riparius water mite diet isolate 8251-BHL040517-GBD21831_6481-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTAGAACTTTATACATTATTTTTGGGGATTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGCATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATAGCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608679 Chironomus riparius water mite diet isolate 8254-BHL040517-GBD28687_18724-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTGTTGGGGCTTGATCCGGAATCGTGGGAACTTCATTAAGAATGTTTATTCGAGCCAAATTAGGACGACCCGGAACTTTCATTGGGGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608680 Chironomus riparius water mite diet isolate 8259-BHL040517-GBD7268_23876-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGACTTGATCCGGAACAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGGGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTGCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608681 Chironomus riparius water mite diet isolate 8266-BHL040517-GBD9288_19625-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTATGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTATAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTGCCTCTAATACTAGGAGCACCTCACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608682 Chironomus riparius water mite diet isolate 8282-BHL040517-GBD20518_6759-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGTAATAGTGGAAACTTCATTAAGAATGCTTATTCGAGTAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTATTTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTCACATAGCCTTTCCTCAAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTTCTTCCTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608683 Chironomus riparius water mite diet isolate 8289-BHL040517-GBD25724_15646-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCATACTTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGAATTGTCCCCCTAATACTTGGAGCACCTGACATAGCTGTTCCTCGAATAAATAATATAAGTTTCTGACTTTGACCCCCCTCTCTTACTCTTCTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608684 Chironomus riparius water mite diet isolate 8295-BHL040517-GBD22384_15349-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTACGAATGCTTATTCGAGCAGAATTAGGACGACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGATGTAATTACTGCACATGCTTTTATTCTAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608685 Chironomus riparius water mite diet isolate 8298-BHL040517-GBD24143_9507-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAACAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAAAAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTGCTTCTTTCTAGTTCGTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608686 Chironomus riparius water mite diet isolate 8299-BHL040517-GBD15576_14975-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATGCTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTAGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGAGCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACCCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608687 Chironomus riparius water mite diet isolate 8300-BHL040517-GBD2841_20230-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGGCGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTCCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACCCTTCTTCTATCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608688 Chironomus riparius water mite diet isolate 8306-BHL040517-GBD28490_19610-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATCTTTGGGGCTTGATCCGGAATAGTTGGAACTTCATTAAGAATGCTTATTTGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCTACCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGGTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608689 Chironomus riparius water mite diet isolate 8314-BHL040517-GBD11522_2385-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAGTTAGGACGCCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACAGAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCCTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608690 Chironomus riparius water mite diet isolate 8330-BHL040517-GBD2151_15959-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGTCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGATCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTCCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACACAGCTTTTCCTCGAATAAACAATATAAGGTTCTGACTTTTACCCCCCTCTCTTACTCATCTTCTTTCTAGTACTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608691 Chironomus riparius water mite diet isolate 8334-BHL040517-GBD24400_21468-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGAAACGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGTATTCGGAAACTGACTTGTCCCCCTAATACTCGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608692 Chironomus riparius water mite diet isolate 8335-BHL040517-GBD10166_15578-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGCTTTATCCGGGATAATGGGAACTTCATTTAGGATGGTTATTTGAGCAGAATTTGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608693 Chironomus riparius water mite diet isolate 8344-BHL040517-GBD20929_3806-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTAGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATATTTGGAGCACCTGACATGGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTAATTCTTTCTAGATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608694 Chironomus riparius water mite diet isolate 8349-BHL040517-GBD15238_13670-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGAAGATGATCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTCATAGTGATACCAATTTTAATTGGAGGGTTCGGAAACTGACTTGTCCTCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTCTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608695 Chironomus riparius water mite diet isolate 8353-BHL040517-GBD18284_11052-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACTTTATTTTTGGGGCCTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTCCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTCGGAGCCCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608696 Chironomus riparius water mite diet isolate 8359-BHL040517-GBD20328_17580-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTCGATCCGGCATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATGTGAGGATTCTGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCGCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608697 Chironomus riparius water mite diet isolate 8364-BHL040517-GBD21056_17877-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGTGAACTTCATTATGAATGCTTATTCGAACAGAATTAGGACGACCCGGAACTCTCATTGGAGATGCCCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTAGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608698 Chironomus riparius water mite diet isolate 8367-BHL040517-GBD24561_19779-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGAGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGACGGATTCGGAAACTGATCTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608699 Chironomus riparius water mite diet isolate 8368-BHL040517-GBD10051_4605-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGCTCTGAAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTTGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTATCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCAAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608700 Chironomus riparius water mite diet isolate 8372-BHL040517-GBD25153_22414-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGTTTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608701 Chironomus riparius water mite diet isolate 8376-BHL101416-GBD11998_10564-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGTTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608702 Chironomus riparius water mite diet isolate 8560-BHL101416-GBD19100_9183-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGAAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGATCCGGAACTTTCATCGGAGATGACCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATGCTTGAAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTGTTACCCCCCTCTCTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608703 Chironomus riparius water mite diet isolate 8598-BHL101416-GBD11311_11344-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGACCAGAATTAGGACGACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGTTTTCGGAAACTGACTTGTCCCCCTAATAATTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608704 Chironomus riparius water mite diet isolate 8610-BHL101416-GBD25985_15552-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTAATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCACTAACCCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608705 Chironomus riparius water mite diet isolate 8621-BHL101416-GBD12878_14911-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCCGAAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGATCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACCTGTCCCCCTAATACTTGGAACACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTGCTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608706 Chironomus riparius water mite diet isolate 8636-BHL101416-GBD24318_6743-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAGTTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCCCCTGAAATAGCTTTTCCTCGAATAAATAAAATAAGTTTCTGACTCTTACCCCCCTCTCATACCCTCCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608707 Chironomus riparius water mite diet isolate 8650-BHL101416-GBD18375_25619-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACCTTATTTTTGGGGCTTGATCCGGTATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATAGTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTATCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608708 Chironomus riparius water mite diet isolate 8661-BHL101416-GBD29141_16143-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTGATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTAACTCTACTACGATCTAGTTCTTTCGTAGAAAATGGAGGTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608709 Chironomus riparius water mite diet isolate 8664-BHL101416-GBD6631_14147-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGCTGTAGTTACCGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTATTACTTGGAACACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCGTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608710 Chironomus riparius water mite diet isolate 8682-BHL101416-GBD15623_12825-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATTCGAGCAGAATTATGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGTTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACCCTACTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608711 Chironomus riparius water mite diet isolate 8701-BHL101416-GBD12985_20160-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGGGGCTTCATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGGTTTTACTATAATTTTTCACATAGTTATACCAATTTTATTTGGAGGGTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGCTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608712 Chironomus riparius water mite diet isolate 8762-BHL101416-GBD15845_3821-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCTTAACTTTCATTGGAGATGACCATATTTATAATGTTATAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTGGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608713 Chironomus riparius water mite diet isolate 8771-BHL101416-GBD25590_19362-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTGTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCATCCGCTGTCTAGTTATTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608714 Chironomus riparius water mite diet isolate 8774-BHL101416-GBD10013_13477-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGTTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTACTATCTAGTTCTCTCGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608715 Chironomus riparius water mite diet isolate 8777-BHL101416-GBD26404_16116-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACGTTATACATTATTTTTGGGGCTTGATCCGGACTAGTGGGCACTTCATTAAGAATGCTTGTTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608716 Chironomus riparius water mite diet isolate 8840-BHL101416-GBD20674_9921-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGAGAACTTCATTAAGAATACTTAATCGAACAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608717 Chironomus riparius water mite diet isolate 8855-BHL101416-GBD10890_14375-Lq60 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGGAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608718 Chironomus riparius water mite diet isolate 8909-BHL032417-GBD7733_13253-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATATTTTTTTGCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCTCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTTACTCTGCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608719 Chironomus riparius water mite diet isolate 8919-BHL032417-GBD25314_5708-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTAATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTATTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608720 Chironomus riparius water mite diet isolate 8945-BHL032417-GBD15221_11859-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATGATGTTGTAGTTACTGCACATGCTTTTGTTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGACCCCCTAATACTTAGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTTACTCTTCTTCTTTCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608721 Chironomus riparius water mite diet isolate 8948-BHL032417-GBD12882_14298-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCGGGAACTTTCATTGGAGATGAACAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAACATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTATCTAGTTCTTTCGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608722 Chironomus riparius water mite diet isolate 8955-BHL032417-GBD24491_4905-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACAACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCAGACATAGCCTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608723 Chironomus riparius water mite diet isolate 8960-BHL032417-GBD26948_11658-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGACTTGTTCCCCTAATACTAGGAGCACCTGACATAGCTTTTCCTCGAATAAGTAATATAAGTTTCTGACTTTTTCCCCCCTTTCTGACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608724 Chironomus riparius water mite diet isolate 8965-BHL032417-GBD14612_2559-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCTACCCGGAACTTTCATTGGAGACGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAAATGGAGGATTGGGAAACTGACTGGTCACCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608725 Chironomus riparius water mite diet isolate 9000-BHL032417-GBD6995_7201-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGCCCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCCCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608726 Chironomus riparius water mite diet isolate 9012-BHL032417-GBD13726_26777-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTGCCTCTAATACTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608727 Chironomus riparius water mite diet isolate 9017-BHL032417-GBD14486_2196-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGCTGTAGTTACTGCACATGCTTTTGTTATAATTTTTTTCCTAGTTATACCAATTTTAATTGGAGGATTCGGTACCTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCTAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGCGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608728 Chironomus riparius water mite diet isolate 9023-BHL032417-GBD28426_11352-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTCTTATAATTTTTTTCATAGTTATACCAATTTTAATTGGTGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAACAATATAAGTTTCTGACTTTTACCCCCCTTTCTTACCCTTCTTCTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608729 Chironomus riparius water mite diet isolate 9024-BHL032417-GBD18268_2977-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGATCTTTCATTGGAGATGACCAATTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGGTATACCAATTTTAATTGGAGGATTAGGAAACTGACTTGTCCCCCTAATACTTGGAGCTCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTTTCTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608730 Chironomus riparius water mite diet isolate 9043-BHL032417-GBD7536_14947-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACAACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTAGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTTACTCTACTTCTTTCAAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608731 Chironomus riparius water mite diet isolate 9049-BHL032417-GBD14589_3225-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACAAAAGTTATAATTTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCACCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGTCTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACCGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608732 Chironomus riparius water mite diet isolate 9064-BHL032417-GBD25774_20244-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTGTCTTACACTTCATCTAGCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608733 Chironomus riparius water mite diet isolate 9074-BHL032417-GBD29519_13716-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCTGGACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCGCTTACTCATCGTCTTTCTAGTTCTTTCTTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608734 Chironomus riparius water mite diet isolate 9075-BHL032417-GBD23650_11284-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTCGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTTCCTAACGCCACTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608735 Chironomus riparius water mite diet isolate 9084-BHL032417-GBD4759_17072-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCGTATTCGAGAAGAATGAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCGTTTATTATAATTTTTTTCATAGTTATACCAATTTTAAGTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608736 Chironomus riparius water mite diet isolate 9111-BHL032417-GBD15340_9251-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGATCTTTCATTGGTGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTGACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608737 Chironomus riparius water mite diet isolate 9119-BHL032417-GBD23929_8451-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGCCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTGATACCAATTTTAATTGGAGGACTCGGAAACTGACTTGTCCCCCTAATACTTGGTGCTCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTAACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608738 Chironomus riparius water mite diet isolate 9125-BHL032417-GBD7721_19830-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACGTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCAGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCATCATAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTTACTCTTCTCCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608739 Chironomus riparius water mite diet isolate 9139-BHL032417-GBD6468_18414-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGTGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGCGCAGAATTAGGCCGACCCGGCACTTTCATTGGAGATGACCAAATTTATAATGTTGTCGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTAGACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTTACTCTTCTTCTTTCTAGTTCTTTCGGAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608740 Chironomus riparius water mite diet isolate 9140-BHL032417-GBD17083_21885-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCTGGAATAGTTGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGTCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATTCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGCTCTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608741 Chironomus riparius water mite diet isolate 9155-BHL032417-GBD28762_16445-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAGAATTAGGACAACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTGGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCGCTAACTCTTCTACTATCAAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608742 Chironomus riparius water mite diet isolate 9166-BHL032417-GBD26684_9716-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGAACAGGAACTTTCATTGGAGATGACCAATTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGAGTCGGAAACTGATTCGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTGTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608743 Chironomus riparius water mite diet isolate 9171-BHL032417-GBD14283_3486-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGAGGGAACTACATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGATGTAGGTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCTCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608744 Chironomus riparius water mite diet isolate 9172-BHL032417-GBD20069_24881-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCTCTAATACTTGGAGCTCCTGATATAGCTTTTCCACGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTAACCCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608745 Chironomus riparius water mite diet isolate 9193-BHL032417-GBD10088_10398-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAGACTGATTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTAACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608746 Chironomus riparius water mite diet isolate 9197-BHL032417-GBD13088_3827-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTGGGGCAGAATTAGGCCGACCCGAAACTTTCATTGGAGATGACCAAATTTATAATGTGGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608747 Chironomus riparius water mite diet isolate 9201-BHL032417-GBD11996_2748-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCAAATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCCCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTTACTCTTCTTCTTTCTTATTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608748 Chironomus riparius water mite diet isolate 9234-BHL032417-GBD20844_27779-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTATGAATGCTTATTCGAGCAGAATTAGGTCGTCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTTTCTTACACTACTTCTATCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608749 Chironomus riparius water mite diet isolate 9237-BHL032417-GBD26765_15559-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATCTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCAACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTGTTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCTCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608750 Chironomus riparius water mite diet isolate 9239-BHL032417-GBD21944_9913-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTCGTAGTTACCGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGAATTCGGAAACTGACTTGTCCTCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCAGCTTCTTGCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608751 Chironomus riparius water mite diet isolate 9248-BHL032417-GBD16376_4977-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGATATACCAATTGTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTGGGAGCACCTGACATAGCTTTTCCTCGACTAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTCGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608752 Chironomus riparius water mite diet isolate 9262-BHL032417-GBD23315_27042-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCACCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCACTCTAACTCTTCTTCTTTCTAGTCCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608753 Chironomus riparius water mite diet isolate 9268-BHL032417-GBD21491_27161-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGAGCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTAACTCTTCTACTTTCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608754 Chironomus riparius water mite diet isolate 9273-BHL032417-GBD14318_20746-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGCGGGAACTTCATTACGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGCTTCGGAAACTGACCTGTCCCCCTAATACTTGGAGCACCTGACATGGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCATTCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608755 Chironomus riparius water mite diet isolate 9284-BHL032417-GBD18417_20734-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGTGCAGAATTAGGACAACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCGTACTCTGCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608756 Chironomus riparius water mite diet isolate 9305-BHL032417-GBD18783_11280-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGTATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608757 Chironomus riparius water mite diet isolate 9308-BHL032417-GBD26785_7610-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCATATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATCTTAATTGTAGGATTCGGAAACTGACTTGTGCCCCTAATACTTGGAGCACCTGACATAGCTATTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608758 Chironomus riparius water mite diet isolate 9311-BHL032417-GBD13933_8914-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGCACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCTCCTGACATAGCTTTTCCGCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCACTTACCCTTCTTCTATCGAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608759 Chironomus riparius water mite diet isolate 9318-BHL032417-GBD15002_11466-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCTCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCACTTACCCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608760 Chironomus riparius water mite diet isolate 9321-BHL032417-GBD16485_17367-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTTGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCTACACGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCGTTCTTACTCTACATCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608761 Chironomus riparius water mite diet isolate 9324-BHL032417-GBD21394_3845-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGTCCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACGTAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTTACTCTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608762 Chironomus riparius water mite diet isolate 9337-BHL032417-GBD27736_17321-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGTTACTTCATTTAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTCTTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCGAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608763 Chironomus riparius water mite diet isolate 9345-BHL032417-GBD15703_10706-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATACGAGCAGAATTAGGTCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCACCTAATACTTGGAGCACCTGGCATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTGTCTTACTCTGCTTCTTTCTAGTACGTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608764 Chironomus riparius water mite diet isolate 9347-BHL032417-GBD8353_17033-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGAATGCCTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTGGTTACTGCACATGCTTTTATTATAATTCCTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATGTAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608765 Chironomus riparius water mite diet isolate 9355-BHL032417-GBD15998_5388-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGTAACTTTCACTGGAGATGACCATATTTATAATGTTGTAGTTACTGCACATGCTGTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTGGGAAACTGAGTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608766 Chironomus riparius water mite diet isolate 9367-BHL032417-GBD29309_14832-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGTACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGTCGACCCGGAACTTTAATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCCCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCAGACTTTTACCCCCCTCTCTTACTCTTCTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608767 Chironomus riparius water mite diet isolate 9378-BHL032417-GBD27860_9275-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCATTTATTATAATTTTCTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATGGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTCCCCCCCTGTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608768 Chironomus riparius water mite diet isolate 9403-BHL032417-GBD18568_25211-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGAACCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGTATTCGGAAACTGACTTGTCCCCCTAATACTGGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTGTCTGACTTTTACCCCCCTATCTAACTCTTCGTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608769 Chironomus riparius water mite diet isolate 9412-BHL032417-GBD26365_11846-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGTAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCACCACTCTTACGCTGCTGCGTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608770 Chironomus riparius water mite diet isolate 9429-BHL032417-GBD2918_13234-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGTCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTCTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCATCTCTTACTCTTCTTCTATCTAGTTCTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608771 Chironomus riparius water mite diet isolate 9448-BHL032417-GBD22081_11023-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGAGACGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTCTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608772 Chironomus riparius water mite diet isolate 9462-BHL032417-GBD2637_11388-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTTGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGATTTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGCTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTATAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608773 Chironomus riparius water mite diet isolate 9464-BHL032417-GBD26871_11626-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTATGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCGTTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCGTAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCAACTGACATAGCTTTTCCTCGAATAAAGAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACATCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608774 Chironomus riparius water mite diet isolate 9505-BHL032417-GBD27737_8768-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGAAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTATTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTGAATTGGAGGATTCGGAAACTGACATGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCATACTCATCTTCATTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608775 Chironomus riparius water mite diet isolate 9517-BHL032417-GBD29289_16866-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACCTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCCTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTTCCCCCCTCGCTGAC	Using NCBI BLASTN in June 2018, this sequence was 98.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608776 Chironomus riparius water mite diet isolate 9529-BHL032417-GBD27425_22969-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGTACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGACGACCAAATTTATAATGTTGTAGTTACCGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCATCTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608777 Chironomus riparius water mite diet isolate 9561-BHL032417-GBD14428_18847-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTTGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATGGCTTTTCCTCGAATAAATATTATAAGTTTCTGACTTTTACCCCCTTCTCTTACTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608778 Chironomus riparius water mite diet isolate 9592-BHL032417-GBD10755_16789-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608779 Chironomus riparius water mite diet isolate 9742-BHL040517-GBD5716_11392-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608780 Chironomus riparius water mite diet isolate 9989-BHL040517-GBD6638_17175-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTCTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608781 Chironomus riparius water mite diet isolate 10036-BHL040517-GBD4905_12545-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGCACTTCATTGAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTATTACCCCCCTCACTTACCCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608782 Chironomus riparius water mite diet isolate 10055-BHL040517-GBD10271_10212-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTTTACTTTATTTTTGGGGCTTGGTCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTACTTCTACCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608783 Chironomus riparius water mite diet isolate 10065-BHL040517-GBD7575_10249-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTGTACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCCTTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608784 Chironomus riparius water mite diet isolate 10097-BHL040517-GBD7396_16697-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACGTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGCATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTGACCCCCCTCTCTTACTCTTCATAAATCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608785 Chironomus riparius water mite diet isolate 10120-BHL040517-GBD23132_26759-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAACTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATATTAATTGGAGGATTTGGAAACTGACTTGTCCCACTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608786 Chironomus riparius water mite diet isolate 10125-BHL040517-GBD8226_17389-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCGCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGGGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTACATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608787 Chironomus riparius water mite diet isolate 10145-BHL040517-GBD15378_23052-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTTTTCCCCCCTCACTAACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608788 Chironomus riparius water mite diet isolate 10173-BHL040517-GBD23985_20722-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGTAGAATTAGGACGACCCGGAACTTTCTTTGGAGATGACCAAATTTATAATGCTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTACTTTCTAGTGCAGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608789 Chironomus riparius water mite diet isolate 10178-BHL040517-GBD8219_22045-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATCTGGAAACTGACTTGTACCCCTAATACTTGGAGCTCCTGTCATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608790 Chironomus riparius water mite diet isolate 10180-BHL040517-GBD4868_9445-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGTCTTGCTCCGGAATAGTGCGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGATGTCGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGATTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCGCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608791 Chironomus riparius water mite diet isolate 10188-BHL040517-GBD9369_12747-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTACACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTTGAGCAGAATTAGGACGGCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCGTACGCTGCTTCGTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608792 Chironomus riparius water mite diet isolate 10189-BHL040517-GBD18347_21069-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAACTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATATTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTGCTGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608793 Chironomus riparius water mite diet isolate 10190-BHL040517-GBD22988_24581-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTATACTTTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTCGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608794 Chironomus riparius water mite diet isolate 10196-BHL040517-GBD20775_11416-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCAGACATAGTTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608795 Chironomus riparius water mite diet isolate 10202-BHL040517-GBD16097_10128-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGCTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGTTTTTCCTCGAATAATTAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608796 Chironomus riparius water mite diet isolate 10210-BHL040517-GBD10587_11477-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGTACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGAACAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTGATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608797 Chironomus riparius water mite diet isolate 10215-BHL040517-GBD27079_12033-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTAATTTGAGCAGAATTAGGACGACCCGGCACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTGCTCTTCTTCTATCTAGTTCTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608798 Chironomus riparius water mite diet isolate 10222-BHL040517-GBD27905_11754-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCTCTAATACTTGGAGCACCTGCCATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCCACTAACTCTTCTACTATCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608799 Chironomus riparius water mite diet isolate 10247-BHL040517-GBD21002_12171-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTATGAATGCTTATTTGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTAGGAAACTGACTTGTCCCCCTAATACTTGGAGCAACTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCAACATCTTTCTAGTACTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608800 Chironomus riparius water mite diet isolate 10271-BHL040517-GBD24014_9026-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGTTTGATCCGGAATAGTGGGAACTTCATTAAGAATTCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGTTTTTCCTCGAATAATTAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTACTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608801 Chironomus riparius water mite diet isolate 10277-BHL040517-GBD19825_27475-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTAGGAGCACCTGACATAGTTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTACTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608802 Chironomus riparius water mite diet isolate 10288-BHL040517-GBD18446_13113-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCTCCTAATACTTGGAGCACCTGACATAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTGCCTCTTTCGAGTTCGTTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608803 Chironomus riparius water mite diet isolate 10296-BHL040517-GBD20118_8561-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGTACTTCATTATGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCACCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCATCGCTTACTCTTCTTCTTTCGAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608804 Chironomus riparius water mite diet isolate 10312-BHL040517-GBD6803_14984-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGTCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATCGGAGGATTCGGAAACTGACTTGTCCCCCTAACACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCATACTCTTCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608805 Chironomus riparius water mite diet isolate 10353-BHL040517-GBD23688_11247-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGTATGCTTATTCGAGCCAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608806 Chironomus riparius water mite diet isolate 10376-BHL040517-GBD3411_15624-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTAGAGCAGAATTAGGACGACCCGGAACTCTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCTCTAATACTTGGAGCCCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608807 Chironomus riparius water mite diet isolate 10378-BHL040517-GBD17557_8169-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGTAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTAACTCTACTTATTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608808 Chironomus riparius water mite diet isolate 10380-BHL040517-GBD17393_4544-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTGATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCATATTTATAATGTTGTAGGTACTGCACATGCATTTATTATAATTTTTTTCATAGGTATACCAATTTTAATTGGAGGATTGGGAAACTGACTTGTCCCCCTAATACTTGGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608809 Chironomus riparius water mite diet isolate 10404-BHL040517-GBD24774_19952-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCCTTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTGCCTCGAATAAATAATATAAGTTTCTGACTTGTACCCCCCGCGCTTACACGACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608810 Chironomus riparius water mite diet isolate 10434-BHL040517-GBD14195_9900-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGGACTTCCTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTATCCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608811 Chironomus riparius water mite diet isolate 10436-BHL040517-GBD9287_16700-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTACAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCTCCTAATACTTGGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACGTTTACCCCCCTCTCTTACTCTTCTTCGTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608812 Chironomus riparius water mite diet isolate 10453-BHL040517-GBD16356_25372-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCACGAATAAATAATATAAGATTCTGACTCTTACCCCCCTCTCTTACTCTGCTTCTTTCTAGTACATTAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608813 Chironomus riparius water mite diet isolate 10458-BHL040517-GBD29120_12692-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACCTTATTTTTGGGGCTTGATCCGGAATAGTGGGTACTTCCTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTGATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTTCTACTATCTAGTTCTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608814 Chironomus riparius water mite diet isolate 10462-BHL040517-GBD12562_8857-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACACGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCAGCTCTTACGCTTCTTCTATCTAGTGCTGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608815 Chironomus riparius water mite diet isolate 10472-BHL040517-GBD8253_19254-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTGTTTGAGCAGCATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCGCTCTTACACTTCATCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608816 Chironomus riparius water mite diet isolate 10484-BHL040517-GBD25908_24054-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTTGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACCATATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTCAATTGGAGGATTCGGAAATTGACTTGTTCTCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608817 Chironomus riparius water mite diet isolate 10515-BHL040517-GBD15928_4649-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCTGAACTTTCATTGGAGATGACCAAATTTATAATGTAGTAGTTACTGCACATGCTTTTATAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTGGGAAACTGACTAGTCACCCTAATACTTGGAGCCCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608818 Chironomus riparius water mite diet isolate 10522-BHL040517-GBD22926_12217-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGCACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACACGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGGTTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608819 Chironomus riparius water mite diet isolate 10523-BHL040517-GBD14491_2575-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGGTGTAGGTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGAATGGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGCAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608820 Chironomus riparius water mite diet isolate 10524-BHL040517-GBD24247_25210-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGCACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTAACTCTTCTTATTTCTAATTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608821 Chironomus riparius water mite diet isolate 10526-BHL040517-GBD14490_2717-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTGGATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTGATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTAGGAACCTGACTTGTCCCCCTAATACTTGGAGCTCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608822 Chironomus riparius water mite diet isolate 10557-BHL040517-GBD2533_16858-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTCGGACGCCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATCCGGAAACTGATTTGTCCCCCTAATACTTGGAGCCCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTATCTAGTTCTTTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608823 Chironomus riparius water mite diet isolate 10564-BHL040517-GBD15296_2710-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACATCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGTAACTTTCATTGGAGATGACCATATTTATAATGTTGTAGTAACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTAGGAAACTGACTTGTCCCTCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTTCCCCCCTCTCTTTCTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608824 Chironomus riparius water mite diet isolate 10569-BHL040517-GBD6650_20930-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGCACTTCTTTAAGAATGTTTATTCGAGCAGAATTCGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATATTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608825 Chironomus riparius water mite diet isolate 10570-BHL040517-GBD14977_17119-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTTTATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATCCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCAAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608826 Chironomus riparius water mite diet isolate 10599-BHL040517-GBD23245_26238-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATGCTTATTCGAGCTGAATTAGGACGACCCGGAACTTTCTTTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTCATAGTTGTACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGTCATAGCTTTTCCTCGAATAAATGATATAAGATTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608827 Chironomus riparius water mite diet isolate 10603-BHL040517-GBD16129_4639-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTAGCAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGTTTTTCCTCGAATAATTAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGCGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608828 Chironomus riparius water mite diet isolate 10605-BHL040517-GBD6872_20795-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATTGGAACTTCATTAAGAATGCTTATTCGGGCAGAATTATGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTCTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608829 Chironomus riparius water mite diet isolate 10610-BHL040517-GBD26433_14507-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGATCACCTGACAAAACTTTTCCTCGAAAAAAAAAAATAAGGTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608830 Chironomus riparius water mite diet isolate 10617-BHL040517-GBD11158_15257-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCAGGAATAATGGGAACTTCATTAAGTATGCTTATTCGAGCAGAATTAGGACTACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608831 Chironomus riparius water mite diet isolate 10621-BHL040517-GBD11892_15341-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAACAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTCTCTAGTACGTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608832 Chironomus riparius water mite diet isolate 10628-BHL040517-GBD14717_5758-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGAGGGAACTTCATTAAGAATGCGTATGCGAGCAGAATCAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTGTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTTCTCTTCTTCTTTCTCGTTCTTTCGTAGAAAATGGCGCTGGAA	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608833 Chironomus riparius water mite diet isolate 10630-BHL040517-GBD2194_14485-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGGATGTTTATTCGAGCAGAATTAGGACGCCCCGGTACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCGCCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608834 Chironomus riparius water mite diet isolate 10645-BHL040517-GBD28445_9818-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATATTGGGAACTTCATTAAGAATGCTTATTCCAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATTACCAAATTTATAATGTTGTAGTTACTGCACCTGCTTTTATTATAATTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608835 Chironomus riparius water mite diet isolate 10665-BHL040517-GBD14352_2821-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGGTGTAGTTACTGCACATGCATTTATTGTAATTTTTTTCATAGATATACCAATTTTAATTGGAGGATTGGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGTTTTTCCTCGAATAATTAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTCCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608836 Chironomus riparius water mite diet isolate 10668-BHL040517-GBD17165_2372-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGCGGGAACTTCATTAAGAATGCTTATTCGAGCAGAAGTAGGACGACCCGGAACTTTCATTGGAGCTGACCAAATTTATAATGATGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATGCGGAAACTGACTTGTCCCCCTAATACTTGGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608837 Chironomus riparius water mite diet isolate 12199-BHL040517-GBD19100_9183-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGAAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGATCCGGAACTTTCATCGGAGATGACCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATGCTTGAAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTGTTACCCCCCTCTCTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608838 Chironomus riparius water mite diet isolate 12237-BHL040517-GBD11311_11344-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGACCAGAATTAGGACGACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGTTTTCGGAAACTGACTTGTCCCCCTAATAATTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608839 Chironomus riparius water mite diet isolate 12249-BHL040517-GBD25985_15552-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTAATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCACTAACCCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608840 Chironomus riparius water mite diet isolate 12260-BHL040517-GBD12878_14911-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCCGAAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGATCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACCTGTCCCCCTAATACTTGGAACACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTGCTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608841 Chironomus riparius water mite diet isolate 12275-BHL040517-GBD24318_6743-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAGTTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCCCCTGAAATAGCTTTTCCTCGAATAAATAAAATAAGTTTCTGACTCTTACCCCCCTCTCATACCCTCCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608842 Chironomus riparius water mite diet isolate 12289-BHL040517-GBD18375_25619-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACCTTATTTTTGGGGCTTGATCCGGTATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATAGTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTATCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608843 Chironomus riparius water mite diet isolate 12300-BHL040517-GBD29141_16143-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTGATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTAACTCTACTACGATCTAGTTCTTTCGTAGAAAATGGAGGTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608844 Chironomus riparius water mite diet isolate 12303-BHL040517-GBD6631_14147-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGCTGTAGTTACCGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTATTACTTGGAACACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCGTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608845 Chironomus riparius water mite diet isolate 12321-BHL040517-GBD15623_12825-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATTCGAGCAGAATTATGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGTTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACCCTACTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608846 Chironomus riparius water mite diet isolate 12340-BHL040517-GBD12985_20160-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGGGGCTTCATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGGTTTTACTATAATTTTTCACATAGTTATACCAATTTTATTTGGAGGGTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGCTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608847 Chironomus riparius water mite diet isolate 12401-BHL040517-GBD15845_3821-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCTTAACTTTCATTGGAGATGACCATATTTATAATGTTATAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTGGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608848 Chironomus riparius water mite diet isolate 12410-BHL040517-GBD25590_19362-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTGTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCATCCGCTGTCTAGTTATTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608849 Chironomus riparius water mite diet isolate 12413-BHL040517-GBD10013_13477-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGTTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTACTATCTAGTTCTCTCGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608850 Chironomus riparius water mite diet isolate 12416-BHL040517-GBD26404_16116-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACGTTATACATTATTTTTGGGGCTTGATCCGGACTAGTGGGCACTTCATTAAGAATGCTTGTTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608851 Chironomus riparius water mite diet isolate 12479-BHL040517-GBD20674_9921-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGAGAACTTCATTAAGAATACTTAATCGAACAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608852 Chironomus riparius water mite diet isolate 12558-BHL040517-GBD23498_14547-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGATCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGTACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTAACTCTTCTTCGTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608853 Chironomus riparius water mite diet isolate 12640-BHL040517-GBD25983_8316-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTATATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTATCTTACTCTACCTCGTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608854 Chironomus riparius water mite diet isolate 12641-BHL040517-GBD24513_21447-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTGTTCGAGCAGAATTAGGACGACCCGTAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTCGTCCCCCTAATACTTGGAGCACCTGACGTAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608855 Chironomus riparius water mite diet isolate 12729-BHL040517-GBD25014_23908-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGTACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCCCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608856 Chironomus riparius water mite diet isolate 12789-BHL040517-GBD2257_15405-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGAAACTTTCATTGGAGATGACCAAATTTATAACGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTTCCCTCACTTACTCTACTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608857 Chironomus riparius water mite diet isolate 12855-BHL040517-GBD20594_23866-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATGCATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACAACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTACACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTAACTCTTCTTCTATCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608858 Chironomus riparius water mite diet isolate 13555-BHL040517-GBD22152_24113-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAAAATTAGGACGACCCGGAACTATCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAGCTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCATCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTTGTAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608859 Chironomus riparius water mite diet isolate 13580-BHL040517-GBD6627_8869-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGGATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAAAACTTGGAGCACCTGACATAGCTTTTCCCCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTATCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGCAAC	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608860 Chironomus riparius water mite diet isolate 13595-BHL040517-GBD22883_9121-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGAGCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTATCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608861 Chironomus riparius water mite diet isolate 13601-BHL040517-GBD21907_15606-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGCACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCTCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTATTACCCCCCTCTCTTACCCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608862 Chironomus riparius water mite diet isolate 13612-BHL040517-GBD28620_18982-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTAGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608863 Chironomus riparius water mite diet isolate 13640-BHL040517-GBD6802_16987-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTCGGGGCTTGATCCGGAATAGTGGGGACTTCATTAAGAATGCTTATTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGATCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608864 Chironomus riparius water mite diet isolate 13643-BHL040517-GBD23482_10790-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTCGGACGACCCGGAACTTTCATTGGAGATGACCAAGTTTATAATGTTGTAGTTCCTGCACATTCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACGCTGCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608865 Chironomus riparius water mite diet isolate 13648-BHL040517-GBD12041_10295-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGATCTTTATACATTATTTTTGGTGCTTGATCCGGAATAGTGGGAACTTCCTTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACACCCCTCTCTTACTCTTCTTCTTTCTAGTACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608866 Chironomus riparius water mite diet isolate 13651-BHL040517-GBD19594_5640-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCTAGCAGAATTAGGACGACCCGGATCTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCACAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTAGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608867 Chironomus riparius water mite diet isolate 13652-BHL040517-GBD21250_26595-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAATTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGAGAACTTCATTAAAAATGCTTACGCGAACAGAATGAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTTCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGTTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608868 Chironomus riparius water mite diet isolate 13685-BHL040517-GBD4374_12016-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGTTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGCTTTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTGCTAGTTCTTTCATAGAAAAGGGAGCTGGAACAGGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608869 Chironomus riparius water mite diet isolate 13687-BHL040517-GBD17497_5360-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTAACTCGAGCAGAATTAGGACGACCCGGAACATTCATGGGAGATGACCAAATTTATAATGTTGTAGTTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTAGGAAACTGACTTGTCCCCCTAATACTTGGAGCTCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608870 Chironomus riparius water mite diet isolate 13689-BHL040517-GBD17957_3084-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGAGGGAACTTCATTAAAAATGCGTATTCGAGCCGAATTAGGACGAACCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTATTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGGGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTATCCCCCTCTCTTACTCTTCTTCTTTCTAGCTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608871 Chironomus riparius water mite diet isolate 13693-BHL040517-GBD15791_5804-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTGATTCGAGCAGAATTAGGACGACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTTACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTCCTCTTCTTCTTTCTCGATCTTTCGTAGAAAATGGAGCTGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608872 Chironomus riparius water mite diet isolate 13739-BHL040517-GBD24267_23722-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTTTACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGAGTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCACTCTTACTCTTCATCATTCTAGTTCTTTCGTAGAAAATGGCGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608873 Chironomus riparius water mite diet isolate 13740-BHL040517-GBD26818_17684-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGAGCTTGATCCTGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAGTACTTGGAGCACCTGACATAGCTTTTCCTCGAACAAATAATATAAGTTTCTGACTTTTACCCTCCTCGCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608874 Chironomus riparius water mite diet isolate 13742-BHL040517-GBD23295_25893-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCTGAATAGTGTTAACTTCATTATGAATTCTTACTCGAGCAGAATTAGGACGAACCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTGCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608875 Chironomus riparius water mite diet isolate 13750-BHL040517-GBD14931_5577-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACTACCCGGAACTTTCATTGGAGATGACCATATTTATAATGGTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTGGGAAACTGACAGGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608876 Chironomus riparius water mite diet isolate 13764-BHL040517-GBD16533_15608-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGGTTCTGACTATTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTACTGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608877 Chironomus riparius water mite diet isolate 13780-BHL040517-GBD25571_17717-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAATATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCCCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAACTGGAGGATTCGGAAACTGACTTGTACCCCTAATACTTGGAGTACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTGACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608878 Chironomus riparius water mite diet isolate 13782-BHL040517-GBD5700_12311-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGGCGACCCGGATCTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCCTGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608879 Chironomus riparius water mite diet isolate 13785-BHL040517-GBD28595_17863-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGTTTGATCCGGAATAGTGGGAACTTCATTTAGAATGCTTACTCGAGTAGAATTAGCACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTACTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608880 Chironomus riparius water mite diet isolate 13794-BHL040517-GBD12009_21661-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTTGGAACTTCATTTAGAATGTTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATGATATAAGTTTCTGACTTGTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608881 Chironomus riparius water mite diet isolate 13795-BHL040517-GBD18376_3886-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAAGTAGGACGACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGCATAAATAATATAATTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608882 Chironomus riparius water mite diet isolate 13808-BHL040517-GBD23669_14298-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGAGGGAACTTCACTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCTGAACTTTCATTGGAGATGACAAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608883 Chironomus riparius water mite diet isolate 13817-BHL040517-GBD14003_18905-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTCGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTAGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTGACTCTTTTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608884 Chironomus riparius water mite diet isolate 13820-BHL040517-GBD10602_9490-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTAGGGCTTGATCCGGAATAGTTGGAACTTCATTAAGAATGCTTACTCGAGCCGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACACTTCTGCTTTCTAGTGCTTGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608885 Chironomus riparius water mite diet isolate 13829-BHL040517-GBD17012_2484-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTAATTCGAGCAGAACTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAGTAGTTACTGCACATGCATTTATTATAATTTTTTACATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTAGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTCTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608886 Chironomus riparius water mite diet isolate 13834-BHL040517-GBD19101_7969-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGAAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTACTACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATCTTTACCCCCCTCTCGTACTCTGCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608887 Chironomus riparius water mite diet isolate 13847-BHL040517-GBD29232_18231-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGTATAGTGGGAACTTCATTAAGAATGCTTATTCGAGTAGAATTAGGACGACCCGGAACTTTCATTGAAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGCTTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608888 Chironomus riparius water mite diet isolate 13851-BHL040517-GBD20201_5102-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCACTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAATTTTCTGACTTTTACCCCCCTCTCTGACTCTACTTCTTTCTAGTTCTTGCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608889 Chironomus riparius water mite diet isolate 13861-BHL040517-GBD29509_13417-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGTTTATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATACAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608890 Chironomus riparius water mite diet isolate 13864-BHL040517-GBD9611_24391-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTAGGAGCATCTGATATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTAGCTAGAACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608891 Chironomus riparius water mite diet isolate 13865-BHL040517-GBD22062_12205-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGTTTTTCCTCGAATAAACAATATAAGTTTCTGACTTTTACCCCCCTCTCCTACTCAGCCTCTTGCGAGTTCTTGCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608892 Chironomus riparius water mite diet isolate 13873-BHL040517-GBD16016_24918-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGGGGGAACTTCATTTAGAATGCTTACTCGAGCAGAGTTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTGACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608893 Chironomus riparius water mite diet isolate 13880-BHL040517-GBD7386_12328-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCAGTATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGAGTCGGAAACTGAATTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTAGTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608894 Chironomus riparius water mite diet isolate 13898-BHL040517-GBD26798_13251-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAATTTTATACATTATTTTTGGGGCTTCATCCGGAATAGTGGGAACTTCATTTAGAATGTTTATTCGAGTAGAATTAGGAGGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCCCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTCCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608895 Chironomus riparius water mite diet isolate 13904-BHL040517-GBD6986_6478-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTATGAATGCTTACTCGAGCAGAATTAGGACGAGCCGGTACTTTCATTGGAGATGACCAAAGTTATAATGTTGTAGTCACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTGCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608896 Chironomus riparius water mite diet isolate 13930-BHL040517-GBD5481_19862-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTCCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATATTAATTGGAGGATTCGGAAACTGACTAGTCCCCATAATACTTGGAGCACCTGACATAGCTTTTCCTCGGATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608897 Chironomus riparius water mite diet isolate 13949-BHL040517-GBD23965_7138-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCCTTAAGTATGCTTATTCGAGCCGAATTAGGACGACCCGGGACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACACCCCTCTCTTACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608898 Chironomus riparius water mite diet isolate 13950-BHL040517-GBD7141_22164-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTGGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTACTACTTTCTAGCTCTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608899 Chironomus riparius water mite diet isolate 13956-BHL040517-GBD26118_8532-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCCTTAAGAATGCTTATTCGATCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTGTAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTATCTAGATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608900 Chironomus riparius water mite diet isolate 13957-BHL040517-GBD13949_4449-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACATCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGTAACTGTCATTGGAGATGACCAAATTTATAATGTACTAGTTACTGCACATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTAGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608901 Chironomus riparius water mite diet isolate 13962-BHL040517-GBD24821_25250-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTATGTATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGCAACTGACTTGTCCACCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACGCTTCTTCTATCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608902 Chironomus riparius water mite diet isolate 13964-BHL040517-GBD18580_15744-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTTGATTAAATAATATAAGTTTCTGACTTTTACCCCCCTCGCTTACACTTCATCTTGCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608903 Chironomus riparius water mite diet isolate 13969-BHL040517-GBD11540_27472-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTTATTCGAACAGAATTAGGACGACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTTGAGGATTCGGAAACTGACTTGTCCCTCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608904 Chironomus riparius water mite diet isolate 13975-BHL040517-GBD10929_26811-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTTTACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATATATAATGTTGTAGTTACTGCACATGCATTTATAATAATTTTTTTCATAGTTATAGCAATTTTAATTGGAGTATTCGGAAACTGACTTGTCCCCCTAATAATTGGAGCACCTGACATAGCTTTTCCTCGAATAAAAAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608905 Chironomus riparius water mite diet isolate 13982-BHL040517-GBD4191_14648-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGTGAACTTCATTAAGATTGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGACACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACGCTTCTTCTGTCTAGTTCTTTCGCAGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608906 Chironomus riparius water mite diet isolate 13997-BHL040517-GBD18812_17608-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAAAGTTGTGGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTTGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608907 Chironomus riparius water mite diet isolate 14008-BHL040517-GBD27054_17418-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACAACCAGGAACTTTCATTGGAGATGACCAAATTTATATTGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTATAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTTACTCTTCTTCTGTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608908 Chironomus riparius water mite diet isolate 14011-BHL040517-GBD24960_5678-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGTAGAATTAGGACGACCCGGATCTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGGCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTACTTCTTTCTAGTTCTGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608909 Chironomus riparius water mite diet isolate 14015-BHL040517-GBD15990_10733-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGAACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTCAGAATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAATTATAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTATCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608910 Chironomus riparius water mite diet isolate 14016-BHL040517-GBD11435_22689-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGTATGCTTATTCGAGCAGAGTTAGGTCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608911 Chironomus riparius water mite diet isolate 14021-BHL040517-GBD17757_29118-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGATCTTCATTTAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCACGAATAAATAATATAAGATTCTGACTATTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608912 Chironomus riparius water mite diet isolate 14023-BHL040517-GBD10869_15415-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACAACCTGGAACTTTCATTGGTGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCTTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608913 Chironomus riparius water mite diet isolate 14024-BHL040517-GBD13537_4808-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCGGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAAGTAGGACGACCCGGAACTTTCATTGGAGATGACCATATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTGGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCCAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608914 Chironomus riparius water mite diet isolate 14025-BHL040517-GBD11127_18538-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAACCTTGTAGTTACGGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAATTATAATTGGAGGATTCGGAAACTGACTTATCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608915 Chironomus riparius water mite diet isolate 14028-BHL040517-GBD13637_25277-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGTGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGTCCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGTTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608916 Chironomus riparius water mite diet isolate 14032-BHL040517-GBD10593_20956-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGAGGCTTGATCCGGACTAGTGGGAACTTCACTAAGAATGCTTATCCGAGCAGAATTAGGAAGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCATTTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTCACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608917 Chironomus riparius water mite diet isolate 14033-BHL040517-GBD16809_3715-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCTGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTATTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAATTGGAGGATTCGGAAACTGACTCGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGCGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608918 Chironomus riparius water mite diet isolate 14035-BHL040517-GBD14647_5894-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAAGTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGGTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAAATGACTTGTCCCCCTAATACTTGGATCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTCCTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGCGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608919 Chironomus riparius water mite diet isolate 14036-BHL040517-GBD24499_4788-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATATTTTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCCTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAACTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608920 Chironomus riparius water mite diet isolate 14037-BHL040517-GBD21790_22979-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTCACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTGGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608921 Chironomus riparius water mite diet isolate 14038-BHL040517-GBD27042_12381-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGAAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGTACGACCCGGAACTTTCATTGGAGATGACCAATTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATATATAATATAAGTTTCTGATTTTTACCCCCCTCTCATACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608922 Chironomus riparius water mite diet isolate 14046-BHL040517-GBD17954_10658-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTCGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAATTATACCAATTATAATTGGAGGATTCGGAAACTGACTTTTGCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCCCTTACTCTTCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608923 Chironomus riparius water mite diet isolate 14047-BHL040517-GBD12286_26013-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTCGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTGTAATGTTGTAGTCACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATTCTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608924 Chironomus riparius water mite diet isolate 14048-BHL040517-GBD23177_3566-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGTGAACTTCATTATGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACATGTCTCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCATCTTCTTTCTAGTTCTTGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608925 Chironomus riparius water mite diet isolate 14051-BHL040517-GBD21897_24174-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAGCTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATCCTAATTGGAGGATTCGGTAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTTCCCCCCTCTCTTACTTTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608926 Chironomus riparius water mite diet isolate 14055-BHL040517-GBD24255_19829-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGCCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTTATGCTTTTATTATAATTTTTTTCATAATTATACCAATTATAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACGTAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608927 Chironomus riparius water mite diet isolate 14056-BHL040517-GBD27764_9184-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGTAAAAATAATATAAGTTTCTGACTATTACCCCCCTCACTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608928 Chironomus riparius water mite diet isolate 14063-BHL040517-GBD23563_15888-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATGCTTATCCGAACAGAATTATGACGACCCGGAACTTTCCTTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTACTTTCTAGTTCTGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608929 Chironomus riparius water mite diet isolate 14067-BHL040517-GBD22100_14925-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGAACAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAAATATACCAATTTTAATTGGAGGATTCGGAAACTGACTTATCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608930 Chironomus riparius water mite diet isolate 14069-BHL040517-GBD6480_22521-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTACTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCATCTCTTACTCCTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608931 Chironomus riparius water mite diet isolate 14072-BHL040517-GBD21416_23828-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGAGATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCACTCTAACTCAGCTTCTTTCTAGTTCGTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608932 Chironomus riparius water mite diet isolate 14077-BHL040517-GBD2966_13609-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACCTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATCGTTATACCAATTTTAATTGGAGGATTCTGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTTCGTCTTTCTAGTCCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608933 Chironomus riparius water mite diet isolate 14078-BHL040517-GBD22487_5568-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGTACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACACGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608934 Chironomus riparius water mite diet isolate 14080-BHL040517-GBD8674_22057-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGCATTAGGATGACCCGAAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAATTATAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATGGCTTTTCCTCGAATAAATAATATAAGTTTCTGAATTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608935 Chironomus riparius water mite diet isolate 14082-BHL040517-GBD18993_24698-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATATTTATACCAATTATAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTACTACTTTCTAGTTCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608936 Chironomus riparius water mite diet isolate 14083-BHL040517-GBD8878_24971-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTATGACAACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAAATATAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTCGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608937 Chironomus riparius water mite diet isolate 14084-BHL040517-GBD20462_16950-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATGCTTATTCGAGTTGAATTATGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTCATTGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCGTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608938 Chironomus riparius water mite diet isolate 14085-BHL040517-GBD27029_22578-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATACTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCTCTAATACTTGGAGCCCCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608939 Chironomus riparius water mite diet isolate 14091-BHL040517-GBD29490_15344-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCACTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACCGCACATGCTTTTATTACAATTTTTTTCATAATTATACCAATTATAATTGGAGGAGTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGAATTTTACACCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608940 Chironomus riparius water mite diet isolate 14092-BHL040517-GBD4710_11763-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGTAGAATTAGGACGACCCGGAACATTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTGTCCTCGAATAAATAATATAAGTGTCTGACTTTTACCCCCCTCTCTTACTCTTCATCATTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608941 Chironomus riparius water mite diet isolate 14096-BHL040517-GBD9732_18135-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACGTTATTTTTGGGGCCTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCGATTTTAATTGGAGGATTGGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACACTTCTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608942 Chironomus riparius water mite diet isolate 14098-BHL040517-GBD6275_7611-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAGCTTTCATTGGAGATGACCAAATATATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTAGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTATGATTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608943 Chironomus riparius water mite diet isolate 14099-BHL040517-GBD12997_15151-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGTTTGTTCCGGAATAGTGGGAACTTCATTGAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGTACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTCCTTCATTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608944 Chironomus riparius water mite diet isolate 14100-BHL040517-GBD12268_21658-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGCCCTGGAACTTTCATTGGAGATGACCAAATTTATAGTGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608945 Chironomus riparius water mite diet isolate 14102-BHL040517-GBD21601_11063-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCTGAATAGTGGGAACTTCATTAAGAATGCTTATTCAAGCAGAATTAGGACGATCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCAGACTATTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608946 Chironomus riparius water mite diet isolate 14103-BHL040517-GBD13248_13738-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGCGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGCACCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTAAACTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608947 Chironomus riparius water mite diet isolate 14104-BHL040517-GBD9192_8301-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGTACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTGACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608948 Chironomus riparius water mite diet isolate 14106-BHL040517-GBD20384_10077-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTCTACATTATTTTTGGTGCTTGATCCGGAATAGTGGGAACTTCCTTAAGAATGCTTATCCGAGCAGAATTAGGACGAACCGGAACTTTCATTTGAGATGACCAAATTTATAATGTTGTAGTTACTGTACATGCTTTTATTATAATTTTTTTCATTGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608949 Chironomus riparius water mite diet isolate 14114-BHL040517-GBD16964_5194-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTAATCCGAGCAAAATTAGGACGACCCTGAACTTTCATTGGAGATGACCAAATTTATAATGTAGTAGTTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608950 Chironomus riparius water mite diet isolate 14117-BHL040517-GBD24375_14563-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTAGTCCCTCTAATACTTGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTATCCCCCTCTCTTACTCTTCTTCTTTCTAGTACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608951 Chironomus riparius water mite diet isolate 14120-BHL040517-GBD15965_5640-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGTAACTTTCAATGGAGATGACCAAATTTATAATGTTGTAGTTACTGTACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGTTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGCGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608952 Chironomus riparius water mite diet isolate 14121-BHL040517-GBD17913_16526-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGTATAGTAGGAACTTCTTTAAGAATGCTTATTCGAGCAGAACTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAATTATAATTGGAGGATTGGGAAACTGACTTGTCCCTCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608953 Chironomus riparius water mite diet isolate 14123-BHL040517-GBD16653_6326-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGGTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCGGAATTATACCAATTATAATTGGAGGATTTGGAAACTGACTTATCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608954 Chironomus riparius water mite diet isolate 14126-BHL040517-GBD21407_19471-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTAGTGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAATTATAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACAAAGCTTTTCCTCGAATAAATAATATAAGTTTCGGACTTTTACCCCCCTCTCATACTCATCTTCATTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608955 Chironomus riparius water mite diet isolate 14128-BHL040517-GBD24541_6870-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTGTACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAACAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCATCCTCTTTCTAGTTCTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608956 Chironomus riparius water mite diet isolate 14137-BHL040517-GBD4698_21681-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGTGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATGATAATTTTTTTCATAGTTATACCAATTATAATTGGAGGATTTGGAAACTGACTTGTCATCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608957 Chironomus riparius water mite diet isolate 14139-BHL040517-GBD20655_26274-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAAATTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTATTGGAGATGTCCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAATTATAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTTCCCCCCTCTCTTACTCATCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608958 Chironomus riparius water mite diet isolate 14140-BHL040517-GBD6411_20787-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACCTTATTTTTGGGGCTTGATCCGGAATAGTGGGGACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTCGTAGTTACTGCACATGCCTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCATCTCTAACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608959 Chironomus riparius water mite diet isolate 14142-BHL040517-GBD18920_25733-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACCTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGTACATGCTTTTATTATAATTTTTTTCATAATTGTACCAATTATAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCTCTCTTACGCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608960 Chironomus riparius water mite diet isolate 14595-BHL040517-GBD17269_10715-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTTTGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCAGACATAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608961 Chironomus riparius water mite diet isolate 14601-BHL040517-GBD12656_27842-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608962 Chironomus riparius water mite diet isolate 14609-BHL040517-GBD6533_13615-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTAGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTATGACGACCAGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCACTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608963 Chironomus riparius water mite diet isolate 14656-BHL040517-GBD24840_18788-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCATACTCTTCTTCTTTCTAGTTCATTCGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608964 Chironomus riparius water mite diet isolate 14666-BHL040517-GBD23751_10919-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGTCTTATCCCCCTAATACTTGGAGCACCTGACATAGCTTCTCCTCGAATAAATAACATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCCTCGTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608965 Chironomus riparius water mite diet isolate 14674-BHL040517-GBD26801_23858-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGATGACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTAGGAGCACCTGACATAGCTTTTTCTCGAATAAATAATATAAGTTTCTGACTTTACCCCCCCTCTCATACTCTTCTTCTTTCTAGATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608966 Chironomus riparius water mite diet isolate 14689-BHL040517-GBD21086_5681-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCTAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCGACTTCGGTCTAGTTCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608967 Chironomus riparius water mite diet isolate 14690-BHL040517-GBD19580_18563-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACAACCAGGAACATTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTAGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608968 Chironomus riparius water mite diet isolate 14697-BHL040517-GBD13328_25139-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCCTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCGTTTCCTCGCATAAATAATATAAGTTTCTGACTTTTACCCACCTCTCTTACTCTGCTTCGTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608969 Chironomus riparius water mite diet isolate 14700-BHL040517-GBD5523_11091-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGATGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCCGAAACTGACTTGTCCCCCTAATAATTGGAGCACCTGAAATAGCTTTTCCTCGAATAAAAAATAAAAGTTTCTGACCTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608970 Chironomus riparius water mite diet isolate 14702-BHL040517-GBD25006_24744-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATCTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTGCTCTTCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608971 Chironomus riparius water mite diet isolate 14710-BHL040517-GBD17775_24108-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCACTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTTTTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACGCTACGACTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608972 Chironomus riparius water mite diet isolate 14717-BHL040517-GBD23191_4971-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCCTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGGCGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTACAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTTTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608973 Chironomus riparius water mite diet isolate 14721-BHL040517-GBD16209_26826-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAAAGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGACTCAATAATATAAGTTTCTGACTTTTACCCCCCTCTCGAACTCGTCTTCGTTCTAGTTCTTTCGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608974 Chironomus riparius water mite diet isolate 14722-BHL040517-GBD13097_27082-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGGTCCGGAATAGTGGGAACTCCATTAAGAATGCTTGTTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTATTACCCCCCTCTCTTACTCTACTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608975 Chironomus riparius water mite diet isolate 14764-BHL040517-GBD27963_18791-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATTACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTAGGAGCACCTGACATAGCTTTTCCGCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608976 Chironomus riparius water mite diet isolate 14773-BHL040517-GBD27051_13851-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACACGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTACTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608977 Chironomus riparius water mite diet isolate 14782-BHL040517-GBD9597_23082-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACCTTATTTTGGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATGCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCCTCTTTCTAGTGCCTTCGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608978 Chironomus riparius water mite diet isolate 14795-BHL040517-GBD22977_22047-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTTATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGAGGACCCGGAACTTTCATTGGAGCTGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGGCATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCGTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608979 Chironomus riparius water mite diet isolate 14804-BHL040517-GBD22538_9725-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCTGAATTAGGACAACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTATAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCACCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608980 Chironomus riparius water mite diet isolate 14805-BHL040517-GBD17151_2207-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGAGCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCATCTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGTACCTGACATAGCGTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTCCGTAGAAAATGGTGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608981 Chironomus riparius water mite diet isolate 14810-BHL040517-GBD10229_5042-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGCACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCGTTACCCCCCTCTCTTACTCTTCTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608982 Chironomus riparius water mite diet isolate 14811-BHL040517-GBD23296_4934-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAAATGGAGGATTCGGAAACTGACTTGTCCCGCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCGGACTTTGACCCCCCTCTCTTACTCGTCTGCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608983 Chironomus riparius water mite diet isolate 14814-BHL040517-GBD24406_16735-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATTCTTATTCTAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTTTAATGTTGTAGTTACTGCACATTCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGTAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608984 Chironomus riparius water mite diet isolate 14817-BHL040517-GBD26496_17124-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTTACTCGTCTTCCATCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608985 Chironomus riparius water mite diet isolate 14820-BHL040517-GBD27740_9250-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATCCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACAAAGCTTTTCCTCGAATAAATAATATAAGTTACGGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608986 Chironomus riparius water mite diet isolate 14826-BHL040517-GBD13339_25153-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCCTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGCAACTGACTTGTCCTCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCCACTCTTACACTTCTTCGATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608987 Chironomus riparius water mite diet isolate 14833-BHL040517-GBD23408_8121-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGACCTTCATTAAGAATGTATATTCGAGCAGAATTAGGACGACTCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTTTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608988 Chironomus riparius water mite diet isolate 14837-BHL040517-GBD7870_9482-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTCTTGGGGCTTGATCCGGAATAGTGGGAACTTCCTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATCATGTTGTAGTTACTGCACATGCTTTTATTATCATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGGATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608989 Chironomus riparius water mite diet isolate 14840-BHL040517-GBD6433_21247-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGAGCTTGATCCGAAATAGTGGGCACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCGTCTCTTACTCTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608990 Chironomus riparius water mite diet isolate 14842-BHL040517-GBD21448_14819-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAACTAGGACGACCCGGAACTTTCATTGGAGATGACCAAGTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATATTTTTTTTCATTGTTATACCATTTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTACTCGAATAAATAATATAAGTTTCTGACGTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608991 Chironomus riparius water mite diet isolate 14855-BHL040517-GBD18022_3947-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGGTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTTGGGTTTCTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTGGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTTTTTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608992 Chironomus riparius water mite diet isolate 14865-BHL040517-GBD29243_17602-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGGTTATCAGAGTAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGGGGATTTGGAAACTGACATGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608993 Chironomus riparius water mite diet isolate 14867-BHL040517-GBD28401_11394-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGACTTGTTCCTCTTATACTTGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608994 Chironomus riparius water mite diet isolate 14875-BHL040517-GBD9446_17984-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATTGCTTTTCCTCGCATAAACAATATAAGTTTCTGACTTTTACCCCCCTCTCCTACACTTCTTCGGTCTAGTTCTTTCGTAGAAAATGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608995 Chironomus riparius water mite diet isolate 14880-BHL040517-GBD18029_23098-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCTCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTGACTCTTCTACTTTCTAGTTCATTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW608996 Chironomus riparius water mite diet isolate 14882-BHL040517-GBD26349_11029-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGTACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATATTATAAGTTTCTGACTATTACCCCCCTCTCTTACTCTTCTACTAGCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608997 Chironomus riparius water mite diet isolate 14890-BHL040517-GBD28245_20826-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCCCCTGACATAACTTTTCCCCGAAAAAAAAATAAAAGGTTCTGGCTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608998 Chironomus riparius water mite diet isolate 14891-BHL040517-GBD14326_21053-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACTTTATTTTTGGGGCTTGATCCGGAATACTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGCCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATCTGGAAACTGACTTGTCCCCCTAATACTTGGAGCCCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW608999 Chironomus riparius water mite diet isolate 14906-BHL040517-GBD14016_4855-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTGATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGCTGTAGTTACTGCACATGCTTTTATTATGATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTAGGAAACTGACTGGTCCCCCTAATACTTGGAGCCCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609000 Chironomus riparius water mite diet isolate 14913-BHL040517-GBD9736_4188-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGTGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTTGGAAGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGTATTCGGAAACTGACTTGTCCTCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTGCTTCTTTCTAGTTCTTGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609001 Chironomus riparius water mite diet isolate 14916-BHL040517-GBD29518_16737-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGACTTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTACTTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTC	Using NCBI BLASTN in June 2018, this sequence was 98.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609002 Chironomus riparius water mite diet isolate 14940-BHL040517-GBD21756_5994-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTATGAATGCTTATTCGTGCAGAATTAGGACGACCCGGAACTTCCAATGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTCACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTCTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609003 Chironomus riparius water mite diet isolate 14960-BHL040517-GBD2549_16615-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCCCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATACATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTACTACTGTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609004 Chironomus riparius water mite diet isolate 14971-BHL040517-GBD20839_26920-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACTTTATTTTTGGGGCTTGATCCGGAGTAGTGGGAACTTCATTTAGAATTCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609005 Chironomus riparius water mite diet isolate 14974-BHL040517-GBD13293_19449-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCAGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACGTTTACCCCCCTCTAGTACTCTTCGTCTTTCGAGTTCTTTCGGAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609006 Chironomus riparius water mite diet isolate 14975-BHL040517-GBD24370_25732-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTATGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTAGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTACTACTAACTAGATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609007 Chironomus riparius water mite diet isolate 14980-BHL040517-GBD21504_15587-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGTACTTTCATTGGAGATGACCAAATTTATAATGTTATAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTTTTCCCCTAATATTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609008 Chironomus riparius water mite diet isolate 14995-BHL040517-GBD15524_14870-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGTTGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGCTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTAATTTCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609009 Chironomus riparius water mite diet isolate 14999-BHL040517-GBD26567_17814-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGCTCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAATTTTACTTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATTTAAGTTTCTGACTTTTACCCCCCGCTCTGACTCTTCTGCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609010 Chironomus riparius water mite diet isolate 15005-BHL040517-GBD15452_24259-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGACTTAGGACGACCCGGTACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTACCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTAACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609011 Chironomus riparius water mite diet isolate 15006-BHL040517-GBD16705_24797-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACAACCCGGAACTTTCATTGGCGATTACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAAGAGTGGGAGCATCTGACATAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609012 Chironomus riparius water mite diet isolate 15012-BHL040517-GBD6785_24343-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAACATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609013 Chironomus riparius water mite diet isolate 15017-BHL040517-GBD18524_28773-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTTGGAACTTCATTTAGAATGCTTATTCGAGCAGAATTATGACAACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTTCTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609014 Chironomus riparius water mite diet isolate 15024-BHL040517-GBD29444_14698-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAATTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGTAGCCCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609015 Chironomus riparius water mite diet isolate 15026-BHL040517-GBD10391_27391-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGAGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACACTTCCTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609016 Chironomus riparius water mite diet isolate 15027-BHL040517-GBD18075_15302-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATTTTAATTCGTGCTGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCGTCGTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609017 Chironomus riparius water mite diet isolate 15037-BHL040517-GBD11191_2232-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTATATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTTACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTATCCTCGAATAAATAATATAAGTTTCTGACCATTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609018 Chironomus riparius water mite diet isolate 15039-BHL040517-GBD14319_28800-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGGATAGTGGGAACTTCATTAAGACTGCTTATTCGAGCAGAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTACCCCTAATACTTGGAGCATCTGACATAACTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609019 Chironomus riparius water mite diet isolate 15070-BHL040517-GBD14287_12157-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTAATGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATACCTTTTCCTCCAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACACTGCGTCTGTCCAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609020 Chironomus riparius water mite diet isolate 15099-BHL040517-GBD6627_10835-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCCCTAAGTATGTTTATTCGAGCAGAATTAGGACGACCCGGAACATTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609021 Chironomus riparius water mite diet isolate 15108-BHL040517-GBD20784_26455-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCCTCTAATACTTGGAGCTCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTTCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609022 Chironomus riparius water mite diet isolate 15117-BHL040517-GBD14199_12580-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGATGACCAAATTTATAATGTTGTAGTTATTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTAGTCCCCCTAATACTTGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTACTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609023 Chironomus riparius water mite diet isolate 15134-BHL040517-GBD22131_19694-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGGTTATTCGAGCAAAATTAGGACGACACGGAATTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTCTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTTTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609024 Chironomus riparius water mite diet isolate 15147-BHL040517-GBD19288_22074-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGTACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACCTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCCAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609025 Chironomus riparius water mite diet isolate 15159-BHL040517-GBD15587_5107-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACTACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATGCCCATTTTAATTGGAGGATTAGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTTCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609026 Chironomus riparius water mite diet isolate 15167-BHL040517-GBD24619_23670-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCATGGACTTTCATTGGAGATGACCAAATGTATAATGTTGTAGTTACTGCACATGCCTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCCTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609027 Chironomus riparius water mite diet isolate 15181-BHL040517-GBD5631_24072-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCCTTAAGTATGCTTATTCGAGCAAAATTAGGACGACCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTTCTTTCGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609028 Chironomus riparius water mite diet isolate 15182-BHL040517-GBD2804_14825-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTGTACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAGGAATGCTTATTCGAGCAGATTTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTGCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCCTACTCGTCTTCTGTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609029 Chironomus riparius water mite diet isolate 15187-BHL040517-GBD22336_16753-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCGTATTCGAGCAGAATTAGGACAACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGCTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609030 Chironomus riparius water mite diet isolate 15192-BHL040517-GBD13264_12147-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTCGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATCTTAATTGGAGGATTCGGAAATTGATTTGTTCCCCTAATACTTGGAGCACCTGACATGGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTGACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609031 Chironomus riparius water mite diet isolate 15203-BHL040517-GBD15106_29067-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTTGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTTTTACTCATCTTCTATCTAGTTCTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609032 Chironomus riparius water mite diet isolate 15205-BHL040517-GBD17724_27756-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAACGGTTATTCTAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGCTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCACCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTGCTCTTCTTCTTTCTAGTTTTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609033 Chironomus riparius water mite diet isolate 15209-BHL040517-GBD20343_17192-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTTTACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTACCCCTAATACTTGAAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTATTTCTAGATCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609034 Chironomus riparius water mite diet isolate 15221-BHL040517-GBD25025_19063-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGTAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACACGGAACTTTCATTGGAGATGACCAAATTTATAATGGTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGAGTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTAGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609035 Chironomus riparius water mite diet isolate 15232-BHL040517-GBD8999_25092-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGTCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCTCCCTCTCTAACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609036 Chironomus riparius water mite diet isolate 15242-BHL040517-GBD27459_14872-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAACTAGGACGAACCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAACACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609037 Chironomus riparius water mite diet isolate 15243-BHL040517-GBD5579_19026-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTACATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCTAATAAATAATACAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCTTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609038 Chironomus riparius water mite diet isolate 15256-BHL040517-GBD14350_6227-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCAAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACCGACTTGTCCCCCTAATCCTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCTCCTCTCTTACTCTTCTTCTTTTTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609039 Chironomus riparius water mite diet isolate 15260-BHL040517-GBD20081_28354-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGGACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTACCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCGCGCTTACACGCCTGCTGTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609040 Chironomus riparius water mite diet isolate 15279-BHL040517-GBD7243_11101-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGTCCTTGATCCGGAATAGTGGGAACTTCCTTAAGAATGCTTATTCGAGCAGAATTAGGACAACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTTTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609041 Chironomus sp. water mite diet isolate 627-BHL072216-GBD13772_7916-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCTTGATCTGATATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGCTACTGCACATGCCTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTTACTTTTACCCCCCTCTCTTACTCCTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609042 Chironomus sp. water mite diet isolate 720-BHL072216-GBD14508_12037-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTTTACTTTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTCTTAGTATGCTTATTCGAGCAGAATTAGGACGTCCTGGTACTTTTATTGGTGATGACCAAATTTATAATGTAGTTGTAACTGCTCACGCATTTATTATAATTTTTTTCATAGTTATACCAATTCTAATTGGTGGTTTTGGTAATTGACTTGTACCCTTAATATTAGGAGACCCAGATATTGCTTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCTCTTACTCTATTACGATCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR665396, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609043 Chironomus sp. water mite diet isolate 721-BHL072216-GBD12442_27071-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTCTTAGTATGCTTATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTAACTGCCCACGCATTTATTATAATTTTTTTCATAGTTATACCAATTCTAATTGGTGGTTCTGGTAATTGACTTGTACCCTTAATATTAGGAGCTCCTGATATGGCTTTTCCTCGGTTAAATAATTTAAGTTTCTGATTCCTTCCTCCTGCTTTAACTCTT	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR665396, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609044 Chironomus sp. water mite diet isolate 723-BHL072216-GBD10864_24172-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTTTACTTTATTTTTGGGGCTTGATCAGGAATGGTAGGGACTTCTCTTAGTATGCTTATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTAACTGCCCACGCATTTATTATAATTTTTTTCATAGTTATACCAATTCTAATTGGTGGCTTTGGTAATTGACTTGTACCCTTAATATTAGGAGCCCCAGATATGGCTTTCCCCCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCCCTTACCCTTTTACTTTCAAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR665396, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609045 Chironomus sp. water mite diet isolate 724-BHL072216-GBD15993_25451-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTTTACTTTATTTTTGGAGCTTGATCAGGAATGGTAGGGACTTCTCTTAGTATGCTTATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTTGTAACTGCTCACGCATTTATTATAATTTTTTTCATAGTTATACCAATTCTAATTGGTGGATTTGGTAATTGACTTGTACCCTTAATATTAGGAGCCCCAGATATGGCTTTCCCCCGAATAAATAATATAAGATTTTGACTTCTTCCCCCATCTCTTACTCTATTACTTTCTAGAACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR665396, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609046 Chironomus sp. water mite diet isolate 727-BHL072216-GBD29241_18913-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTTTACATTATTTTTGGAGCTTGATCAGGAATGGTAGGTACTTCTCTTAGTATGCTTATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTTGTAACTGCCCACGCATTTATTATAATTTTTTTCATAGTGATACCAATTCTAATTGGTGGTTTTGGTAATTGACTTGTTCCCTTAATATTAGGAGCCCCAGATATGGCTTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTTACGTTATTACTATCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR665396, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609047 Chironomus sp. water mite diet isolate 731-BHL072216-GBD28028_20295-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTCTTAGTATGCTTATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACTGCACACGCATTTATTATAATTTTTTTCATAGTTATACCAATTCTAATTGGTGGTTTTGGTAATTGACTTGTACCCTTAATATTAGGAGCTCCAGATATGGCTTTCCCCCGAATAAATAATATAAGTTTTTGACTACTTCCCCCATCTCTAACACTATTACTTTCTAGAACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR665396, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609048 Chironomus sp. water mite diet isolate 734-BHL072216-GBD24489_13885-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTTTACTTTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTCTTAGTATGCTTATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTAACTGCCCACGCATTTTTTATAATTTTTTTCATAGTTATACCAATTCTAATTGGAGGTTTTGGTAATTGACTTGTACCCTTAATATTAGGAGCCCCAGATATAGCTTTCCCCCGAATAAATAATATAAGATTTTGACTTCTTCCCCCATCTCTAACTCTTTTACTTGCTAGTGCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR665396, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609049 Chironomus sp. water mite diet isolate 742-BHL072216-GBD10770_10115-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTTTACTTTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTTTTAGTATGTTTATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTAACTGCTCACGCATTTATTATAATTTTTTTCATAGTTATACCAATTCTAATTGGTGGTTTTGGTAATTGACTTGTACCCTTAATATTAGGAGCCCCCGATATGGCTTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCACTAACTCTTCTACTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR665396, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609050 Chironomus sp. water mite diet isolate 743-BHL072216-GBD27903_21703-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTCTTGGTGCTTGATCAGGAATGGTAGGGACTTCTTTTAGTATGCTTATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTGTAGTAACTGCCCACGCATTTATTATAATTTTTTTCATAGTTATACCAATTCTAATTGGAGGTTTTGGAAATTGACTTGTACCCTTAATATTAGGAGCCCCAGATATAGCTTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTTACTCTTTTACGTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR665396, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609051 Chironomus sp. water mite diet isolate 1087-BHL100916-GBD9216_23109-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTTATTCGAGCAGAATTAGGACAACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCCCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAGTTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCCCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTGCTTTCTAGATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609052 Chironomus sp. water mite diet isolate 1206-BHL110116-GBD13201_8878-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAACTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTATTACCCCCCTTACTAACCCTTCTTCTTTCTAGTTCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609053 Chironomus sp. water mite diet isolate 1678-BHL110116-GBD21474_2717-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTACTACCACCATCTC-TAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609054 Chironomus sp. water mite diet isolate 1680-BHL110116-GBD1964_13536-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTC-TAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609055 Chironomus sp. water mite diet isolate 1718-BHL110116-GBD13197_5578-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGCTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609056 Chironomus sp. water mite diet isolate 1736-BHL110116-GBD23215_27060-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAGCTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGATTTGTTCCTCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTGACTCTTTTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609057 Chironomus sp. water mite diet isolate 1807-BHL101516-GBD6949_14897-Ldc86 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTAGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAAGAATATAAGTTTCTGATTTTTGCCCCCCTCACTAACTCTATTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609058 Chironomus sp. water mite diet isolate 2428-BHL072216-GBD6325_14569-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCTTTTACTTTATTTTTGGTGCTTGATCAGGAATGTTAGGGACTACTTTAAGTATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTAAGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTCAATACTAGGGGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTTACATTACTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609059 Chironomus sp. water mite diet isolate 2666-BHL072216-GBD3859_9880-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTTGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACTACCCGGCACTTTCATTGGAGATGACCAAGTTTATAATGTTTTAGTTACTGCACATGCTTTTATTATAATTTTTTTCTTAGTTATACCAATTTTAATTGTAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGTACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGTAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609060 Chironomus sp. water mite diet isolate 2815-BHL032417-GBD16607_8138-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACCTTCATTGGAGATGGCCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609061 Chironomus sp. water mite diet isolate 2839-BHL032417-GBD3461_9142-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTATTGGGGCTTGATCCGGAAAAGTGGAAACTTCATTAAGAATGCTGATTCGAGAAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTATCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAACACCTTACATAGCTCTTCCTCGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609062 Chironomus sp. water mite diet isolate 2904-BHL032417-GBD11187_12702-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAGCTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCGCCAGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGACTACTCCCACCATCTTTAACTCTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609063 Chironomus sp. water mite diet isolate 2913-BHL032417-GBD21502_13620-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGACGACCCGGAACCTTCATTGGAGATGGCCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCGATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR756187, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609064 Chironomus sp. water mite diet isolate 2946-BHL032417-GBD16279_14592-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATCTATTATAATCTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGATATATCTTTCCCTCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609065 Chironomus sp. water mite diet isolate 2978-BHL032417-GBD11157_27870-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACAATATTCTTGGGGCTTGATCCGGAAAAGTGGAAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAACACCTTACATAGCATTTCCTCGAATAAATATTATAAGTTTCTGACTTTTACCCGCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609066 Chironomus sp. water mite diet isolate 2986-BHL032417-GBD20469_19846-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCATTAAGAATCCTTTTTCGAGCAGAACTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACTTGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTTGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCCGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCATTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID KR756187, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609067 Chironomus sp. water mite diet isolate 3044-BHL032417-GBD20835_12560-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGACCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAACTGGAGGATTTGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCATCTCTTAC-CTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609068 Chironomus sp. water mite diet isolate 3067-BHL032417-GBD28052_10787-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTATAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGTGCCCCTGATATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609069 Chironomus sp. water mite diet isolate 3071-BHL032417-GBD24850_18571-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCCTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGGCCAAATTTATAATGTTGTAGTTACTGCACAGGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609070 Chironomus sp. water mite diet isolate 3077-BHL032417-GBD18364_11913-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTTCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTAAAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609071 Chironomus sp. water mite diet isolate 3087-BHL032417-GBD6997_19451-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATATTTTTTTTTTGGAGCTTGATCCGGAAAAGTGGAAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACGTGTCCCCCTAATACTTGGAACACCTTGCATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609072 Chironomus sp. water mite diet isolate 3094-BHL032417-GBD14919_14004-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATATATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609073 Chironomus sp. water mite diet isolate 3165-BHL032417-GBD15975_3626-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTGTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACTACCCGGAACCTTCATTGGAAATGGCCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTACAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609074 Chironomus sp. water mite diet isolate 3192-BHL032417-GBD20388_7698-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATATTTTTTTTTTGGAGCTTGATCCGGAATAGTGGGAACTTCATTAAGAACGCTTATTCGAGCAGAACTAGGACGACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTTGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCATTCTTCTTTCTAGTTCTTTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609075 Chironomus sp. water mite diet isolate 3197-BHL032417-GBD6494_23966-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTATTGGGGCTTGATCCGGAAAAGTGGAAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAGACTGACTTGTCCACCTAATACTTGGAACAACTTACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCATTCCTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609076 Chironomus sp. water mite diet isolate 3199-BHL032417-GBD12047_21935-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATATTTTTTTTTGGAGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCTTTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTATTACTTGGAGCACCTGACATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609077 Chironomus sp. water mite diet isolate 3203-BHL032417-GBD17837_5427-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATGCTTATTCGAGCAGAACTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGGTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGTAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCATACCATTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID KR756187, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609078 Chironomus sp. water mite diet isolate 3219-BHL032417-GBD18402_24760-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACATTCATTGGAGATGGCCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCACGAATAAATAATATAAGATTCTGACTATTACCCCCCTCTCTTACTCTACTTCTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609079 Chironomus sp. water mite diet isolate 3249-BHL032417-GBD20576_11083-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACGTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGAAACCTTCATTGGAGATGGCCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCGCTCTTACCAGACTTCTTGCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609080 Chironomus sp. water mite diet isolate 3260-BHL032417-GBD8245_10396-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGAATCGGAAACTGACTTGTCCCCTTATTACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609081 Chironomus sp. water mite diet isolate 3261-BHL032417-GBD5265_11930-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATAGTTACTGCTCATGCTTTTATTGTAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACCTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609082 Chironomus sp. water mite diet isolate 3297-BHL032417-GBD13280_20970-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCTTATTACTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609083 Chironomus sp. water mite diet isolate 3332-BHL032417-GBD10732_3972-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGTGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACCTTCATTGGAGATGGTCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAATTAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTTTCTAGTGCAGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609084 Chironomus sp. water mite diet isolate 3342-BHL032417-GBD25061_17791-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGATCTTCTTTAAGTTTGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTTTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTGATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGATATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTTACATTATTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609085 Chironomus sp. water mite diet isolate 3443-BHL032417-GBD8793_21871-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTCTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGATATATCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609086 Chironomus sp. water mite diet isolate 3455-BHL032417-GBD6913_14122-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACCTTCATTGGAGATGGCCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGGAACTGATTTGTCCCTCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAATACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609087 Chironomus sp. water mite diet isolate 3463-BHL032417-GBD4992_17187-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACCTTCATTGGAGATGGCCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGATATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTTACATTATTCCATTCAAGTTCATTTGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609088 Chironomus sp. water mite diet isolate 3487-BHL032417-GBD15592_6432-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATGTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGACCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTAGAAAAAAATAATATAAGTTTCTGACTTTTACCCCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609089 Chironomus sp. water mite diet isolate 3543-BHL032417-GBD10237_2544-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGCACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTGCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609090 Chironomus sp. water mite diet isolate 3551-BHL032417-GBD19840_16535-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609091 Chironomus sp. water mite diet isolate 3554-BHL032417-GBD20238_27673-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCCACAAATCATAAAGATATTGGAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTGATTGTAACGGCACATGCTTTTTTTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGATATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACATACATTACTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609092 Chironomus sp. water mite diet isolate 3577-BHL032417-GBD7051_7318-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAACAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACGTGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCTTCCTCTCTTACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609093 Chironomus sp. water mite diet isolate 3630-BHL032417-GBD8244_6431-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGACATTGGAACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGATATAGCTTTCCCCCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609094 Chironomus sp. water mite diet isolate 3636-BHL032417-GBD26435_17017-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTAGAAAAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTAGTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609095 Chironomus sp. water mite diet isolate 3654-BHL032417-GBD13515_25681-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAACAATGCTTATTCGGGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTCACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATATCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACTCCCTTCATTAACT-TTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609096 Chironomus sp. water mite diet isolate 3698-BHL032417-GBD8748_7440-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACATTATATCTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACGTCTTTAAATATGCTAATTCGAGCAGAAATAGGACGACCTGGAACTTTTATTGGAGATGACCAGATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATATTTTTTTTTATAGTTATATCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCTAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609097 Chironomus sp. water mite diet isolate 3709-BHL032417-GBD24647_15292-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAACATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCTCTTACATTACTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609098 Chironomus sp. water mite diet isolate 3742-BHL032417-GBD17137_26045-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATGTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATTCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATTGCTTTTCCTAGAAAAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609099 Chironomus sp. water mite diet isolate 3769-BHL032417-GBD12699_26597-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATACGGAATAGTGGGAACTTCATTAACAATGCTTATTCGATCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCCAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCTCCCTCTCTTACTCATCTTTTTTCTAGTTCCTTCGTAGAAAATTGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609100 Chironomus sp. water mite diet isolate 3771-BHL032417-GBD10523_9289-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGACCAAATTTATAATGTTGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATATATAATATAAGTTTTTGAGTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.1% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609101 Chironomus sp. water mite diet isolate 3803-BHL032417-GBD14173_23058-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCCTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTAGAAAAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTGTTACTTTCTAGTTCAATTGTAGAGAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609102 Chironomus sp. water mite diet isolate 3824-BHL032417-GBD16225_4936-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATGTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCAGACATAGCTTTTCCTAGAAAAAATAATATAAGTTTCTGACTTTTACCCCCTTCATTAACT-TTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609103 Chironomus sp. water mite diet isolate 3847-BHL032417-GBD17905_5340-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTGTAGTTACAGCTCACACATTTATTATAATTTTCTTCATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATATATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609104 Chironomus sp. water mite diet isolate 3880-BHL032417-GBD12686_28375-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGTGAACTTTATTAACAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTCACTGCACATGCTTTTATTATAGTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAGACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCTCCCTCTTTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609105 Chironomus sp. water mite diet isolate 3881-BHL032417-GBD21601_24540-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTGTTGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTTCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATATATAATATAAGTTTTTGAGTTCCCCCCCCATCTTTAACCCTTCTTCTATCTAGTTCAGTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609106 Chironomus sp. water mite diet isolate 3882-BHL032417-GBD18512_18694-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAAGTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609107 Chironomus sp. water mite diet isolate 3917-BHL032417-GBD2168_12046-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATGTTTGGGGCTTGATCCGGAATAGTTGGAACTTCATTTAGAATACTTATTCGAGCAGAATTATGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTAGAAAAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTGCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609108 Chironomus sp. water mite diet isolate 3925-BHL032417-GBD10927_25167-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTGTAGTTACAGCTCACGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609109 Chironomus sp. water mite diet isolate 3978-BHL032417-GBD25367_20172-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCATTCCCTCGAATATATAATATAAGTTTTTGAGTTCTCCCCCCATCATTAACTCTACTACTATCTAGTTCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609110 Chironomus sp. water mite diet isolate 4000-BHL032417-GBD18436_8503-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTATTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCACACATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAAATGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGATATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACATACATTACTCCTTTCAAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609111 Chironomus sp. water mite diet isolate 4041-BHL032417-GBD25394_10868-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAACAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGATTTGTACCTTTAATACTAGGGGCCCCTGATATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACATACATTACTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609112 Chironomus sp. water mite diet isolate 4060-BHL032417-GBD12019_18661-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCTCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTTCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCATCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609113 Chironomus sp. water mite diet isolate 4070-BHL032417-GBD8158_11548-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATATTGTTGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATATATAATATAAGTTTTTGAGTTCTCCCCCCATCTTTAACATTACTATTAGCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.6% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609114 Chironomus sp. water mite diet isolate 4521-BHL032417-GBD23190_16222-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTACTATACTTTTCTTTATCGTTATATCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTGGACTTCTCCCCCCATCTTTAACTCTTCCTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609115 Chironomus sp. water mite diet isolate 4561-BHL032417-GBD12317_28281-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTTCATTATACTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCAAGTAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCGTTTATTATGATTTTCTTTATAGTTATATCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTGGACTTCTCCCCCCATCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609116 Chironomus sp. water mite diet isolate 4625-BHL032417-GBD23348_25064-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTGATTATAATTTTCTTTATAGTTATATCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTTCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTGGACTTCTCCCCCCATCTTTAACCCTACTTCTATCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.4% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609117 Chironomus sp. water mite diet isolate 4635-BHL032417-GBD26509_20741-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTTCATTATACTTCATTTATGGTGCCTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCAAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATATCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTGTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609118 Chironomus sp. water mite diet isolate 4664-BHL032417-GBD3489_20487-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTCGGGGGTTGATCCGGAATTGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTCGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609119 Chironomus sp. water mite diet isolate 4690-BHL032417-GBD28887_14792-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCCAGCAGACTTAGGACGTCCTGGAACTTTTATTGGTGATGACCAATCTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATATCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.1% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609120 Chironomus sp. water mite diet isolate 4724-BHL032417-GBD14694_24357-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTAGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATATCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTGGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609121 Chironomus sp. water mite diet isolate 4736-BHL032417-GBD13991_12936-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTTCATTATACTTCATTCTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAATTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATATCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609122 Chironomus sp. water mite diet isolate 4789-BHL032417-GBD7218_22431-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGGAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACATCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTGGGACTTCTCCCCCCATCTTTAACTCTACTTCTTTCTAGTTCATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609123 Chironomus sp. water mite diet isolate 4835-BHL032417-GBD13609_25429-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCAAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATATCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGATCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACT-TTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.1% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609124 Chironomus sp. water mite diet isolate 4911-BHL032417-GBD25863_15614-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCAAGCAGAATTAGGACGTCCTGGGACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTGTAATATTGGGAGCCCCTGATATAGCATTCCCTCTAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAAC-CTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609125 Chironomus sp. water mite diet isolate 4930-BHL032417-GBD6679_10146-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATATCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACT-TTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609126 Chironomus sp. water mite diet isolate 4997-BHL032417-GBD19225_17079-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATGATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGATCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGAATTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.6% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609127 Chironomus sp. water mite diet isolate 5016-BHL032417-GBD6830_13213-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTTCATTATACTTCATTTTTGGTGCCTTATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCGCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTTGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609128 Chironomus sp. water mite diet isolate 5063-BHL032417-GBD26255_20725-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACCCTATATTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTATGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACCACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCGCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCATCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609129 Chironomus sp. water mite diet isolate 5098-BHL032417-GBD7646_4905-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGACCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTACAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCGCCAGATATGGCCTTCCCTCGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCA---GTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609130 Chironomus sp. water mite diet isolate 5129-BHL032417-GBD12867_28094-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGAATTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609131 Chironomus sp. water mite diet isolate 5145-BHL032417-GBD7293_9428-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGACTTCCCTCGAATAAATAATATAAGTTTTTGAATTCTACCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609132 Chironomus sp. water mite diet isolate 5160-BHL032417-GBD9923_3282-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTATGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGGACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGGGCGCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACT-TTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609133 Chironomus sp. water mite diet isolate 5196-BHL032417-GBD20191_22284-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACTTTATATTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCATCTTCTTTCAAGTACATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609134 Chironomus sp. water mite diet isolate 5197-BHL032417-GBD4236_22463-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGGCTATTACCCCCGTCATTATCATTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609135 Chironomus sp. water mite diet isolate 5204-BHL032417-GBD17597_28083-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGATCTTTATATATTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGCTTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATAGCCTTCCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTACATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609136 Chironomus sp. water mite diet isolate 5215-BHL032417-GBD12031_7561-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATACTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATCCCAATTTTAACTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609137 Chironomus sp. water mite diet isolate 5238-BHL032417-GBD23765_18893-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCCGGAATAGTAGGAACTTCCTTTAGAATATTTATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCGCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTGCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609138 Chironomus sp. water mite diet isolate 5239-BHL032417-GBD26160_10964-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTCCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACCTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATGGATTGGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAAC-ATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609139 Chironomus sp. water mite diet isolate 5240-BHL032417-GBD20435_27553-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCTTTTAGAATGTTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGATTTGTTCCTTTAATATTAGGAGGTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCATTAACTCTTCTACTATCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609140 Chironomus sp. water mite diet isolate 5252-BHL032417-GBD26407_16020-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCCTTTAGAATTTTAATTCGAGCAGAATTAGGACGACCTGGTACTTTTATTGGTGATGATCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTACTCCCCCCATCTTTAACTCTACTACTATCTAGTTCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609141 Chironomus sp. water mite diet isolate 5266-BHL032417-GBD21034_28251-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGATTTGTCCCTTTAATATTAGGAGTTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTACTCCCCCCATCATTAACTCTACTGCTATCTAGTTCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609142 Chironomus sp. water mite diet isolate 5268-BHL032417-GBD26246_17702-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTATATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGATGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTAAGTCTTCCTCTTTCTAGTAGTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609143 Chironomus sp. water mite diet isolate 5278-BHL032417-GBD19043_22739-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTCTTAGAATTTTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTTGTCCCTTTAATATTAGGAGCGCCAGATATAGCCTTCCCTCGAATAAATAATATAAGATTTTGACTACTCCCCCCATCTTTAACTCTACTTCTATCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.4% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609144 Chironomus sp. water mite diet isolate 5286-BHL032417-GBD27992_19628-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCTTTTAGAATATTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTTGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTCTAATATTAGGAGCGCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTACTACTATCTAGTTCGTTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609145 Chironomus sp. water mite diet isolate 5287-BHL032417-GBD11357_10481-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTCTTTACTTTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGAACAGATTTATAATGTAGTTGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGAGCCCCTGATATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACATACATTATTCCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609146 Chironomus sp. water mite diet isolate 5295-BHL032417-GBD10322_16056-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTTTATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACATCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCGCCCCCCATCTTTAACACTTCATCAATCTAGTGCATTAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609147 Chironomus sp. water mite diet isolate 5298-BHL032417-GBD10257_20952-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACCTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAATTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.1% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609148 Chironomus sp. water mite diet isolate 5313-BHL032417-GBD5510_13176-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACATCCTGGATCTTTTATTGGTGATGATCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAACTGGAGGATTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGAATACTCCCCCCATCTTTAACTCTACTTCTTTCTAGTTCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609149 Chironomus sp. water mite diet isolate 5336-BHL032417-GBD22088_7118-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGATTTGTTCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAACATAAGTTTTTGACTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAACATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609150 Chironomus sp. water mite diet isolate 5337-BHL032417-GBD17520_6052-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGACTGCA---GTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609151 Chironomus sp. water mite diet isolate 5341-BHL032417-GBD25402_7854-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGATGCCTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCTGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCGCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609152 Chironomus sp. water mite diet isolate 5397-BHL032417-GBD26006_6017-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGCACTTTTATTGGTGATGACCAAATTTATAATGTAGTTGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTACCTTTAATATTAGGAGCGCCAGATATAGCCTTCCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCAAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609153 Chironomus sp. water mite diet isolate 5399-BHL032417-GBD7955_16243-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATATAGTTGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTTGTGCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609154 Chironomus sp. water mite diet isolate 5411-BHL032417-GBD25057_7018-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTGTCCCTTTAATATTAGGAGCGCCAGATATGGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTCCCCCCATCTTTAACTCTACTACTTGCTAGGGCAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609155 Chironomus sp. water mite diet isolate 5416-BHL032417-GBD25956_13471-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCCTTTAGAATATTAATTCGAGCAGAATTAGGACATACTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCCATTTTAATTGGAGGTTTTGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTACTCCCCCCATCTTTAACTCTACTACTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609156 Chironomus sp. water mite diet isolate 5424-BHL032417-GBD25514_8012-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGTACTTCATTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCTGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTTTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609157 Chironomus sp. water mite diet isolate 5436-BHL032417-GBD4541_12349-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTACTTCTATCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609158 Chironomus sp. water mite diet isolate 5437-BHL032417-GBD3890_21627-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTTTATATTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAGTAGTAACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGATTTTGACTACTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTGCTTTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609159 Chironomus sp. water mite diet isolate 5455-BHL032417-GBD26640_18547-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACATTATATTTTATTTTTGGTGCTTGATCAGGAATAGTTGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGTAGGTTTTGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATAGCCTTCCCTCGAATAAATAATATAAGATTTTGAATACTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609160 Chironomus sp. water mite diet isolate 5530-BHL032417-GBD10556_25114-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGTGCTTGATCAGGAATAGTCGGAACTTCCCTTAGTATATTAATTCGAGCAGAATTAGGACGCCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTTGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATAGCCTTCCCTCGAATAAATAACATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTATCTAGAACATGAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.6% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609161 Chironomus sp. water mite diet isolate 5536-BHL032417-GBD18704_3227-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCTCTTAGAATATTAATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAGTTGTTACATCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTTGTCCCTTTAATATTAGGAGCACCAGATATAGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTACTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609162 Chironomus sp. water mite diet isolate 5543-BHL032417-GBD21382_15510-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609163 Chironomus sp. water mite diet isolate 5547-BHL032417-GBD25222_21745-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCTCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAGTAGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCGCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTCCCCCCATCTTTAACACTACTACTATCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.6% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609164 Chironomus sp. water mite diet isolate 5549-BHL032417-GBD19907_15692-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGACTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAGCTAGGACGTCCCGGAACTTTCATTGGAGATGACCAAATTTACAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTATTAATATTCTTCTGTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609165 Chironomus sp. water mite diet isolate 5555-BHL032417-GBD9936_24223-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCCTTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCACGAATAAATAATATAAGATTTTGAATACTACCCCCATCTTTAACTCTACTTCTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.6% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609166 Chironomus sp. water mite diet isolate 5577-BHL032417-GBD23146_6571-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCGATTTTAATTGGAGGTTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609167 Chironomus sp. water mite diet isolate 5586-BHL032417-GBD7114_9091-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATACGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCTTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609168 Chironomus sp. water mite diet isolate 5597-BHL032417-GBD24868_12611-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAGTTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609169 Chironomus sp. water mite diet isolate 5598-BHL032417-GBD15375_26562-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACCTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCATCTTTAACTCTTCTTCTTTCTTGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609170 Chironomus sp. water mite diet isolate 5618-BHL032417-GBD19911_12049-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTCCCCCTAATACTAGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTACAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609171 Chironomus sp. water mite diet isolate 5622-BHL032417-GBD27855_18537-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGGGCCTGATCTGGGATAGTTGGAACTTCTTTAAGAATTCTTATTCGTGCAGAATTAGGACATGCTGGTTCCTTAATTGGAGACGACCAAATTTATAATGTAATTGTTACTGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGTTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAACAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCATCTTTCTTGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609172 Chironomus sp. water mite diet isolate 5623-BHL032417-GBD20571_16053-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCGGCTTCTTTCTAGTTCATCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609173 Chironomus sp. water mite diet isolate 5624-BHL032417-GBD26207_11230-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGAATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTAACTCTTCTACTCTCAAGTACAACCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609174 Chironomus sp. water mite diet isolate 5629-BHL032417-GBD18014_27731-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAAGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCGATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTTGTTCATTTGTAGAAAATGTAGTTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609175 Chironomus sp. water mite diet isolate 5634-BHL032417-GBD4015_19702-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAACTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTTGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609176 Chironomus sp. water mite diet isolate 5637-BHL032417-GBD21769_18364-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAACTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTTGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATAGCCTTCCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTTGTTCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609177 Chironomus sp. water mite diet isolate 5650-BHL032417-GBD8112_10871-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGAATGTTTATTCGAGTAGAATTAGGAGGACCCGGAACATTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTATTACCCCCCTCTCTTACTCTACTTCTATCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609178 Chironomus sp. water mite diet isolate 5652-BHL032417-GBD15985_15805-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAGTTGTTACGGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCGATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATAGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTACTACTATCTTGTTCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609179 Chironomus sp. water mite diet isolate 5668-BHL032417-GBD17811_10174-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCAGCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609180 Chironomus sp. water mite diet isolate 5674-BHL032417-GBD19695_15461-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGAAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTATCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609181 Chironomus sp. water mite diet isolate 5676-BHL032417-GBD9853_15680-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTTTCTTAGAATATTAATTCGAGCAGAATTAGGCCGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAGTGGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGATCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTTGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609182 Chironomus sp. water mite diet isolate 5677-BHL032417-GBD20892_3065-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTGTCTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGGGATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609183 Chironomus sp. water mite diet isolate 5678-BHL032417-GBD15805_1856-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGTACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACACGACAACTATCTAGTACAACCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609184 Chironomus sp. water mite diet isolate 5680-BHL032417-GBD9772_14119-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGCCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTAACCCTACTTCTATCAAGATCATCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609185 Chironomus sp. water mite diet isolate 5682-BHL032417-GBD28010_15044-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATGCTTATTCGAGCAGAATTAGGACAACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACCGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTACTACTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609186 Chironomus sp. water mite diet isolate 5691-BHL032417-GBD19887_22955-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAGGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTATAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACGTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCTTTAACTCTTCTTTTATCAAGCTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609187 Chironomus sp. water mite diet isolate 5692-BHL032417-GBD24984_5701-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCCTGATCTGGGATAGTTGGAACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGAAGATGACCAAATTTATAATGTTATAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCTCTCTCTTACTCTTCTTCTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609188 Chironomus sp. water mite diet isolate 5698-BHL032417-GBD19790_9447-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATTCCGATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCTTTAACTCTTCTTTTATCAAGCTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609189 Chironomus sp. water mite diet isolate 5705-BHL032417-GBD4599_16119-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATACTTTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTTGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCAACCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609190 Chironomus sp. water mite diet isolate 5707-BHL032417-GBD18737_10938-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTTTATATTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACTGCTCACGCATTTATAATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCATCTTTAACCCTTCTTCTTTCTTGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609191 Chironomus sp. water mite diet isolate 5709-BHL032417-GBD8057_14518-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCATTAGAATATTAATTCGAGTAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATGAATAATATAAGTTTTTGACTACTCCCCCCATCTTTAACTCTACTTCTATCTTATTCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609192 Chironomus sp. water mite diet isolate 5711-BHL032417-GBD11053_11985-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTAGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTTGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609193 Chironomus sp. water mite diet isolate 5713-BHL032417-GBD3939_12537-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGACTAGTTCCCTTAATATTAGGAGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCTTTAACTCTTCTTTTATCAAGCTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609194 Chironomus sp. water mite diet isolate 5717-BHL032417-GBD14686_19668-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACCTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGATTTGTCCCTTTAATATTCGGAGCTCCAGATATAGCCTTCCCTCGAATAAATAATATAAGATTTTGACTGCTCCCCCCATCTTTAACTCTTCTTCTTTCTTGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609195 Chironomus sp. water mite diet isolate 5721-BHL032417-GBD12046_25248-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACAACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTCCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCGCTAACTCTACTACTATCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609196 Chironomus sp. water mite diet isolate 5725-BHL032417-GBD25409_20780-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTATAGTTACTGTACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCTCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTACTTTCTAGTACTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609197 Chironomus sp. water mite diet isolate 5727-BHL032417-GBD20281_3578-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATGATTTTCTTTATAGTAATACCTATTTTAATTGGAGGATATGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609198 Chironomus sp. water mite diet isolate 5776-BHL032417-GBD4877_7126-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAATTGGAACTTCTTTAAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCTATCTTTAACTCTTCTTCTTTCTAATTCATTTGTAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609199 Chironomus sp. water mite diet isolate 5788-BHL032417-GBD25915_19064-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAAGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTACACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTAGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCTTCTCTTACTCTTCTACTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609200 Chironomus sp. water mite diet isolate 5819-BHL032417-GBD18682_4544-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGAGTCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCTTCTCTTACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609201 Chironomus sp. water mite diet isolate 5820-BHL032417-GBD16056_6980-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATACATTATTTTTGAGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCAGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGTCTCGGAAATTGACTTGTCCCTTTAATATTAGGAACTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCTATCTTTAACTCTTCTTCTTTCTAATTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609202 Chironomus sp. water mite diet isolate 5839-BHL032417-GBD9622_5816-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGCACTTCATTAAGAATGCTTATTCGAACAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCATAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCGTCACTTACTCTACTACTATCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609203 Chironomus sp. water mite diet isolate 5850-BHL032417-GBD4770_10882-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTACACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACT-TTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609204 Chironomus sp. water mite diet isolate 5852-BHL032417-GBD20378_19877-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCTTCTCTTACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609205 Chironomus sp. water mite diet isolate 5877-BHL032417-GBD7241_22598-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAAATATGGCCTTCCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCTCCTCTCTTACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609206 Chironomus sp. water mite diet isolate 5881-BHL032417-GBD27212_8399-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGTGCTTGATCTGGAATAGTAGGAACTTCCTTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTAGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTACTCCCCCTATCTTTAACTCTACTTCTTTCTAATTCATTTGTAGAAAATGCAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609207 Chironomus sp. water mite diet isolate 5891-BHL032417-GBD6013_10979-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAACAGAATTAGGACGACCCGGAACTTTCATTGGAGTTGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATCTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAATTTTCTGACTTTTACCCCCTTCTCATACTCTTCCTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609208 Chironomus sp. water mite diet isolate 5893-BHL032417-GBD7158_9728-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTCTTGACTTCACCCCCTATCTATAACGCTGCGTCTGTCTAATACATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609209 Chironomus sp. water mite diet isolate 5903-BHL032417-GBD22778_26085-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCTTAATATTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCTTCTCTAACTCTTCTTCTTTCTAGTTCAATCGTAGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609210 Chironomus sp. water mite diet isolate 5906-BHL032417-GBD12328_8310-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGATCTTTATACTTTATTTTTGGTGCTTGATCCGGAATAGTGGGAACTTCCTTAAGAATGTTTATTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTCTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTAGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCTTCTCTTACTCTTCTTCTTTCTAGTACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609211 Chironomus sp. water mite diet isolate 5920-BHL032417-GBD16216_12300-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCGATTTTAATTGGGGGTTTCGGAAATTGATTAGTATCTTTAATGTTAGGGGCCCCTGATATAGCCTTCCCGCGAATAAATAATATAAGATTTTGACTTCTCCCACCGTCTCTTTCTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609212 Chironomus sp. water mite diet isolate 5924-BHL032417-GBD15139_14949-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATCGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGCTTCTGACTATTACCCCCTTCTCTTACACTACTTCTAGCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609213 Chironomus sp. water mite diet isolate 5930-BHL032417-GBD14508_8395-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGCACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATAATAATTTTTTTCATAGTGATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCTTCACTTACCCTTCTTCTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609214 Chironomus sp. water mite diet isolate 5939-BHL032417-GBD8999_12224-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609215 Chironomus sp. water mite diet isolate 5941-BHL032417-GBD20024_6376-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGAACCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTCGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCTATCTTTAACTCTTCTTCTTTCTAATTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609216 Chironomus sp. water mite diet isolate 5949-BHL032417-GBD26703_23950-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCCCATGCTTTTATTATAATTTTTTTCATAGTTAGACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCTTCTCTTACTCTACTACTTGCTAGTACTAGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609217 Chironomus sp. water mite diet isolate 5951-BHL032417-GBD25042_15466-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGATTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGTGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCTTCTCTAACCCTTCTTCTATCTAGTACTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609218 Chironomus sp. water mite diet isolate 5956-BHL032417-GBD19641_5148-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGTGCATGATCAGGAATAATTGGAACTTCTTTAAGAATATTAATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCTTCTCTTACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609219 Chironomus sp. water mite diet isolate 5972-BHL032417-GBD7841_16733-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCTGAATCGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCTGAACTTTCATTGGAGATGATCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCTATCTTTAACTCTTCTTCTTTCTAATTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609220 Chironomus sp. water mite diet isolate 5980-BHL032417-GBD17723_16445-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGCACTTCCTTAAGTATACTTTTTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCCCGAATAAATAATATAAGTTTCTGACTTTTACCCCCGTCTCTTACTCTTCTTCGATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609221 Chironomus sp. water mite diet isolate 5988-BHL032417-GBD19200_28171-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATATTATAAGTTTCTGACTTTTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609222 Chironomus sp. water mite diet isolate 5994-BHL032417-GBD18519_23806-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATTCGGAATTGTGGGAACTTCATTGAGAATGCTTATTCGTGCAGAAATATGACGACACGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCAAAGTTATACCAGTTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609223 Chironomus sp. water mite diet isolate 6068-BHL032417-GBD2254_13667-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTTCAATTTTTTTCATAGTTATACCAATTTTAAATGGAGGTGTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609224 Chironomus sp. water mite diet isolate 6093-BHL032417-GBD10099_16616-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGTAACTTTTATTGGTGACGACCAAATTTATAATGTTGTAGTTACTGCACATACTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTATCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609225 Chironomus sp. water mite diet isolate 6099-BHL032417-GBD23460_8100-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGCATTCTAATTAGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATGTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAAACTGACTTGTCTCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609226 Chironomus sp. water mite diet isolate 6194-BHL032417-GBD28924_14431-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATAGCAGTTTTAAATGGAGAATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGATTAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACACTACTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609227 Chironomus sp. water mite diet isolate 6233-BHL032417-GBD14147_7235-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGACCTTTATACAGTATTTTTGGGGCTTGCTCCGGAATTGTGGGAACTTCATTGGGAATGCTTATTCGAGCAGAAATAGGACGAACAGGAACTTTCATTGGAGATGACCAAAATTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609228 Chironomus sp. water mite diet isolate 6266-BHL032417-GBD8945_22359-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAACAAATAGTATAAGTTTCTGACTTTTACCTCCCTCTCTTACTCTTCTTCTATCTAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609229 Chironomus sp. water mite diet isolate 6284-BHL032417-GBD4519_15743-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACAATATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAAATAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTGTTACCCCCCTCACTTACTCTACTTCTATCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609230 Chironomus sp. water mite diet isolate 6294-BHL032417-GBD25296_13247-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAACTAGGACGACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGTTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTACTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609231 Chironomus sp. water mite diet isolate 6399-BHL032417-GBD22650_4858-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGAATTGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCTCTTGACATGGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCAAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609232 Chironomus sp. water mite diet isolate 6429-BHL032417-GBD9616_21670-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAAATAGGACGACCCGGAACTTTCATGGGAGATGACCAAATTTATAATGTTGTAGTAACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTAAAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTCCTTCATTCTAGTCCTTTCGAAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609233 Chironomus sp. water mite diet isolate 6455-BHL032417-GBD23598_26365-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATGCCTATTCGAGCAGAAATAGGACGACCCGGAACTGTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAAATGGAGGATTCGGAAACTGACTTGTCCCATTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGGATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609234 Chironomus sp. water mite diet isolate 6477-BHL032417-GBD10910_22984-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGCCTTTTCCTCGCATAAATAGTATAATTTTCTGACTTTTACCCCCCTCTCTTACACGTCTTCTGTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609235 Chironomus sp. water mite diet isolate 6483-BHL032417-GBD24553_13313-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGTATGCTTATTCGAGCAGAACTACGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACGAGTTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCACTAACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609236 Chironomus sp. water mite diet isolate 6530-BHL032417-GBD14209_28908-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCCCTTGACCTGGCCTTTCCCCCAATAAATAGTAAAAGTTTCCGACCTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609237 Chironomus sp. water mite diet isolate 6531-BHL032417-GBD25999_7805-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATACTTATTCGAGCAGAAATAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGGTTCGGAAACTGACTAGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609238 Chironomus sp. water mite diet isolate 6545-BHL032417-GBD21203_23118-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAAATTATAATGTTGTAGTTACTGCACATGCCTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCAGCCACTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609239 Chironomus sp. water mite diet isolate 6558-BHL032417-GBD29139_16186-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAACTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTCTTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGAATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTACCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCGCTCTTACTCTTCTTCTGTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609240 Chironomus sp. water mite diet isolate 6570-BHL032417-GBD12197_11043-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAAATGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCAGACATAGCTTTTCCTCGAATAAATAGTATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609241 Chironomus sp. water mite diet isolate 6594-BHL032417-GBD9831_24574-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGTGAACTTCCTTGAGAATGCTTATTCGAGCAGAAATAGGACGACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAAACTGACTTGTCCTCCTAATACTTGGAGCACGTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609242 Chironomus sp. water mite diet isolate 6595-BHL032417-GBD17312_18559-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCTGAATTGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTATTACCCCCATCTCTTACTCTACTTCTTTTTACTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609243 Chironomus sp. water mite diet isolate 6614-BHL032417-GBD21055_24025-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACCTTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATGCTTATTCGAGCAAAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTATTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCACTAACTCTACTACTATCTAGTTCTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609244 Chironomus sp. water mite diet isolate 6748-BHL032417-GBD18074_17274-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTATAGTTACTGCACATGCTTATATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCCGACTTTTACCCCCCTCTCTTACCCTACCTCTATCTAGTTTATTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609245 Chironomus sp. water mite diet isolate 6756-BHL032417-GBD25911_7186-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATACGGACTAGTGGGAACTTCATTACGAATGCTTATTCGAGCGGCATTAGGACGACACGGAACTTTCATTGGCGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCGCTCTTACTCTTCCTCTTTCTAGTTTTTTGGTAGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609246 Chironomus sp. water mite diet isolate 6757-BHL032417-GBD11414_17570-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCAGACATAGCTTTTTCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTAACTCTTCCTCTTTCTAGTTTATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609247 Chironomus sp. water mite diet isolate 6785-BHL032417-GBD18898_14038-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGATGTAGTTACTGCACATGCTTATATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATATTATAAGTTCCTGACTTTTACCCCCCTCTCTTAAACTGCCTCGGTCTAGTTTTTTGGTAGAAAACGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609248 Chironomus sp. water mite diet isolate 6787-BHL032417-GBD5341_13708-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCTCATGCTTATATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTAGGAGCACCTGACATAGCTTTTCCTCGGATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCCTCTTTCTAGTTTATTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609249 Chironomus sp. water mite diet isolate 6791-BHL032417-GBD18318_8618-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTATATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGAATACTTCCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609250 Chironomus sp. water mite diet isolate 6793-BHL032417-GBD4325_18449-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACAAGCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTGTTACCCCCCTCACTTACTCTACCACTATCTAGATCATTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609251 Chironomus sp. water mite diet isolate 6805-BHL032417-GBD11920_5272-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTACACATGCTTGTATTATAATTTTTTTCATCGTTATACCCATTTCAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCCTCTTTCTAGTTTTTTGATAGTAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609252 Chironomus sp. water mite diet isolate 6808-BHL032417-GBD28821_14722-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTCGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCCGAATTAGGACAACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACCTCTTTCTAGTTGATTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609253 Chironomus sp. water mite diet isolate 6816-BHL032417-GBD29450_13729-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTCTAATGTTGTAGTTACTACACATGCTTATATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCGCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCGCGTACTCTTCCTCTTTCTAGTTTGTTGGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609254 Chironomus sp. water mite diet isolate 6823-BHL032417-GBD12258_22674-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGAAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTATATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAAGACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTTCCTCTTTATAGTAGAATGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609255 Chironomus sp. water mite diet isolate 6854-BHL032417-GBD26833_19922-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAATTACTGCACATGCTTATATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCTCGCTTACACTACCTCTGTCTAGTTTTTTGGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609256 Chironomus sp. water mite diet isolate 6856-BHL032417-GBD7145_16588-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCATGATCCGGAATAGTGGGAACTTCATTTAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAGATTTATAATGTTATAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCCTCTTTCTAGTGTATTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609257 Chironomus sp. water mite diet isolate 6860-BHL032417-GBD15442_27128-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTATATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCCTCTTTCTAGTTTTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609258 Chironomus sp. water mite diet isolate 6874-BHL032417-GBD17777_4061-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTCATACATTATTTTTGGGGTTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGTAACTTTCATTGTAGATGACCATATTTATAATGTTGTAGTTACTGCACATGCTTATATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACATGCCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTCCTCTTCCTCTTTCTAGTTTTTTGGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609259 Chironomus sp. water mite diet isolate 6880-BHL032417-GBD2836_17270-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGTACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGAACCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCGTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCCTCTAGCTAGGGGTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609260 Chironomus sp. water mite diet isolate 6917-BHL032417-GBD9422_8766-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACAAAGCTTTTCCACGAATAAATAATATAAGGTTCTGACTTTTACCCCCATCTCTTACTCTACCTCTTTCTAGGTGTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609261 Chironomus sp. water mite diet isolate 6929-BHL032417-GBD3218_15827-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTATATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCCTCTTTCTAGTTTTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609262 Chironomus sp. water mite diet isolate 6969-BHL032417-GBD20866_9666-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGCTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609263 Chironomus sp. water mite diet isolate 6972-BHL032417-GBD24103_18897-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609264 Chironomus sp. water mite diet isolate 6988-BHL032417-GBD21928_14073-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609265 Chironomus sp. water mite diet isolate 7049-BHL032417-GBD16511_9739-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCTCTCAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609266 Chironomus sp. water mite diet isolate 7054-BHL032417-GBD26213_18019-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTGTATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGAAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTATACCGCCCTCTCTTACTCTTCTTCTTTCCAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609267 Chironomus sp. water mite diet isolate 7055-BHL032417-GBD21814_23522-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACCTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCCGACTATTACCCCCCTCTCTTACTCTACTTCTTTCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609268 Chironomus sp. water mite diet isolate 7062-BHL032417-GBD19737_19786-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGTACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609269 Chironomus sp. water mite diet isolate 7065-BHL032417-GBD20433_2300-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATACGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTCTCTGACTTTTACCCCCCTCTCTAACTCTACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609270 Chironomus sp. water mite diet isolate 7072-BHL032417-GBD24057_17305-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATATTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGAACCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTTACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCACTAACTCTACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609271 Chironomus sp. water mite diet isolate 7168-BHL032417-GBD23331_20817-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCCTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGGATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTTCCTCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCCGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609272 Chironomus sp. water mite diet isolate 7170-BHL032417-GBD26207_13328-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTAACTCATCTTCTATCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609273 Chironomus sp. water mite diet isolate 7173-BHL032417-GBD14104_2601-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATATTTTATTTTTGGAGCTTGATCCGGAATGGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTATCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGCTTCTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609274 Chironomus sp. water mite diet isolate 7188-BHL032417-GBD11765_5548-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACAACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGAATTTGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTAACCCTACTACTTTCTAGTTCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609275 Chironomus sp. water mite diet isolate 7193-BHL032417-GBD16650_20565-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACTCCCCTCGCCTACTCAGCTTCTTTCTAGTTCGTGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609276 Chironomus sp. water mite diet isolate 7207-BHL032417-GBD22534_3858-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCACTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATGGCTTTTCCACGAATAAATAATATAAGATTCCGACTTTTACCCCCCTCTCTTACTCTACTACTTTCTAGTGCAGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609277 Chironomus sp. water mite diet isolate 7214-BHL032417-GBD21479_23862-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTATTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTGGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTCTACCCCCCTCTCTGACTCTTCTACTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609278 Chironomus sp. water mite diet isolate 7219-BHL032417-GBD27571_22320-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTAATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTGCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTATTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609279 Chironomus sp. water mite diet isolate 7233-BHL032417-GBD21787_18105-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAGTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTTGTTCCCCTGATACTTGGAGCACCAGACATAGCTCTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTACTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609280 Chironomus sp. water mite diet isolate 7239-BHL032417-GBD24496_24227-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCGCGAATAAATAATATAAGATTCTGACTATTACCCCCCTCTCTAACCCTACTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609281 Chironomus sp. water mite diet isolate 7253-BHL032417-GBD27437_7833-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGGACTTCATTAAGAATGCTTATTTGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATATTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609282 Chironomus sp. water mite diet isolate 7264-BHL032417-GBD23805_16703-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACCTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTTCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTATACCGCCCTCTCTTACGCTTCTTCTTTCCAGTTCGTTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609283 Chironomus sp. water mite diet isolate 7286-BHL032417-GBD24132_13231-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGTGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCTTAATACTTGGAGTACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTACTTTCAAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609284 Chironomus sp. water mite diet isolate 7289-BHL032417-GBD20522_8880-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGATCTTTATACATTATTTTTGGTGCCTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCTAGCAGAATTAGGACGTCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTGGTTACTGCACATGCTTTTATTATAATTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609285 Chironomus sp. water mite diet isolate 7300-BHL032417-GBD23855_14344-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCCTGATCCGGAATAGTGGGTACTTCATTAAGAATGTTTATTCGAGCAGAATTCGGACGCACCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTAACTCTACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609286 Chironomus sp. water mite diet isolate 7321-BHL032417-GBD11276_5472-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGATCTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTTTCTACTTCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609287 Chironomus sp. water mite diet isolate 7339-BHL032417-GBD23506_15851-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCTAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTAACCCTACTACTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609288 Chironomus sp. water mite diet isolate 7345-BHL032417-GBD26038_18431-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGTGCTTGATCCGGAATAGTGGGAACTTCCTTAAGAATGCTTATTCGGGTAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACTCCCCTCTCTAACTCTTCTTCTTTCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609289 Chironomus sp. water mite diet isolate 7350-BHL032417-GBD23606_10573-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTTTACTTTATTTTTGGGACTTGATCCGGAATAGTGGGAACTTCATTAAGAATTCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTGTTACCCCCCTCACTAACTCTACTACTATCTAGATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609290 Chironomus sp. water mite diet isolate 7352-BHL032417-GBD9500_21011-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGTAGGATTTGGAAACTGACTCGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACTCCCCTCTCTAACACTACTACTTTCTAGAACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609291 Chironomus sp. water mite diet isolate 7372-BHL032417-GBD4200_17098-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATGCTTATTCGAGTAGAATTATGACGACCCGGAACTTTCTTTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTACCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTAACCCTACTACTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609292 Chironomus sp. water mite diet isolate 7373-BHL032417-GBD18229_7917-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTACACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAATTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAATCTGACTTCTCCCCCTGATACTTGGGGCACCTGACGTAGCTTTTCCTCGAATAAATAATATAAGTTTCTTACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609293 Chironomus sp. water mite diet isolate 7383-BHL032417-GBD26224_10434-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCTGTAATAATTGGAGCACCAGACATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTATTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609294 Chironomus sp. water mite diet isolate 7385-BHL032417-GBD10546_27367-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATGCTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGAAGATCAAATTTATAATGCTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACCCTACTTCTTTCTAGTGCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609295 Chironomus sp. water mite diet isolate 7409-BHL032417-GBD11396_23949-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGGCGCCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTATAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATATTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTATCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609296 Chironomus sp. water mite diet isolate 7427-BHL032417-GBD14395_3928-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTAGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCTGAACTTTCATTGGAGATGACCATATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTAGGAAACTGACTTGTCCCCCTGATACTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTCCTCCCCTCTCTTTCTCTTCTTCTTTCTAGTTCTTTCGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609297 Chironomus sp. water mite diet isolate 7438-BHL032417-GBD18750_13649-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGTACTTCATTATGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCACTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATAAAAGTGTCTGACTTTTACTCCCCTCTCTTACTCTACGTCATTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609298 Chironomus sp. water mite diet isolate 7440-BHL032417-GBD20569_27867-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGATCTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTACTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACCCTTCTTCTATCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609299 Chironomus sp. water mite diet isolate 7446-BHL032417-GBD3323_11808-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGAATACTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTTGTTCCCCTAATATTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTCCTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609300 Chironomus sp. water mite diet isolate 7449-BHL032417-GBD13853_9931-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTTACTGCTCATGTTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATAGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTCGGAGTACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609301 Chironomus sp. water mite diet isolate 7457-BHL032417-GBD23169_22017-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAACAGAATTAGGACTACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609302 Chironomus sp. water mite diet isolate 7459-BHL032417-GBD3636_16569-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTTGGAACTTCATTAAGAATGCTTATTTGAGCAGAATTAGGACGACACGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGGTTCCGAATTTTACCCCCCTCTCTTACTCTTCTTCTGGCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609303 Chironomus sp. water mite diet isolate 7460-BHL032417-GBD17627_5438-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTGTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCTTAACTTTCATTGGACATGACCAAATTTATAATGATGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTAGGACACTGACTTGTCCACCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609304 Chironomus sp. water mite diet isolate 7466-BHL032417-GBD5164_13760-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGGTTGATCCGGAATAGTGGGAACTTCATTTAGAATGTTTATTCGAGCTGAATTAGGACAACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTACACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTCAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCCGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609305 Chironomus sp. water mite diet isolate 7469-BHL032417-GBD27638_14102-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTTGTTCCCCTGATATTTGGGGCTCCTGACATGGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTGACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609306 Chironomus sp. water mite diet isolate 7478-BHL032417-GBD13727_6182-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCATTAACTTTTATTGGAGACGACCAAATTTATAATGTTGTAGTTACTGCACATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTAGGAAACTGACTAGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609307 Chironomus sp. water mite diet isolate 7490-BHL032417-GBD20235_5498-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGGGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAACAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACCCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609308 Chironomus sp. water mite diet isolate 7493-BHL032417-GBD12434_5572-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCAAACGGAATTAGGTCATCCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCGTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609309 Chironomus sp. water mite diet isolate 7497-BHL032417-GBD22258_10263-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCAATGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTACTAATAACTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609310 Chironomus sp. water mite diet isolate 7509-BHL032417-GBD7281_13304-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGTACTTCATTAAGAATGCTTATTCTAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATATCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATATTATAAGTTTCTGACTTTGACTCCCCTCTCTTACACTTCATCAATCTAGTGCTTGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609311 Chironomus sp. water mite diet isolate 7512-BHL032417-GBD24234_16414-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGAGCTTGAGCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATATTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCTTAATACTTGGAGCTCCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACCCTACTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609312 Chironomus sp. water mite diet isolate 7514-BHL032417-GBD22980_12099-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGAGCCGGTACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCTTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAACATAAGATTCTGACTTTTACCCCCCTCTCTTACACTACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609313 Chironomus sp. water mite diet isolate 7536-BHL040517-GBD15398_9862-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTAGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609314 Chironomus sp. water mite diet isolate 7574-BHL040517-GBD23425_12671-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTCACATAGCTTCTCCTCAAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609315 Chironomus sp. water mite diet isolate 7636-BHL040517-GBD3527_12206-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTCGGACTACCTGGTACTTTAATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609316 Chironomus sp. water mite diet isolate 7650-BHL040517-GBD16655_28433-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609317 Chironomus sp. water mite diet isolate 7666-BHL040517-GBD8890_10445-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCGGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTCACATAGCTTTTCCTCAAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609318 Chironomus sp. water mite diet isolate 7675-BHL040517-GBD15461_10481-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCTGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCATAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTCACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609319 Chironomus sp. water mite diet isolate 7695-BHL040517-GBD16255_11928-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACCCTTTACTTTATTTTTAGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGACCAAATTTATAAAGTTGTAGTTACTGCACATGCTTTTATTATAATCTTTTTCATAGTTATACCAATTTTAATCGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCCTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609320 Chironomus sp. water mite diet isolate 7711-BHL040517-GBD7531_11244-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAACTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCGCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTTACCCTACTTCTATCTAGATCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609321 Chironomus sp. water mite diet isolate 7712-BHL040517-GBD29201_18212-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAGATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTCATAGTTCTACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAACACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCATTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609322 Chironomus sp. water mite diet isolate 7748-BHL040517-GBD20801_23722-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACTTTATTTTTGGGGCTTGGTCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCCCCTAATACTTGGAGCACCTCACATAGCTTTTCCTCGAATAAATAACATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTATCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609323 Chironomus sp. water mite diet isolate 7759-BHL040517-GBD28280_18226-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGTAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCTCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCCACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609324 Chironomus sp. water mite diet isolate 7760-BHL040517-GBD14936_21270-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTATCATTGGAGATGATCAAATTTATAATGTTATTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTGACTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609325 Chironomus sp. water mite diet isolate 7777-BHL040517-GBD17465_12320-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAATTACTCCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTTACTTGTCCCCCTAATACTTGGATCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609326 Chironomus sp. water mite diet isolate 7779-BHL040517-GBD20972_12868-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTGTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATTCTTATTCGAGCAGAATTAGGGCGACCCGGAACTTTGATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609327 Chironomus sp. water mite diet isolate 7781-BHL040517-GBD2153_13952-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGTAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTCCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTAGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACCCTACTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609328 Chironomus sp. water mite diet isolate 7793-BHL040517-GBD23742_12824-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGCACTTCATTAAGAATGTTTATTCGACTAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTGTTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCACTTACCCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609329 Chironomus sp. water mite diet isolate 7807-BHL040517-GBD12601_21376-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGACTTTATACATTATTTTTGGGGCCTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATCTTTTTCATAGTTATACCAATTTTAATCGGAGGTTTCGGAAACTGACTTGTCCCCCTAAAACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCTCCTTCTCTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609330 Chironomus sp. water mite diet isolate 7819-BHL040517-GBD24612_22233-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATCTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609331 Chironomus sp. water mite diet isolate 7844-BHL040517-GBD13435_8279-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTTATTAAGAATGTTTATTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCAGTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609332 Chironomus sp. water mite diet isolate 7846-BHL040517-GBD13098_9342-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCGTTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTTTTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTACTACTTTCTAGTGCTGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609333 Chironomus sp. water mite diet isolate 7865-BHL040517-GBD26945_9012-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGCTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTTACATAGCTTTTCCTCAAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609334 Chironomus sp. water mite diet isolate 7866-BHL040517-GBD4139_9782-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAAATTTCATTGGAGATGACCAAATTTATAATGTTTTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTTCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTAGAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609335 Chironomus sp. water mite diet isolate 7872-BHL040517-GBD10733_11968-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTAATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTAACCCCTCTTCTATCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609336 Chironomus sp. water mite diet isolate 7875-BHL040517-GBD10663_12803-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGCCTTTATATATTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGCCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATCTTTTTCATAGTTATACCAGTTTTAATCGGAGATTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609337 Chironomus sp. water mite diet isolate 7881-BHL040517-GBD22437_15674-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCACTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTAATCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609338 Chironomus sp. water mite diet isolate 7882-BHL040517-GBD26409_8557-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTTTACTTTATTTTTGGGGCTTGATCCGGAATAGTTGGAACTTCATTAAGAATTCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTAACTCCACTGCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609339 Chironomus sp. water mite diet isolate 7887-BHL040517-GBD8004_19592-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTGCATTGTACTTCATTGTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAATTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTGTACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609340 Chironomus sp. water mite diet isolate 7892-BHL040517-GBD23050_16048-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCCCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTATCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609341 Chironomus sp. water mite diet isolate 7897-BHL040517-GBD19151_13506-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609342 Chironomus sp. water mite diet isolate 7906-BHL040517-GBD6241_8473-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTGGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACTCTGAACTGTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGTTTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCGCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609343 Chironomus sp. water mite diet isolate 7913-BHL040517-GBD11766_16591-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTCCTCCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTGCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609344 Chironomus sp. water mite diet isolate 7916-BHL040517-GBD20352_17056-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATCACCAATTTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTATAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAACACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609345 Chironomus sp. water mite diet isolate 7942-BHL040517-GBD11591_24054-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATGCTTATTCGAGCAGAATTATGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCCTAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTATCCCCCTAATACTTGGAGCACCTCACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTGCAGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609346 Chironomus sp. water mite diet isolate 7953-BHL040517-GBD22199_25552-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTTGGAACTTTATTAAGAATTCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATCGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATTATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACATGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTTGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCGTTCTAGTTCTTTCATAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609347 Chironomus sp. water mite diet isolate 7957-BHL040517-GBD16069_13650-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATGGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGAATTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCACGAATAAATAATATAAGATTCCGACTATTACCCCCCTCTCTTACTCTACTTCTTTCTAGTGCTGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609348 Chironomus sp. water mite diet isolate 7961-BHL040517-GBD13255_18037-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGATTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGTCTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609349 Chironomus sp. water mite diet isolate 7976-BHL040517-GBD2798_16518-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTGGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGGATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGTACCTCACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609350 Chironomus sp. water mite diet isolate 7987-BHL040517-GBD26293_20205-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTACTTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTCACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTATCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609351 Chironomus sp. water mite diet isolate 7991-BHL040517-GBD29052_17893-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGTGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGAACCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTCCCACTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609352 Chironomus sp. water mite diet isolate 8009-BHL040517-GBD23148_23253-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTCGTTCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609353 Chironomus sp. water mite diet isolate 8010-BHL040517-GBD24351_15522-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGAAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATACTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAAGTGACTTGTCCCCCTAATACTTGGAGCACTTCACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609354 Chironomus sp. water mite diet isolate 8019-BHL040517-GBD21509_8338-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGTACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGAATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCCGACTATTACCCCCCTCGCTAACTCTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609355 Chironomus sp. water mite diet isolate 8033-BHL040517-GBD13693_5439-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCCTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609356 Chironomus sp. water mite diet isolate 8040-BHL040517-GBD14976_7795-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGTCTTTATACGTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAGGAATGCTTATTCGAGCAGTATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATCTTTTTCATAGTTATACCAATTTTAATCGGAGGTTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTTGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTGGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609357 Chironomus sp. water mite diet isolate 8058-BHL040517-GBD22337_21609-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGTTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGATCAAATTTATAATGTTATAGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCTCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609358 Chironomus sp. water mite diet isolate 8065-BHL040517-GBD21262_20061-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGCACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATCGGAGGTTTCGGAAACTTACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTATTACGCCCCTCTCTTACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609359 Chironomus sp. water mite diet isolate 8084-BHL040517-GBD10668_26187-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATATTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTCTTACCCCCCTCTCTTACTCTTCTTCTTTCCAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609360 Chironomus sp. water mite diet isolate 8086-BHL040517-GBD19905_2312-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCAGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATATTTTTTCTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTCTCCCCCTAATACTTGGAGCACCCGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACATTTACCCCCCTCTCTTACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609361 Chironomus sp. water mite diet isolate 8099-BHL040517-GBD8346_16740-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCAGGAATAGTAGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACGGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCCACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609362 Chironomus sp. water mite diet isolate 8100-BHL040517-GBD8522_5249-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609363 Chironomus sp. water mite diet isolate 8101-BHL040517-GBD3689_20007-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTTGGAACTTCATTAAGAATGCTAATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTCCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCACTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACACTACTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609364 Chironomus sp. water mite diet isolate 8105-BHL040517-GBD13288_16627-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTTGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGATTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTAATGCACATGCTTTTATTATAATTTTTTTCGTAGTTATACCAACTTTAATTAGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAATACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATTGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609365 Chironomus sp. water mite diet isolate 8107-BHL040517-GBD19152_21393-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGAATTGTTCCTCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609366 Chironomus sp. water mite diet isolate 8115-BHL040517-GBD23136_19649-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATGCTTATTCGAGTAGAATTATGACAACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTCACATAGCTTTTCCTCAAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609367 Chironomus sp. water mite diet isolate 8122-BHL040517-GBD18156_25506-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTATGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTACCCCTAATACTTGGAGCACCAGACATAGCATTTCCCCGAATAAATAATATAAGATTCTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609368 Chironomus sp. water mite diet isolate 8125-BHL040517-GBD10478_19985-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTAACTCTACTACTTTCTAGTTCTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609369 Chironomus sp. water mite diet isolate 8137-BHL040517-GBD25059_9707-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATCTTTTTCATAGTTATACCAATTTTAATCGGAGGTTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCCTACACATCTTCAATCTAGTGCTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609370 Chironomus sp. water mite diet isolate 8139-BHL040517-GBD10749_5528-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCTTGATCTGGTATAATAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTTGAGGGTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAACTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCTCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609371 Chironomus sp. water mite diet isolate 8143-BHL040517-GBD5794_17932-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTTATTGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609372 Chironomus sp. water mite diet isolate 8149-BHL040517-GBD20421_20359-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGTTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609373 Chironomus sp. water mite diet isolate 8160-BHL040517-GBD15699_11279-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAGTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGTAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGTACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609374 Chironomus sp. water mite diet isolate 8184-BHL040517-GBD15912_12352-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCTGAATTAGGACAACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTCTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTAGATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609375 Chironomus sp. water mite diet isolate 8191-BHL040517-GBD9648_7232-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCATGATCCGGAATAGTGGGAACTTCTTTAAGAATGCTTATTAGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTATTACCCCCCTCTCTTACACTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609376 Chironomus sp. water mite diet isolate 8193-BHL040517-GBD19924_9800-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAACAGTGGGAACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCTCCAGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609377 Chironomus sp. water mite diet isolate 8217-BHL040517-GBD4299_20506-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGAGCTTGATCCGGAATAGTAGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGATGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTGTTATAATTTTTTTCATAGTTATATCAATTTTAATTGGAGGATTTGGAAACTGATTTGTCCCCCTAATACTTGGAGCCCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTCTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609378 Chironomus sp. water mite diet isolate 8218-BHL040517-GBD24212_14881-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGTACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTTGTCCCCCTAATACTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTAACAATACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609379 Chironomus sp. water mite diet isolate 8220-BHL040517-GBD26163_15152-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTATAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTATTACCCCCCTCTCTTACACTACTACTATCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609380 Chironomus sp. water mite diet isolate 8225-BHL040517-GBD24475_14237-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGAAACTTCATTAAGAATGCTTGTTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACATGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAATACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609381 Chironomus sp. water mite diet isolate 8239-BHL040517-GBD9328_9355-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGCACTTTTTTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCAGAAACTGACATGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACCCTTCTTCTATCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609382 Chironomus sp. water mite diet isolate 8241-BHL040517-GBD3077_18792-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATCTTTTTCATAGTTATACCAATTTTAATCGGAGGTTTCGGAAACTGACTTATCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCT-TTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609383 Chironomus sp. water mite diet isolate 8260-BHL040517-GBD27969_16289-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACTACCAGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTAGTACCCCTAATACTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609384 Chironomus sp. water mite diet isolate 8268-BHL040517-GBD5429_18274-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGGGCCTGATCGGGGTTAGTAGGGACATCCCTAAGAATACTAATTTGTGCTAAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGTCTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCATACTCCTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609385 Chironomus sp. water mite diet isolate 8272-BHL040517-GBD26341_7925-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCTTTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTTTCTAATGCAGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609386 Chironomus sp. water mite diet isolate 8273-BHL040517-GBD27607_8933-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAACTAGGACGACCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCTCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTTCCTCCCTCTCTTACTCTTCTTCTTTCTAGTACTTTCGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609387 Chironomus sp. water mite diet isolate 8275-BHL040517-GBD5096_9356-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCCGGAACAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTTGTTCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609388 Chironomus sp. water mite diet isolate 8280-BHL040517-GBD17647_9736-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGTGCTTGATCCGGAATAGTGGGACCTTTATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTTACATGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTTCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609389 Chironomus sp. water mite diet isolate 8281-BHL040517-GBD26228_9800-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCCTTAAGAATGTTTATTCGAGCAGAATTAGGACGACCTGGAACTTTCATTTGAGATGACCAAATTTATAATGTTGTAGTTACTGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCAGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609390 Chironomus sp. water mite diet isolate 8285-BHL040517-GBD20864_6789-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGGGCCTGATCTGGGATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTAGAGATGACCAAATTTATAAAGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTCACATAGCTTTTCCTCAAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTTTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609391 Chironomus sp. water mite diet isolate 8291-BHL040517-GBD20738_15144-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTCGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGATGATCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTTGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCGCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609392 Chironomus sp. water mite diet isolate 8294-BHL040517-GBD28426_10356-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTCATTGGGGATGATCAAATTTATAATGTTGTAGTTACTCCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609393 Chironomus sp. water mite diet isolate 8296-BHL040517-GBD17188_27486-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCACCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609394 Chironomus sp. water mite diet isolate 8312-BHL040517-GBD12852_6363-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCCTTTACTTTATTTTTAGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTTGAGATGACCAAATTTATAATATTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGGTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACATTTACCTCCCCCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609395 Chironomus sp. water mite diet isolate 8318-BHL040517-GBD13344_6927-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAGTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTGTAGTTATACCAATTTTAATTGGAGAATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGCTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609396 Chironomus sp. water mite diet isolate 8321-BHL040517-GBD21257_18976-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAGGAATGCTTATTCGAGCAGAATTAGGACGAGCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCTCTAATACTTGGAGCACCTGACATAGCTTTTCCACGAATAAATAATATAAGTTTCCGACTGTTACCCCCCTCTCTTACTCTACTACTATCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609397 Chironomus sp. water mite diet isolate 8325-BHL040517-GBD26574_11769-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGTGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATGTAAGTTTCCGACTTTTACCCCCCTCTCTGACTCTTCTACTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609398 Chironomus sp. water mite diet isolate 8329-BHL040517-GBD2126_18676-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGTACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCT-TTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609399 Chironomus sp. water mite diet isolate 8337-BHL040517-GBD14583_8945-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTGTTGGGGCTTGATCCGGAATAGGTGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACAACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTATAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTTACTCTACTTCTTTCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609400 Chironomus sp. water mite diet isolate 8339-BHL040517-GBD7641_21840-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGTGAACTTCATTAAGAATGCTTATTCGAGCAGCATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTACCGACTTTGACCCCCCGCTCCTACACTACTTCTGTCTAGTGCTTGCGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609401 Chironomus sp. water mite diet isolate 8340-BHL040517-GBD14175_10973-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCAATAAGAATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTGTCCCACGAATAAGTAATATAAGTTTCTGACTATTACCTCCTTCTCTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID JF412084, identified in GenBank as Chironomus javanus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609402 Chironomus sp. water mite diet isolate 8343-BHL040517-GBD7936_10520-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTTATTAAGAATGCTTATTCGAGCAGAATTAGGACAACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCAGATGCTTTTATTATAATTTTTTTCCTAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACATGTCCCCCTAATACTTAGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTTTCTAGTGCTTTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609403 Chironomus sp. water mite diet isolate 8351-BHL040517-GBD11352_26224-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAGTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCGTAGTTATACCAATTTTAATTGTAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGTACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATCACCTCCTTCTCTAACCCTTCTTCTTTCTAGATTAGTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609404 Chironomus sp. water mite diet isolate 8354-BHL040517-GBD23782_6215-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTGTTGGGGCTTGATCCGGAATATTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTCTCATTAGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTAACTATACTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609405 Chironomus sp. water mite diet isolate 8357-BHL040517-GBD18431_23792-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGAGGCTTGATCCGGAATAATGGGAACTTCATTAAGTATGCTTATTCGATCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTCTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCTAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTACTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609406 Chironomus sp. water mite diet isolate 8411-BHL101416-GBD16269_13320-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGATCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTCTTGACTTCTTCCCCCATCCTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609407 Chironomus sp. water mite diet isolate 8431-BHL101416-GBD26142_15418-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTCGTCCCCCTAATACTTGGAGCACCTGACGTAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGCTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609408 Chironomus sp. water mite diet isolate 8450-BHL101416-GBD15524_11889-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACACTATTTCTGGGACTTCATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGAACAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTTTAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609409 Chironomus sp. water mite diet isolate 8462-BHL101416-GBD17859_3717-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGAGCTTGATCCGAAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGAGCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609410 Chironomus sp. water mite diet isolate 8463-BHL101416-GBD16515_4533-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACGTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACATCATTAAGAATGCTTGTTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAAGTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTCGTCCCCCTAATACTTGGAGCACCTGACGTAGCTTTTCCTCGAATAAACAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609411 Chironomus sp. water mite diet isolate 8466-BHL101416-GBD8308_18984-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACACTATACTTTATTTTTGGAACTCGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTACACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGATCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTCTTGACTTCTCCCCCCATCCTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.4% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609412 Chironomus sp. water mite diet isolate 8468-BHL101416-GBD7843_9308-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTTCCTTTAATATTAGGAGCCCCAGATATGGCCTTCCCTCGAATAAATAATAAAAGATTTTGACTACTCCCCCCATCTTTAACATTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609413 Chironomus sp. water mite diet isolate 8476-BHL101416-GBD24323_6075-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGGGGCTTCATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCTCTAATGCTTGGAGCACATGACATAGCTTTTCCACGAATAAATAATATAAGTTTCTGACTGTTACCCCCCTCTCTTACTCAACTACTATCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609414 Chironomus sp. water mite diet isolate 8482-BHL101416-GBD17843_19969-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAACTGGAGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGTTCTTTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609415 Chironomus sp. water mite diet isolate 8485-BHL101416-GBD14782_4927-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCCAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609416 Chironomus sp. water mite diet isolate 8494-BHL101416-GBD9211_19362-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTACAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTAATACCTATTTTAATTGGGGAATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTAGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609417 Chironomus sp. water mite diet isolate 8499-BHL101416-GBD20984_27653-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGTAATTGATTACTACCTCTAATATTAGGAGCCCCTGATATAACATTTCCTCGAATAAATAATATAAGATTTTGATTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609418 Chironomus sp. water mite diet isolate 8501-BHL101416-GBD19763_17372-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCTTTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCTTTTAATATTAGGAGCTCCAGATATAGCCTTCCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCATCTTTAACCCTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609419 Chironomus sp. water mite diet isolate 8508-BHL101416-GBD8964_19142-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGAAGCACCTGACATAGCTTTTCCTAGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609420 Chironomus sp. water mite diet isolate 8515-BHL101416-GBD25268_5294-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCGGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTGTAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTAGTGCCATTAATATTAGGAGCACCTGATATGGCATTTCCTCGAATAAATAATACAAGATTTTGACTTTTA-CCCCCTCCCTTAACATTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609421 Chironomus sp. water mite diet isolate 8520-BHL101416-GBD21771_11617-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTAGTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAACACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTCTTTGACTTTTACCCCCTTCTTTAACTTTACTTCTTTCTAGATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609422 Chironomus sp. water mite diet isolate 8525-BHL101416-GBD20995_22929-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCGGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609423 Chironomus sp. water mite diet isolate 8528-BHL101416-GBD21252_3092-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACCTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACATGGTACTTTTATTGGAGATGACCAAATCTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACATGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609424 Chironomus sp. water mite diet isolate 8530-BHL101416-GBD14974_19719-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGATATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGGAAACTAACTTGT-CCCATAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCTCTCTTACTCTACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609425 Chironomus sp. water mite diet isolate 8535-BHL101416-GBD17315_22665-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACCTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATCTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGATCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTCTTGACTTCTCCCCCCATCCTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609426 Chironomus sp. water mite diet isolate 8536-BHL101416-GBD24983_16674-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTCTGGGGCTTCACCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTTCTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATGCTAGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTGACTCATCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609427 Chironomus sp. water mite diet isolate 8556-BHL101416-GBD12876_26079-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGGTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGATGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.1% identical to accession ID GU944724, identified in GenBank as Chironomus circumdatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609428 Chironomus sp. water mite diet isolate 8558-BHL101416-GBD4880_13488-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGGTTTTATTATAATTTTTCTCATAGCTATACCAATTTTAATTGGAGGGTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCCCCTGATATAGCATTTCCTCGAATAAATAAAATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTGCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609429 Chironomus sp. water mite diet isolate 8572-BHL101416-GBD25259_25301-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGGGGCTTCATCCGGAATAGTGGGAACTTCATTAAGCATGCTTATTCGAGCAGAATTAGGACGAACAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGACTAAATAATATAAGTTTCTTACTTTTACCCCCCACTCTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609430 Chironomus sp. water mite diet isolate 8581-BHL101416-GBD19768_14970-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACAGCTCATACTTTTTTTATAATTTTTTTCATAGTTATACCAATTTTAATTGGGGGATTCGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609431 Chironomus sp. water mite diet isolate 8584-BHL101416-GBD3457_20840-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACGTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTGTTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCCTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTGGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTTATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTTGCTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAAAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609432 Chironomus sp. water mite diet isolate 8599-BHL101416-GBD14760_23246-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGATGAATTAGGTCACCCAGGAACTTTAATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGAAGGATTCGGAAACTGACTTGTCCCCCTAATACTTAGAACACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609433 Chironomus sp. water mite diet isolate 8614-BHL101416-GBD24434_14820-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCTTTAGAATATTAATTCGAGCAAAATTAGGACATCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGATTTCTCCCCCCATCTTTAACTCTTTTACTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609434 Chironomus sp. water mite diet isolate 8624-BHL101416-GBD8124_22916-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAATAGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGATCCGGAACTTTCGTTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCACTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609435 Chironomus sp. water mite diet isolate 8625-BHL101416-GBD12059_7096-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACGTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTGTTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTCGTCCCCCTAATACTTGTAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609436 Chironomus sp. water mite diet isolate 8629-BHL101416-GBD25232_7134-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAAGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATCTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAATTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609437 Chironomus sp. water mite diet isolate 8633-BHL101416-GBD8671_23795-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGGGGCTTCATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTCTTGACTTCTCCCCCCATCCTTAACACTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609438 Chironomus sp. water mite diet isolate 8634-BHL101416-GBD11339_11257-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACATTATATTTTATTTTTGGAGCTTGATCAGGTATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGCACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTATTGACTTCTCCCCCCATCTTTAACTCTTTTCTTTCTAGTTCATGAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609439 Chironomus sp. water mite diet isolate 8640-BHL101416-GBD16651_2382-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTGGAGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAACGTTGTAGTTACTGCACATGGTTTTATTATAATTTTTCTCATAGGTATACCAATTTTAATTGGAGGGTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGCTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609440 Chironomus sp. water mite diet isolate 8642-BHL101416-GBD25724_14138-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGTATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTACTCCCCCCATCATTAACACTTTTTCTTTCTAGTTCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609441 Chironomus sp. water mite diet isolate 8649-BHL101416-GBD26454_6921-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGCTCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGATGATCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAAAAAATAATATAAGTGTCTGACTTTTACCCCCCACTCTTACTCATCTACTTTCTAGTTCTTTCGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609442 Chironomus sp. water mite diet isolate 8652-BHL101416-GBD3032_12356-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAACTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTGCCATTAATATTAGGAGCACCTGATATGGCATTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCTTCCTTAACATTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609443 Chironomus sp. water mite diet isolate 8660-BHL101416-GBD7541_22684-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGACACCCAGGAACTTTAATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATACGGAAACTGACTTGTTCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCCTCTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609444 Chironomus sp. water mite diet isolate 8662-BHL101416-GBD12687_18192-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGAAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGATCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGACTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCCCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTATCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609445 Chironomus sp. water mite diet isolate 8669-BHL101416-GBD25424_17514-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGGACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTCTCCCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCTCCTAATACTTGGAACACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCGTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609446 Chironomus sp. water mite diet isolate 8672-BHL101416-GBD27489_16912-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCTGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGATGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGTAGTTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609447 Chironomus sp. water mite diet isolate 8683-BHL101416-GBD24059_25224-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGGGGCTTCATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAAGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTGATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCACTTACCCATCTTCTATCTAGATCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609448 Chironomus sp. water mite diet isolate 8685-BHL101416-GBD26839_23827-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATTCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGTACTTTCATTGGAGATGACCAAATTTATAATGTTATAGTTACTGCACATGCTGTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCATCTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609449 Chironomus sp. water mite diet isolate 8689-BHL101416-GBD18073_24778-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTGGAGCTTGATCCGAAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGATCCGGAACCTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCGGATAAAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609450 Chironomus sp. water mite diet isolate 8690-BHL101416-GBD10227_21132-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGAAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGTATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATGGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609451 Chironomus sp. water mite diet isolate 8704-BHL101416-GBD13480_8784-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGAACAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACATGGCATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCTCCTCTCTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609452 Chironomus sp. water mite diet isolate 8705-BHL101416-GBD28059_10714-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGTACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609453 Chironomus sp. water mite diet isolate 8715-BHL101416-GBD27040_7213-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGGGGCTTCATCCGCAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCTGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTAATACCAGTTTTAATTGGAGGATTCGGAAACTGATTTGTACCCCTAATACTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTGGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609454 Chironomus sp. water mite diet isolate 8716-BHL101416-GBD3349_9093-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTCCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCACCCAGCTTTAACCCTTCTT-TTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609455 Chironomus sp. water mite diet isolate 8717-BHL101416-GBD4970_18887-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAGTGTTGTAGTTACTGCACATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCAAATAAACAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609456 Chironomus sp. water mite diet isolate 8725-BHL101416-GBD28785_14026-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATAGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTCTACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGATCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTAACTCTACTACTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609457 Chironomus sp. water mite diet isolate 8747-BHL101416-GBD21623_19146-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTTTACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAATTAGTACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTATAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCTCTCTTACACTTCATCATGCTAGTTCTTTCGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609458 Chironomus sp. water mite diet isolate 8779-BHL101416-GBD16640_16587-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGAATTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTCCCACTAATACTGGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609459 Chironomus sp. water mite diet isolate 8780-BHL101416-GBD20276_10804-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACCTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTTTAGTTACTGCACATGGTTTTATTATAATTTTTCTCATAGTTATACCAATTTTAATTGGAGGGTGCGGAAACTGACTCGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCATTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609460 Chironomus sp. water mite diet isolate 8782-BHL101416-GBD5635_6172-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTCCCCCTAATATTGGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609461 Chironomus sp. water mite diet isolate 8787-BHL101416-GBD10605_4100-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCCGAATAGTGGGAACTTCATTAAGCATACTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGGTTTTATTATAATTTTTCTCATAGTTATACCAATTTTAATTGGAGGGTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAGGCTTCTGACTTTTATCCCCCTCTCTTACTCTTCTTCGTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609462 Chironomus sp. water mite diet isolate 8791-BHL101416-GBD11800_3162-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACATTATATTTTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTTGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCATCTTTAACTCTTTTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609463 Chironomus sp. water mite diet isolate 8792-BHL101416-GBD25441_5489-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCTTTTAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAATTTTAATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609464 Chironomus sp. water mite diet isolate 8801-BHL101416-GBD11653_16331-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGGTTTTATTATAATTTTTCTCATAGTTATACCAATTTTAATTGGGGGGTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATGAGCTTCTGATTTTTACCCCCATCTCTTACACTACTTCTGTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609465 Chironomus sp. water mite diet isolate 8804-BHL101416-GBD6320_8262-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAACACCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTACTACCATCTAGTACACTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609466 Chironomus sp. water mite diet isolate 8805-BHL101416-GBD24811_16294-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACCTGATCAGGAATAGTAGGAACTTCCCTTAGAATACTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCCTCTTTAACTCTTTTTCTTTCTAGTACATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609467 Chironomus sp. water mite diet isolate 8807-BHL101416-GBD6204_11805-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTATGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTATCCCCCTAATACTTGGAACACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTACTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609468 Chironomus sp. water mite diet isolate 8810-BHL101416-GBD12610_22269-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGTGGCTTGATCCGAAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGATCCGGAACTCTCATTGAAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTGTAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATCTGGAAACTGACATGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609469 Chironomus sp. water mite diet isolate 8823-BHL101416-GBD12498_28645-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACATTATATTTTATTTTTGGAGCTTGATCTGGTATAATAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCTTTTAATATTAGGAGCACCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGTGCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.4% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609470 Chironomus sp. water mite diet isolate 8828-BHL101416-GBD7695_24736-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCGCCCCCCATCTTTAACACATTTTCTATATAGTGCATTAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609471 Chironomus sp. water mite diet isolate 8832-BHL101416-GBD10836_12757-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCCTCATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCATCTCTTTCTCAACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609472 Chironomus sp. water mite diet isolate 8838-BHL101416-GBD11991_11288-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGAAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGTAGAATTAGGACGATCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGATGATTCGGATACTGACATGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609473 Chironomus sp. water mite diet isolate 8844-BHL101416-GBD16361_10366-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGTTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609474 Chironomus sp. water mite diet isolate 8847-BHL101416-GBD16979_2101-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGAAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGATCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAATTGGAGGATTCGGAAACTGACATGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609475 Chironomus sp. water mite diet isolate 8848-BHL101416-GBD8813_26484-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGGTTTTATTATAATTTTTCTCATAGTTATACCAATTTTAATTGGAGGGTTCGGAAACTGACTTGCTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGCATAAATAATATAAGCTTCTGACTTTTTCCCCCTCTCTTACTCAACCTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609476 Chironomus sp. water mite diet isolate 8851-BHL101416-GBD10909_17494-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCCGGAACTTTTATTGGTGATGCCCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATGATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATAGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCATCTTTAACTCTTTTTCTTTCTAGATCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609477 Chironomus sp. water mite diet isolate 8915-BHL032417-GBD2867_12592-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609478 Chironomus sp. water mite diet isolate 8922-BHL032417-GBD11726_4221-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTAGAACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCATTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTTACCCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609479 Chironomus sp. water mite diet isolate 8936-BHL032417-GBD9497_24760-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACCTCTTTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609480 Chironomus sp. water mite diet isolate 8956-BHL032417-GBD14201_5561-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTACTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGAATGGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609481 Chironomus sp. water mite diet isolate 8988-BHL032417-GBD7652_13067-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCTGGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTACACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609482 Chironomus sp. water mite diet isolate 9004-BHL032417-GBD9465_20885-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTGGCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609483 Chironomus sp. water mite diet isolate 9015-BHL032417-GBD19435_27591-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATGCTTATTCGAGCAGAATTAGGACAACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTACTACTTTCTAGTGCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609484 Chironomus sp. water mite diet isolate 9063-BHL032417-GBD28456_19262-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGTATAGTGGGAACTTCATTAAGAATGCTTATTCGAGTAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGAAAACTGACTTGTCCCTCTAATATTGGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTCCCCCCCTCACTAACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609485 Chironomus sp. water mite diet isolate 9085-BHL032417-GBD24369_14965-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGGTTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTTTTCCCCCCTCTATTACACTACTACTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609486 Chironomus sp. water mite diet isolate 9098-BHL032417-GBD14785_10772-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGCTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCACTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTTACACTTCATCATGCTAGTGCTTTCGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609487 Chironomus sp. water mite diet isolate 9103-BHL032417-GBD5433_12384-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACGTCCTTAAGTATATTAATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR756187, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609488 Chironomus sp. water mite diet isolate 9109-BHL032417-GBD6450_22782-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCCGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCACTTACTCTACTACTGTCTAGTTCTATCGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609489 Chironomus sp. water mite diet isolate 9117-BHL032417-GBD5747_12289-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGCCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTTCTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609490 Chironomus sp. water mite diet isolate 9186-BHL032417-GBD26773_10424-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGCATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTAATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCCCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTTCCCCCCTTACTTACTCTACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609491 Chironomus sp. water mite diet isolate 9195-BHL032417-GBD9155_24939-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAACTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACAGCACATGCTTTTGTTATAATTTTTTTCATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTTACTCTTCTACTATCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609492 Chironomus sp. water mite diet isolate 9204-BHL032417-GBD9536_22251-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTTGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTTTCTTACTCTTCTTCTGTCTAGTACGGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609493 Chironomus sp. water mite diet isolate 9206-BHL032417-GBD20545_17570-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGAATGCTTGTTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTGTTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609494 Chironomus sp. water mite diet isolate 9222-BHL032417-GBD26160_11466-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGTACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTACTACCCCCGTCACTAACTCTACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609495 Chironomus sp. water mite diet isolate 9231-BHL032417-GBD25556_23385-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTTGTCCCTCTAATACTTGGAGCTCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTAACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609496 Chironomus sp. water mite diet isolate 9252-BHL032417-GBD14010_28404-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACCTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTTCCCCTAATACTAGGAGCACCTGACATAGCTTTTCCCCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609497 Chironomus sp. water mite diet isolate 9315-BHL032417-GBD25470_8686-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTAATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGTCCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTTACTCTTCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609498 Chironomus sp. water mite diet isolate 9327-BHL032417-GBD9837_5170-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACTTTATTTTTGGTGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTTTCCCACTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609499 Chironomus sp. water mite diet isolate 9332-BHL032417-GBD18778_12446-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTTATTCGAGCAGAATTAGGCCGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTTACTTGTCCCCCTAATACTTGGTGCACCTGACATAGCTTTTCCCCCAATAAATAATATAAGGTTCTGACTTTTACCCCCCTTTCTTACTCTACTACTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609500 Chironomus sp. water mite diet isolate 9334-BHL032417-GBD4807_18922-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCCTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTTGTCCCCCTAATACTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTTCTACTTTCAAGTACATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609501 Chironomus sp. water mite diet isolate 9349-BHL032417-GBD9561_4911-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGAGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGCCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTATCTAGTTCTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609502 Chironomus sp. water mite diet isolate 9353-BHL032417-GBD10748_3134-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAACTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609503 Chironomus sp. water mite diet isolate 9364-BHL032417-GBD3680_14495-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTCGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCAACCCGGAACTTTCATTGGAGATGACCAACTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTCTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAACAATATAAGATTCTGACTTTTACCCCCCTTTCTTACTCTACTCCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609504 Chironomus sp. water mite diet isolate 9380-BHL032417-GBD28657_17509-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTCGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGTCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTTTACTATTATCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609505 Chironomus sp. water mite diet isolate 9397-BHL032417-GBD14901_22564-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAAAACTTGGACGACGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAGTTGTCACAGCGCACGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609506 Chironomus sp. water mite diet isolate 9413-BHL032417-GBD22209_4963-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGAGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTACACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCACTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCATCTCTTACTCTACTTCTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609507 Chironomus sp. water mite diet isolate 9439-BHL032417-GBD14996_16186-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACACTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTACATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609508 Chironomus sp. water mite diet isolate 9525-BHL032417-GBD6014_19542-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACCTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGGCCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAACTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609509 Chironomus sp. water mite diet isolate 9528-BHL032417-GBD4972_6953-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGTACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATACTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCAGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTGGTACCCCCCTTACTTACTCTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609510 Chironomus sp. water mite diet isolate 9532-BHL032417-GBD27014_12262-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACATTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCACGAATAAATAATATAAGATTCTGACTATTACCCCCCTCTCTTACTCTACTTCTTTCAAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609511 Chironomus sp. water mite diet isolate 9537-BHL032417-GBD27118_20928-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCAGGCTAACACATCATCAATCTAGTGCTTGCGTAGAAAATGGAGCTGAAAC	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609512 Chironomus sp. water mite diet isolate 9882-BHL040517-GBD14674_9901-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAGTAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAATCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609513 Chironomus sp. water mite diet isolate 9892-BHL040517-GBD16965_13670-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609514 Chironomus sp. water mite diet isolate 9907-BHL040517-GBD10787_10839-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609515 Chironomus sp. water mite diet isolate 9914-BHL040517-GBD25761_6973-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACATCTCACGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609516 Chironomus sp. water mite diet isolate 9921-BHL040517-GBD22766_3332-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAAGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAACAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609517 Chironomus sp. water mite diet isolate 9941-BHL040517-GBD19796_5071-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGCTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR756187, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609518 Chironomus sp. water mite diet isolate 9964-BHL040517-GBD22286_3119-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTGGTTACAGCTCGCGCATTTATTATAATTTTCTTTATAGTTATACCAACTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609519 Chironomus sp. water mite diet isolate 9976-BHL040517-GBD11442_26096-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATATTTTATTTTTGGAGCTTGATCGGGGATACTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609520 Chironomus sp. water mite diet isolate 9990-BHL040517-GBD27338_7543-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATACATTATTTTTGGGGCCTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTACACATGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCACCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609521 Chironomus sp. water mite diet isolate 9993-BHL040517-GBD14315_23885-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCCCTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAGTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATGAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609522 Chironomus sp. water mite diet isolate 9995-BHL040517-GBD18157_17385-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCATCTTCAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609523 Chironomus sp. water mite diet isolate 9997-BHL040517-GBD26786_22292-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTATCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCATAGAAAATGAAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609524 Chironomus sp. water mite diet isolate 10001-BHL040517-GBD24532_5803-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTATCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609525 Chironomus sp. water mite diet isolate 10003-BHL040517-GBD10744_12621-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATACGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609526 Chironomus sp. water mite diet isolate 10031-BHL040517-GBD16466_28424-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGTTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCATCTCTAACATTATTACTTTCGAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609527 Chironomus sp. water mite diet isolate 10041-BHL040517-GBD11868_6804-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTCATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCATCTCTAACATTATTACTTTCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609528 Chironomus sp. water mite diet isolate 10049-BHL040517-GBD21549_17353-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGTATAGTAGGAACTTCCCTTAGAATATTCATTCGAGCAGAATTAGGACGTCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATAGTTACAGCTCACGCATTTACTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609529 Chironomus sp. water mite diet isolate 10054-BHL040517-GBD8885_4422-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTTCATTATACTTCACTTTTGGTGACTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTGCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.1% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609530 Chironomus sp. water mite diet isolate 10058-BHL040517-GBD21433_8696-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTTGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609531 Chironomus sp. water mite diet isolate 10062-BHL040517-GBD25870_6196-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGTGCTTGATCCGGAATAGTTGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGATTTTATTATAATTTTTTTCTTAGGTATACCAGTTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACCTGACATAGCTTTTACTCGAATAAATAATATAAGTTTTTGATTATTACCTCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609532 Chironomus sp. water mite diet isolate 10070-BHL040517-GBD15794_5348-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTTGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTC-TATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609533 Chironomus sp. water mite diet isolate 10072-BHL040517-GBD18768_9919-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCTTAATACTTGGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTTACCCTTCTTCTATCAAGATCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609534 Chironomus sp. water mite diet isolate 10075-BHL040517-GBD16126_23758-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTGTATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATCAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609535 Chironomus sp. water mite diet isolate 10077-BHL040517-GBD13009_27260-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTATCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609536 Chironomus sp. water mite diet isolate 10084-BHL040517-GBD23057_11924-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTTTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID JF412084, identified in GenBank as Chironomus javanus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609537 Chironomus sp. water mite diet isolate 10089-BHL040517-GBD17723_13020-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609538 Chironomus sp. water mite diet isolate 10090-BHL040517-GBD7589_19412-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGCGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGTCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609539 Chironomus sp. water mite diet isolate 10091-BHL040517-GBD9128_11815-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609540 Chironomus sp. water mite diet isolate 10111-BHL040517-GBD13682_20647-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCGATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609541 Chironomus sp. water mite diet isolate 10119-BHL040517-GBD21173_26370-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCCAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609542 Chironomus sp. water mite diet isolate 10127-BHL040517-GBD12590_25997-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTCTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCCTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609543 Chironomus sp. water mite diet isolate 10157-BHL040517-GBD24777_17059-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGACTAGTGGGAACTTCATTAAGAATGCCTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGCGATGACCAAATTTATAATGTTGTGGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTACCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCATACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609544 Chironomus sp. water mite diet isolate 10191-BHL040517-GBD16639_10762-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCCTTAAGAATGCTTATTTGAGCAGAATTAGGACGCCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTCTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTATCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609545 Chironomus sp. water mite diet isolate 10200-BHL040517-GBD2056_17482-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609546 Chironomus sp. water mite diet isolate 10204-BHL040517-GBD21322_6299-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTATGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATTGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCACGCTTACTCAGCTTCTTTCTAGTACGTGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609547 Chironomus sp. water mite diet isolate 10207-BHL040517-GBD17602_15401-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609548 Chironomus sp. water mite diet isolate 10213-BHL040517-GBD10755_12980-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTTTAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGTGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCCTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609549 Chironomus sp. water mite diet isolate 10218-BHL040517-GBD22579_20802-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAGTAGTTACAGCTCGCGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCCTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609550 Chironomus sp. water mite diet isolate 10219-BHL040517-GBD18068_2060-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATTCTTATTCGAGCAGAATTAGGACGACCCGGATCTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTACTACTATCTAGATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609551 Chironomus sp. water mite diet isolate 10220-BHL040517-GBD6203_19392-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATAGTTACAGCTCACGCATTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAACATAAGATTTTGACTACTCCCACCATCTTTAACTCTACTTCTTTCTAGTACATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609552 Chironomus sp. water mite diet isolate 10223-BHL040517-GBD25415_15703-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCCTTAAGAATGTTTATTTGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTTCTACTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609553 Chironomus sp. water mite diet isolate 10230-BHL040517-GBD10718_24724-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATTCTTATTTGAGCAGAATTAGGACGACCGGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCCCCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609554 Chironomus sp. water mite diet isolate 10240-BHL040517-GBD18048_7588-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATCGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609555 Chironomus sp. water mite diet isolate 10292-BHL040517-GBD5523_16404-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGATCTTTATATTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCTTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACCCTTCTTCTATCTAGTTCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609556 Chironomus sp. water mite diet isolate 10302-BHL040517-GBD18487_21985-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTCGGTGTCTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATCCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGTCATAGCTTTTCCTCGAATAAATGATATAAGTTTCTGACTTTTACCCCCCGCTCTTACTCTACTTCATTCTAGTTCTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609557 Chironomus sp. water mite diet isolate 10304-BHL040517-GBD25564_14256-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGAACCGGATCTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGACTTATCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTACTATCTAGTTCTTTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609558 Chironomus sp. water mite diet isolate 10311-BHL040517-GBD3017_13324-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATGTTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGCTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTCTGACTACTACCACCTCCACTAATCCTATTAGCTTC-TTCTGCTGC---CGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609559 Chironomus sp. water mite diet isolate 10313-BHL040517-GBD22757_27424-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGGACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTAGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609560 Chironomus sp. water mite diet isolate 10333-BHL040517-GBD29135_12681-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCCTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTCGGTCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609561 Chironomus sp. water mite diet isolate 10343-BHL040517-GBD19377_2814-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAAAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCCCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609562 Chironomus sp. water mite diet isolate 10361-BHL040517-GBD23503_25509-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGTCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCTCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCACTAACTCTACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609563 Chironomus sp. water mite diet isolate 10383-BHL040517-GBD23244_7580-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTTCCCCCTCACTTACTCTACTACTTTCTAGTTCTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609564 Chironomus sp. water mite diet isolate 10399-BHL040517-GBD16629_7352-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATCGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTCGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCGCTTACACTTCATCAATCTAGTGCTTGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609565 Chironomus sp. water mite diet isolate 10405-BHL040517-GBD16250_9553-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609566 Chironomus sp. water mite diet isolate 10414-BHL040517-GBD20098_6098-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTATCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609567 Chironomus sp. water mite diet isolate 10417-BHL040517-GBD25237_25566-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAAAATTAGGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATAGTTACAGCTCATGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTACATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609568 Chironomus sp. water mite diet isolate 10421-BHL040517-GBD2038_15000-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTTGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTATACCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCACCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609569 Chironomus sp. water mite diet isolate 10426-BHL040517-GBD21175_23998-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAAAATTAGGACGTCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATGTAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609570 Chironomus sp. water mite diet isolate 10433-BHL040517-GBD25799_23790-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATACTTGGAGCACCCGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.4% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609571 Chironomus sp. water mite diet isolate 10461-BHL040517-GBD18952_3910-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTATCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCCTACCCTACTTCTTTCTACTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609572 Chironomus sp. water mite diet isolate 10467-BHL040517-GBD26850_15814-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGTCCCGGAACTTTCATTGGAGGTGACCAAATTTATAATGTTATAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTAGTTCCCCTAATACTTGGAGCGCCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609573 Chironomus sp. water mite diet isolate 10470-BHL040517-GBD16047_14460-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACATCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609574 Chironomus sp. water mite diet isolate 10478-BHL040517-GBD18123_27453-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCCTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAACTAGGACGACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTTCCCCCCTCTCTAACTCTTCTTCTTTCTAGTACATTCGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609575 Chironomus sp. water mite diet isolate 10479-BHL040517-GBD8708_4271-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTATCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609576 Chironomus sp. water mite diet isolate 10492-BHL040517-GBD29649_15099-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATAGCCTCCCCTCGAATAAATAATATAAGTTTTTGACTACTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609577 Chironomus sp. water mite diet isolate 10503-BHL040517-GBD11276_2642-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGTGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGTTAATTCGAGCTGAATTAGGACAACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTCGTCCCCCTAATACTTGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609578 Chironomus sp. water mite diet isolate 10504-BHL040517-GBD13307_5341-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAATGGGTACAGCTCATGCATTTATTATAATTTTTTTCGTAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAGAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609579 Chironomus sp. water mite diet isolate 10505-BHL040517-GBD2575_16617-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCTGAATTAGGACAACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTCTACCCCCTTCTCTAACCCTACTACTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609580 Chironomus sp. water mite diet isolate 10506-BHL040517-GBD28723_19737-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATTCTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCTCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTATTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTTCTATCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609581 Chironomus sp. water mite diet isolate 10507-BHL040517-GBD5779_21621-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTCGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATACGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGAACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609582 Chironomus sp. water mite diet isolate 10509-BHL040517-GBD22712_21331-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTACTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609583 Chironomus sp. water mite diet isolate 10513-BHL040517-GBD26006_21056-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTCTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609584 Chironomus sp. water mite diet isolate 10519-BHL040517-GBD9753_14761-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATGCTTATTCGAGCAGAATTATGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATTGTTATACCAATTTTAATTGGAGGATTCGGAAACTGAATAGTCCCCCTAATACTTGGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTACTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609585 Chironomus sp. water mite diet isolate 10528-BHL040517-GBD23644_22796-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGTCCCGGAACTTTCATTGGAGATGACCAAATTCATAATGTTGTAGTTACTGCTTATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTTTCCCCCTAATACTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTACATTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609586 Chironomus sp. water mite diet isolate 10556-BHL040517-GBD2745_19039-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGAGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATATTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGTTTTTCCTCGAATAATTAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTACTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609587 Chironomus sp. water mite diet isolate 10565-BHL040517-GBD13948_27935-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609588 Chironomus sp. water mite diet isolate 10568-BHL040517-GBD22117_13991-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCCTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTATCTAGTTCTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609589 Chironomus sp. water mite diet isolate 10579-BHL040517-GBD25076_13269-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTGGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATAGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGACATAGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609590 Chironomus sp. water mite diet isolate 10582-BHL040517-GBD26962_16221-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGAGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCTGGAACATTCATAGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTACCCCTAATACTTGGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609591 Chironomus sp. water mite diet isolate 10586-BHL040517-GBD28494_11562-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAAAATTAGGACGAGCCGGAACTTTAATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCTCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609592 Chironomus sp. water mite diet isolate 10592-BHL040517-GBD17959_25978-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCTGAATTAGGACGAACCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTAACTCTTCTACTTTCTAGTAGTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609593 Chironomus sp. water mite diet isolate 10613-BHL040517-GBD14080_11700-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACTTTTTATATTATTTTTGGTGCTTGATCAGGAATAGTAGGTACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATACAAGTTTTTGACCTCGCCCCTCAACTTTAACACTTCATCAATCTAGTGCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609594 Chironomus sp. water mite diet isolate 10620-BHL040517-GBD27311_12309-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGAGCTTGATCCGGTATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGTACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCTCTAATATTTGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCTTCACTTACTCTTCTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609595 Chironomus sp. water mite diet isolate 10622-BHL040517-GBD29014_13617-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGAAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGAAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTAACTCTACAACTATCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609596 Chironomus sp. water mite diet isolate 10658-BHL040517-GBD24601_22374-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAACGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTAATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTATTACCCCCCTCTCTAACTCTACTACTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609597 Chironomus sp. water mite diet isolate 10660-BHL040517-GBD6138_22256-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTTTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTATTACCCCCCTCTCTTACTCTACTACTTTCTAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609598 Chironomus sp. water mite diet isolate 10662-BHL040517-GBD19572_20974-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTAGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATCCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609599 Chironomus sp. water mite diet isolate 12050-BHL040517-GBD16269_13320-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGATCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTCTTGACTTCTTCCCCCATCCTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609600 Chironomus sp. water mite diet isolate 12070-BHL040517-GBD26142_15418-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTCGTCCCCCTAATACTTGGAGCACCTGACGTAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGCTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609601 Chironomus sp. water mite diet isolate 12089-BHL040517-GBD15524_11889-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACACTATTTCTGGGACTTCATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGAACAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTTTAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609602 Chironomus sp. water mite diet isolate 12101-BHL040517-GBD17859_3717-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGAGCTTGATCCGAAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGAGCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609603 Chironomus sp. water mite diet isolate 12102-BHL040517-GBD16515_4533-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACGTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACATCATTAAGAATGCTTGTTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAAGTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTCGTCCCCCTAATACTTGGAGCACCTGACGTAGCTTTTCCTCGAATAAACAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609604 Chironomus sp. water mite diet isolate 12105-BHL040517-GBD8308_18984-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACACTATACTTTATTTTTGGAACTCGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTACACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGATCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTCTTGACTTCTCCCCCCATCCTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.4% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609605 Chironomus sp. water mite diet isolate 12107-BHL040517-GBD7843_9308-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTTCCTTTAATATTAGGAGCCCCAGATATGGCCTTCCCTCGAATAAATAATAAAAGATTTTGACTACTCCCCCCATCTTTAACATTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609606 Chironomus sp. water mite diet isolate 12115-BHL040517-GBD24323_6075-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGGGGCTTCATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCTCTAATGCTTGGAGCACATGACATAGCTTTTCCACGAATAAATAATATAAGTTTCTGACTGTTACCCCCCTCTCTTACTCAACTACTATCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609607 Chironomus sp. water mite diet isolate 12121-BHL040517-GBD17843_19969-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAACTGGAGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGTTCTTTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609608 Chironomus sp. water mite diet isolate 12124-BHL040517-GBD14782_4927-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCCAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609609 Chironomus sp. water mite diet isolate 12133-BHL040517-GBD9211_19362-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTACAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTAATACCTATTTTAATTGGGGAATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTAGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609610 Chironomus sp. water mite diet isolate 12138-BHL040517-GBD20984_27653-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGTAATTGATTACTACCTCTAATATTAGGAGCCCCTGATATAACATTTCCTCGAATAAATAATATAAGATTTTGATTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609611 Chironomus sp. water mite diet isolate 12140-BHL040517-GBD19763_17372-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCTTTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCTTTTAATATTAGGAGCTCCAGATATAGCCTTCCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCATCTTTAACCCTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609612 Chironomus sp. water mite diet isolate 12147-BHL040517-GBD8964_19142-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGAAGCACCTGACATAGCTTTTCCTAGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609613 Chironomus sp. water mite diet isolate 12154-BHL040517-GBD25268_5294-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCGGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTGTAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTAGTGCCATTAATATTAGGAGCACCTGATATGGCATTTCCTCGAATAAATAATACAAGATTTTGACTTTTA-CCCCCTCCCTTAACATTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609614 Chironomus sp. water mite diet isolate 12159-BHL040517-GBD21771_11617-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTAGTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAACACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTCTTTGACTTTTACCCCCTTCTTTAACTTTACTTCTTTCTAGATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609615 Chironomus sp. water mite diet isolate 12164-BHL040517-GBD20995_22929-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCGGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609616 Chironomus sp. water mite diet isolate 12167-BHL040517-GBD21252_3092-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACCTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACATGGTACTTTTATTGGAGATGACCAAATCTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACATGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609617 Chironomus sp. water mite diet isolate 12169-BHL040517-GBD14974_19719-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGATATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGGAAACTAACTTGT-CCCATAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCTCTCTTACTCTACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609618 Chironomus sp. water mite diet isolate 12174-BHL040517-GBD17315_22665-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACCTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATCTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGATCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTCTTGACTTCTCCCCCCATCCTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609619 Chironomus sp. water mite diet isolate 12175-BHL040517-GBD24983_16674-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTCTGGGGCTTCACCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTTCTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATGCTAGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTGACTCATCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609620 Chironomus sp. water mite diet isolate 12195-BHL040517-GBD12876_26079-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGGTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGATGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.1% identical to accession ID GU944724, identified in GenBank as Chironomus circumdatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609621 Chironomus sp. water mite diet isolate 12197-BHL040517-GBD4880_13488-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGGTTTTATTATAATTTTTCTCATAGCTATACCAATTTTAATTGGAGGGTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCCCCTGATATAGCATTTCCTCGAATAAATAAAATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTGCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609622 Chironomus sp. water mite diet isolate 12211-BHL040517-GBD25259_25301-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGGGGCTTCATCCGGAATAGTGGGAACTTCATTAAGCATGCTTATTCGAGCAGAATTAGGACGAACAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGACTAAATAATATAAGTTTCTTACTTTTACCCCCCACTCTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609623 Chironomus sp. water mite diet isolate 12220-BHL040517-GBD19768_14970-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACAGCTCATACTTTTTTTATAATTTTTTTCATAGTTATACCAATTTTAATTGGGGGATTCGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609624 Chironomus sp. water mite diet isolate 12223-BHL040517-GBD3457_20840-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACGTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTGTTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCCTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTGGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTTATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTTGCTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAAAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609625 Chironomus sp. water mite diet isolate 12238-BHL040517-GBD14760_23246-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGATGAATTAGGTCACCCAGGAACTTTAATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGAAGGATTCGGAAACTGACTTGTCCCCCTAATACTTAGAACACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609626 Chironomus sp. water mite diet isolate 12253-BHL040517-GBD24434_14820-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCTTTAGAATATTAATTCGAGCAAAATTAGGACATCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGATTTCTCCCCCCATCTTTAACTCTTTTACTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609627 Chironomus sp. water mite diet isolate 12263-BHL040517-GBD8124_22916-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAATAGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGATCCGGAACTTTCGTTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCACTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609628 Chironomus sp. water mite diet isolate 12264-BHL040517-GBD12059_7096-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACGTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTGTTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTCGTCCCCCTAATACTTGTAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609629 Chironomus sp. water mite diet isolate 12268-BHL040517-GBD25232_7134-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAAGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATCTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAATTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609630 Chironomus sp. water mite diet isolate 12272-BHL040517-GBD8671_23795-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGGGGCTTCATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTCTTGACTTCTCCCCCCATCCTTAACACTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609631 Chironomus sp. water mite diet isolate 12273-BHL040517-GBD11339_11257-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACATTATATTTATTTTTGGAGCTTGATCAGGTATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGCACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTATTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGTTCATGAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609632 Chironomus sp. water mite diet isolate 12279-BHL040517-GBD16651_2382-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTGGAGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAACGTTGTAGTTACTGCACATGGTTTTATTATAATTTTTCTCATAGGTATACCAATTTTAATTGGAGGGTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGCTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609633 Chironomus sp. water mite diet isolate 12281-BHL040517-GBD25724_14138-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGTATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTACTCCCCCCATCATTAACACTTTTTCTTTCTAGTTCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609634 Chironomus sp. water mite diet isolate 12288-BHL040517-GBD26454_6921-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGCTCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGATGATCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAAAAAATAATATAAGTGTCTGACTTTTACCCCCCACTCTTACTCATCTACTTTCTAGTTCTTTCGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609635 Chironomus sp. water mite diet isolate 12291-BHL040517-GBD3032_12356-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAACTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTGCCATTAATATTAGGAGCACCTGATATGGCATTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCTTCCTTAACATTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609636 Chironomus sp. water mite diet isolate 12299-BHL040517-GBD7541_22684-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGACACCCAGGAACTTTAATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATACGGAAACTGACTTGTTCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCCTCTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609637 Chironomus sp. water mite diet isolate 12301-BHL040517-GBD12687_18192-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGAAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGATCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGACTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCCCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTATCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609638 Chironomus sp. water mite diet isolate 12308-BHL040517-GBD25424_17514-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGGACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTCTCCCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCTCCTAATACTTGGAACACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCGTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609639 Chironomus sp. water mite diet isolate 12311-BHL040517-GBD27489_16912-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCTGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGATGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGTAGTTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609640 Chironomus sp. water mite diet isolate 12322-BHL040517-GBD24059_25224-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGGGGCTTCATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAAGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTGATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCACTTACCCATCTTCTATCTAGATCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609641 Chironomus sp. water mite diet isolate 12324-BHL040517-GBD26839_23827-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATTCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGTACTTTCATTGGAGATGACCAAATTTATAATGTTATAGTTACTGCACATGCTGTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCATCTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609642 Chironomus sp. water mite diet isolate 12328-BHL040517-GBD18073_24778-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTGGAGCTTGATCCGAAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGATCCGGAACCTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCGGATAAAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609643 Chironomus sp. water mite diet isolate 12329-BHL040517-GBD10227_21132-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGAAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGTATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATGGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609644 Chironomus sp. water mite diet isolate 12343-BHL040517-GBD13480_8784-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGAACAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACATGGCATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCTCCTCTCTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609645 Chironomus sp. water mite diet isolate 12344-BHL040517-GBD28059_10714-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGTACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609646 Chironomus sp. water mite diet isolate 12354-BHL040517-GBD27040_7213-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGGGGCTTCATCCGCAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCTGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTAATACCAGTTTTAATTGGAGGATTCGGAAACTGATTTGTACCCCTAATACTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTGGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609647 Chironomus sp. water mite diet isolate 12355-BHL040517-GBD3349_9093-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTCCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCACCCAGCTTTAACCCTTCTT-TTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609648 Chironomus sp. water mite diet isolate 12356-BHL040517-GBD4970_18887-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAGTGTTGTAGTTACTGCACATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCAAATAAACAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609649 Chironomus sp. water mite diet isolate 12364-BHL040517-GBD28785_14026-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATAGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTCTACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGATCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTAACTCTACTACTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609650 Chironomus sp. water mite diet isolate 12386-BHL040517-GBD21623_19146-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTTTACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAATTAGTACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTATAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCTCTCTTACACTTCATCATGCTAGTTCTTTCGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609651 Chironomus sp. water mite diet isolate 12418-BHL040517-GBD16640_16587-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGAATTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTCCCACTAATACTGGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609652 Chironomus sp. water mite diet isolate 12419-BHL040517-GBD20276_10804-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACCTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTTTAGTTACTGCACATGGTTTTATTATAATTTTTCTCATAGTTATACCAATTTTAATTGGAGGGTGCGGAAACTGACTCGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCATTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609653 Chironomus sp. water mite diet isolate 12421-BHL040517-GBD5635_6172-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTCCCCCTAATATTGGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609654 Chironomus sp. water mite diet isolate 12426-BHL040517-GBD10605_4100-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCCGAATAGTGGGAACTTCATTAAGCATACTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGGTTTTATTATAATTTTTCTCATAGTTATACCAATTTTAATTGGAGGGTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAGGCTTCTGACTTTTATCCCCCTCTCTTACTCTTCTTCGTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609655 Chironomus sp. water mite diet isolate 12430-BHL040517-GBD11800_3162-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACATTATATTTTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTTGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCATCTTTAACTCTTTTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609656 Chironomus sp. water mite diet isolate 12431-BHL040517-GBD25441_5489-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCTTTTAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAATTTTAATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609657 Chironomus sp. water mite diet isolate 12440-BHL040517-GBD11653_16331-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGGTTTTATTATAATTTTTCTCATAGTTATACCAATTTTAATTGGGGGGTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATGAGCTTCTGATTTTTACCCCCATCTCTTACACTACTTCTGTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609658 Chironomus sp. water mite diet isolate 12443-BHL040517-GBD6320_8262-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAACACCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTACTACCATCTAGTACACTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609659 Chironomus sp. water mite diet isolate 12444-BHL040517-GBD24811_16294-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACCTGATCAGGAATAGTAGGAACTTCCCTTAGAATACTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCCTCTTTAACTCTTTTTCTTTCTAGTACATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609660 Chironomus sp. water mite diet isolate 12446-BHL040517-GBD6204_11805-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTATGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTATCCCCCTAATACTTGGAACACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTACTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609661 Chironomus sp. water mite diet isolate 12449-BHL040517-GBD12610_22269-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGTGGCTTGATCCGAAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGATCCGGAACTCTCATTGAAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTGTAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATCTGGAAACTGACATGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609662 Chironomus sp. water mite diet isolate 12462-BHL040517-GBD12498_28645-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACATTATATTTATTTTTGGAGCTTGATCTGGTATAATAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCTTTTAATATTAGGAGCACCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGTGCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.4% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609663 Chironomus sp. water mite diet isolate 12467-BHL040517-GBD7695_24736-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCGCCCCCCATCTTTAACACATTTTCTATATAGTGCATTAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609664 Chironomus sp. water mite diet isolate 12471-BHL040517-GBD10836_12757-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCCTCATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCATCTCTTTCTCAACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609665 Chironomus sp. water mite diet isolate 12477-BHL040517-GBD11991_11288-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGAAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGTAGAATTAGGACGATCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGATGATTCGGATACTGACATGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609666 Chironomus sp. water mite diet isolate 12483-BHL040517-GBD16361_10366-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGTTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609667 Chironomus sp. water mite diet isolate 12486-BHL040517-GBD16979_2101-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGAAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGATCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAATTGGAGGATTCGGAAACTGACATGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609668 Chironomus sp. water mite diet isolate 12487-BHL040517-GBD8813_26484-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGGTTTTATTATAATTTTTCTCATAGTTATACCAATTTTAATTGGAGGGTTCGGAAACTGACTTGCTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGCATAAATAATATAAGCTTCTGACTTTTTCCCCCCTCTCTTACTCAACCTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609669 Chironomus sp. water mite diet isolate 12490-BHL040517-GBD10909_17494-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCCGGAACTTTTATTGGTGATGCCCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATGATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATAGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGATCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609670 Chironomus sp. water mite diet isolate 13577-BHL040517-GBD20247_22513-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTCGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCGTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609671 Chironomus sp. water mite diet isolate 13594-BHL040517-GBD7002_22965-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTGTTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTTGTCCCCCTAATACTGGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTATTACCCCCCTCTCTTACTCTTCTTCTTTCTAGATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609672 Chironomus sp. water mite diet isolate 13618-BHL040517-GBD12533_25567-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGTTTATTCGAGCAGAATTAGGACAACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCACTAACTCTACTTCTATCTAGATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609673 Chironomus sp. water mite diet isolate 13620-BHL040517-GBD28793_19596-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATCTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGAAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACGCTTTTACTTTCAAGTAGAGTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609674 Chironomus sp. water mite diet isolate 13622-BHL040517-GBD2580_17309-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609675 Chironomus sp. water mite diet isolate 13641-BHL040517-GBD16614_9468-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGCTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATATCTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTACTACTTTCTAGATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609676 Chironomus sp. water mite diet isolate 13654-BHL040517-GBD7726_20389-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATTCTTATTCGAGCAGAATTAGGACAACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTTTTCTTCTTTCTAGAACTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609677 Chironomus sp. water mite diet isolate 13664-BHL040517-GBD5591_15135-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTAATTCGAGCAGAATTAGGACGACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACACTACTTCTATCTAGAACTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609678 Chironomus sp. water mite diet isolate 13666-BHL040517-GBD25658_12449-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGGAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAGAACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609679 Chironomus sp. water mite diet isolate 13677-BHL040517-GBD25117_6850-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCTCTAATACTTGGAGCACCTGTCACAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCGCTAACTCAGCTACTTTCTAGAACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609680 Chironomus sp. water mite diet isolate 13679-BHL040517-GBD12702_8364-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTTCCCCCCTCTCCTACACGACATCTGTCTAGTTCTTGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609681 Chironomus sp. water mite diet isolate 13681-BHL040517-GBD16054_21912-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTAGTCCCCCTAATACTTGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTAACTCTTCTACTTTCTAGAACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609682 Chironomus sp. water mite diet isolate 13712-BHL040517-GBD7647_10992-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGTTTATTCGAGTAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGATTTTATTATATTTTTTTTCATAATTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGTAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTGCTTCTTTCTAGAACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609683 Chironomus sp. water mite diet isolate 13722-BHL040517-GBD16354_27251-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACCACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTCATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAGGTTTCTGACTTTTACCCCCCTCACTAACTCTACTACTTTCTAGATCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609684 Chironomus sp. water mite diet isolate 13723-BHL040517-GBD24974_13294-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGTTTACTCGAGCAGAATTAGGACGACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTCCCCCTAATACTTGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTAACTCTTCTACTTTCTAGTACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609685 Chironomus sp. water mite diet isolate 13732-BHL040517-GBD13063_27661-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTATATTTTATTTTTGGAGCATGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCATCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609686 Chironomus sp. water mite diet isolate 13743-BHL040517-GBD28850_11978-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACCTTATTTTTGGGGCTTGATCCGGAATAGTGGGCCCTTCATTAAAACTGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTGACTCTTCTTCTTTCTAGATCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609687 Chironomus sp. water mite diet isolate 13745-BHL040517-GBD12880_28388-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTGGGGGCTTGATCCGGCATAGTGGGAACTTCATTAAGAATTCTTACTCGAGCAGAATTAGGAGGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTACTTCGATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609688 Chironomus sp. water mite diet isolate 13761-BHL040517-GBD23714_22831-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCCTTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTTACTCTTCTTCTATCTAGAACATTCGTAGAGAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609689 Chironomus sp. water mite diet isolate 13784-BHL040517-GBD18323_14350-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTATGACGACCCGGAACTTTCCTTGGAGATGACCAAATTTATAATGTTCTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCACGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTACTACTTTCTAGTGCTGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609690 Chironomus sp. water mite diet isolate 13787-BHL040517-GBD25742_11108-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGTTTATTCGAGCAGAATTAGGACGACCCGGATCTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGAAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATCACCCCCTTCTCTTACCCTACTTCTTTCTAGATCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609691 Chironomus sp. water mite diet isolate 13788-BHL040517-GBD26152_12670-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTCATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTAGTACCCCCCTCACTAACTCTACTACGTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609692 Chironomus sp. water mite diet isolate 13791-BHL040517-GBD22401_19309-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCCTAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCTCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTAACCCTTCTTCTTTCTAGATCATCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609693 Chironomus sp. water mite diet isolate 13802-BHL040517-GBD22121_18560-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATCTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCATTTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGATCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609694 Chironomus sp. water mite diet isolate 13805-BHL040517-GBD24361_12564-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCAGTAAAAATCCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAGTGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609695 Chironomus sp. water mite diet isolate 13811-BHL040517-GBD22338_13150-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATGCTTATTCGAGTAGAATTAGGACGACCAGGAACTTTCCTTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCAGACATAGCTTTTCCACGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTACTTCTTTCTAGTGCTGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609696 Chironomus sp. water mite diet isolate 13812-BHL040517-GBD26409_14942-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTTTACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCCTTAAGTATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTATTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609697 Chironomus sp. water mite diet isolate 13827-BHL040517-GBD17779_8045-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTTGGTACTTCATTAAATATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCATAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCATCGCTTACTCAGCTTCTTGCGAGAACGTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609698 Chironomus sp. water mite diet isolate 13837-BHL040517-GBD4615_20467-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAGCTTCATTAAAAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTTGTCCCCCTAATACTAGGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTACTACTATCTAGATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609699 Chironomus sp. water mite diet isolate 13844-BHL040517-GBD7854_9713-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTTATTCGAGCAGAATTAGGACAACCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTAATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCACGAATAAATAATATAAGATTCTGACTATTACCCCCCTCTCTTACTCTACTTCTTTCTAGAACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609700 Chironomus sp. water mite diet isolate 13854-BHL040517-GBD24885_10914-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCCTGATCAGGAATAGTGGGCACTTCTTTAAGAATTCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609701 Chironomus sp. water mite diet isolate 13868-BHL040517-GBD17601_10811-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATGCTTACTCGAGTAGAATTAGGACGACCCGGAACTTTCTTTGGAGATAACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGAATTGTCCCCCTAATACTTGGAGCACCTGACGTAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTACTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609702 Chironomus sp. water mite diet isolate 13872-BHL040517-GBD17565_21542-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCCTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTCGGACGACCCGGTACTTTCATTGGAGATGATCAAATTTATAATGTAGTTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609703 Chironomus sp. water mite diet isolate 13878-BHL040517-GBD16027_24530-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGATCTTTATATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTTTCCCCCTAATATTTGGAGCACCTGACATAGCTTTTCCACGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTTACTCTACTACTTTCAAGAACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609704 Chironomus sp. water mite diet isolate 13879-BHL040517-GBD14803_16892-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCCTTTATTATAATTTTTTTCATAGTAATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTACCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609705 Chironomus sp. water mite diet isolate 13888-BHL040517-GBD25739_7462-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTATACTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACCCTACTTCTTTCTAGATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609706 Chironomus sp. water mite diet isolate 13889-BHL040517-GBD23664_4335-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGTCGACCCGGCACTTTCATTGGAGAAGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTACTACTATCTAGATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609707 Chironomus sp. water mite diet isolate 13894-BHL040517-GBD28677_12122-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATTCTTACTCGAGCAGAATTAGGACCACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTAGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTACTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609708 Chironomus sp. water mite diet isolate 13913-BHL040517-GBD23494_14833-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCACTAATACTTGGAGCACCTGATATGGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCCCTAACACTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609709 Chironomus sp. water mite diet isolate 13917-BHL040517-GBD24120_10312-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTCATTGGAGATGACCAATTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTCTACCCCCCTCACTTACTCTACTACTTTCTAGATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609710 Chironomus sp. water mite diet isolate 13921-BHL040517-GBD8796_8576-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGATATTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCTCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTATTACCCCCCTCACTTACTCTACTACTGTCTAGATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609711 Chironomus sp. water mite diet isolate 13929-BHL040517-GBD2635_13714-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTCGTCCCCCTAATACTTGGAGCTCCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCACTTACTCTACTTCTATCAAGATCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609712 Chironomus sp. water mite diet isolate 13933-BHL040517-GBD21498_3069-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGATTAGTGGGTACTTCATTAAAAATTCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTTACCCTACTTCTTTCTAGATCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609713 Chironomus sp. water mite diet isolate 13938-BHL040517-GBD14514_23351-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTTTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCACGAATAAATAATATAAGATTCTGACTATTACCCCCCTCTCTTACTCTACTTCTTTATAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609714 Chironomus sp. water mite diet isolate 13943-BHL040517-GBD18510_17708-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGTACTTCATTAAGTATGCTTACTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTTTCCTCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCACTCTTACTCAGCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609715 Chironomus sp. water mite diet isolate 13944-BHL040517-GBD25657_20858-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTTATTCGAGTAGAATTAGGACAACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATATTAATTGGAGGATTCGGAAACTGACTTGTACCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACCCTACTTCTTTCTAGAGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609716 Chironomus sp. water mite diet isolate 13955-BHL040517-GBD23730_18328-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCTAATAAATAATATAAGTTTCTGACTTTTACCCCCCGCTCTAACACGGCTTCGTACTAGAACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609717 Chironomus sp. water mite diet isolate 13970-BHL040517-GBD24457_25868-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCGCGCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609718 Chironomus sp. water mite diet isolate 13976-BHL040517-GBD10284_22244-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACACTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAACAATATAAGAGTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609719 Chironomus sp. water mite diet isolate 13979-BHL040517-GBD16123_14783-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATTCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAAGACGACCCGGAACTTTCATTGGAGACGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTTTCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609720 Chironomus sp. water mite diet isolate 14017-BHL040517-GBD9467_14704-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTACATTAATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTACTGACTTTTACCCCCCTCTCTTAATCTACATCTGTCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609721 Chironomus sp. water mite diet isolate 14020-BHL040517-GBD21851_11986-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAACTTATAATGTTGTAGTTACTGTACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609722 Chironomus sp. water mite diet isolate 14026-BHL040517-GBD19963_22427-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGACGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAATTATAATTGGTGGATTCGAAAACTGACTTGTCCCCCTAGTACATGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTGCCCCCCTCTCTTACGCGTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609723 Chironomus sp. water mite diet isolate 14030-BHL040517-GBD13584_28918-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGCTCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGCCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAATTATAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609724 Chironomus sp. water mite diet isolate 14031-BHL040517-GBD11186_23597-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGAATACTTATTCGAGCAAAATTAGGACGACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAATTATAATTGGAGGATTTGGAAATTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609725 Chironomus sp. water mite diet isolate 14042-BHL040517-GBD2963_12466-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGATGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAATTATAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTAACATAGCTTTTCCTCGAATAAATAATATAAGAGTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609726 Chironomus sp. water mite diet isolate 14043-BHL040517-GBD10602_19469-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATCAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCACCTAATACTTGGAGCTCCTGTCATAGCTTTTCCTCGAATAAAAAATATAAGTGTCTGACTTTTACCCCCCTCTCCTACTCTGCCTCTTTCTAGTTCGTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609727 Chironomus sp. water mite diet isolate 14071-BHL040517-GBD6033_21266-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGTGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAATTATAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAACAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCGATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609728 Chironomus sp. water mite diet isolate 14073-BHL040517-GBD23098_17043-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGTAGCACCTGACACAGCTTGACCTCGAATAAATAATATAAGTTTCTGATTATTACCCCCCGCTCCTACTCTTCTTCATTCTAGTTCTTTCGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609729 Chironomus sp. water mite diet isolate 14075-BHL040517-GBD13382_8002-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGTCCTGGAACTTTCATTGGTGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTCCCACTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCATCTCTTACTCTACTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609730 Chironomus sp. water mite diet isolate 14079-BHL040517-GBD25646_20416-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGTATAGTGGGAACTTCCTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTAACCCTACTACTAACTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609731 Chironomus sp. water mite diet isolate 14094-BHL040517-GBD14727_1965-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGACTGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTCGTAGTTACTGCACATGCCTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCACTTACTCTTCTTCTATCTAGTTCTGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609732 Chironomus sp. water mite diet isolate 14095-BHL040517-GBD26122_18638-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACAACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAATTATAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACGTAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609733 Chironomus sp. water mite diet isolate 14101-BHL040517-GBD18078_16849-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTATCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609734 Chironomus sp. water mite diet isolate 14110-BHL040517-GBD23263_22417-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGAGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATTCTTATTCGAGCAGAATTAGGACAACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTAACTCTTCTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609735 Chironomus sp. water mite diet isolate 14113-BHL040517-GBD13052_7756-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTCGTAGTTACTGCACATGCCTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCTCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTTCTTCCTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609736 Chironomus sp. water mite diet isolate 14118-BHL040517-GBD4787_15599-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATCCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTATAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCACTTACTCTACTACTAGCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609737 Chironomus sp. water mite diet isolate 14124-BHL040517-GBD25958_14139-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTTTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTTCCCCTAATACTTGAAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609738 Chironomus sp. water mite diet isolate 14125-BHL040517-GBD10416_17970-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACTACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAACTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTAACCCTTCTTCTATCTAGTACATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609739 Chironomus sp. water mite diet isolate 14127-BHL040517-GBD9066_7891-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATTCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCCCTAATATTTGGAGCACCTGACACAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609740 Chironomus sp. water mite diet isolate 14129-BHL040517-GBD19001_7753-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTTTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTTGAGATGACCAAATTTATAATGTTGTGGTTACTGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAATTATAATTGGAGGATTCGGAAACTGACTTATCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609741 Chironomus sp. water mite diet isolate 14134-BHL040517-GBD9889_23904-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTTGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAATTATAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGAAATAGCTTTTCCTCGAACAAATAATATAAGTTTCTGACTACTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609742 Chironomus sp. water mite diet isolate 14135-BHL040517-GBD21495_24331-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAAAATTTTAATTCGACTAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACGGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609743 Chironomus sp. water mite diet isolate 14136-BHL040517-GBD28354_21330-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTATCTCTAATATTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTCCCCCCCTCTCTTACTCTTCTACTTTCTAGTACTTTCGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609744 Chironomus sp. water mite diet isolate 14141-BHL040517-GBD28031_15964-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTAGGAACTTCATTAAGAATGCTTTTTCGAGCAGAATTAGGATGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTCATAATTATACCAATTATAACTGGAGGATTCGGAAACTGACTTATCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609745 Chironomus sp. water mite diet isolate 14143-BHL040517-GBD28638_15681-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTCGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATACTTATACCAATTATAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGAATTTTACCCCCCTCACTAACACTACTTCTTTCTAGTTCTGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609746 Chironomus sp. water mite diet isolate 14220-BHL040517-GBD10351_6378-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTTACATTACTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609747 Chironomus sp. water mite diet isolate 14222-BHL040517-GBD4310_9757-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTACTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609748 Chironomus sp. water mite diet isolate 14258-BHL040517-GBD10245_26317-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTACTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAAATGACTTATGCCTTTAATACTAGGGGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609749 Chironomus sp. water mite diet isolate 14269-BHL040517-GBD9772_5231-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCTAATTTTAATTGGTGGTTTTGGAGATTGACTTGTACCTTTAATACTAGGGGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTTACATTACTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609750 Chironomus sp. water mite diet isolate 14309-BHL040517-GBD26500_23935-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTAGGACAACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGGTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTAGTACCTTTAATACTAGGGGCCCCAGACATAGCTTTCCCCCGAATAAATAATATAAGATTCTGATTACTTCCCCCATCACTAACATTACTACTTTCAAGTTCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609751 Chironomus sp. water mite diet isolate 14333-BHL040517-GBD15344_25381-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCTTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTACTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGAGATGACCAGATTTATAATGTAGTAGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAACTGACTTGTCCCTTTAATACTAGGGGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTTACATTACTCCTTTCAAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609752 Chironomus sp. water mite diet isolate 14346-BHL040517-GBD21696_11855-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTACTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCAGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609753 Chironomus sp. water mite diet isolate 14357-BHL040517-GBD14807_9563-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTACTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACACGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTCCATAGTTATGCCAATTTTATTTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609754 Chironomus sp. water mite diet isolate 14370-BHL040517-GBD11508_16780-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCTTTATCAGGAATGGTAGGGACTACTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCGGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCGTAGTTATGCCAATTGTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGAATACTTCCCCCATCACTTACATTACTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609755 Chironomus sp. water mite diet isolate 14450-BHL040517-GBD16781_18905-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTAGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609756 Chironomus sp. water mite diet isolate 14465-BHL040517-GBD21826_22779-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTACTTTACGTATGCTTATTCGAGCAGAATTAGGACGAGCCGGCACTTTTGTTGGCGACGAGCAGATTTATAATGTAGTTGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATATTAGGGGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTAACATTACTCCTATCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609757 Chironomus sp. water mite diet isolate 14473-BHL040517-GBD7611_12981-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTACTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAATAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609758 Chironomus sp. water mite diet isolate 14515-BHL040517-GBD23773_15487-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACTTTATTTTTGGTACTTGATCAGGAATGGTAGGGACTTCTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGATTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTAACATTACTCCTTTCAAGATCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609759 Chironomus sp. water mite diet isolate 14523-BHL040517-GBD8079_13949-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACTTTATTTTTGGTGCTTGATCAGGAATGGTTGGGACTACTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCAGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTTGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGAGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTGCCCCCATCACTTACATTACTCCTATCAAGATCATTTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609760 Chironomus sp. water mite diet isolate 14542-BHL040517-GBD25220_10268-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGAACTACTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTGTTGGCGACGACCAAATTTATAATGTAGTTGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGTGCCCCTGATATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGACTACTTCCCCCATCACTAACATTACTACTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609761 Chironomus sp. water mite diet isolate 14557-BHL040517-GBD3217_14085-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTACTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGATCTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609762 Chironomus sp. water mite diet isolate 14626-BHL040517-GBD13923_7861-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATTCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTGCTTCTTTCTAGTTCGTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609763 Chironomus sp. water mite diet isolate 14638-BHL040517-GBD12872_20079-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609764 Chironomus sp. water mite diet isolate 14643-BHL040517-GBD8901_4023-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTTTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609765 Chironomus sp. water mite diet isolate 14655-BHL040517-GBD25191_15763-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTTATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609766 Chironomus sp. water mite diet isolate 14708-BHL040517-GBD14333_19525-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAAGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609767 Chironomus sp. water mite diet isolate 14720-BHL040517-GBD5137_22269-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGTGCTGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCTCTCGTACTCTTCTTCTTTCTAGTTTTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609768 Chironomus sp. water mite diet isolate 14778-BHL040517-GBD9895_11888-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGCCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATATTTGGAGCACCTGACATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCTCACTTACTCTACTACTATCTAGCTTTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609769 Chironomus sp. water mite diet isolate 14780-BHL040517-GBD16738_2639-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTGGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACCGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGTACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTATTCTTATTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609770 Chironomus sp. water mite diet isolate 14784-BHL040517-GBD2450_11727-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGCACTTCATTAAGAATTCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCGCGAATAAATAATATAAGATTCTGACTATTACCCCCCTCTCTTACCCTTCTTCTATCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609771 Chironomus sp. water mite diet isolate 14799-BHL040517-GBD7497_9354-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGTCCCGGAACCTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGACTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTTGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609772 Chironomus sp. water mite diet isolate 14806-BHL040517-GBD24899_16070-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTCGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTTCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACAC-TATTATTAGTAAGAAGTATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609773 Chironomus sp. water mite diet isolate 14851-BHL040517-GBD8207_17021-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAAGTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGCATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATTCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTGACCCCCCTCTCTTACACTTCATCAATCTATTGCTTGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609774 Chironomus sp. water mite diet isolate 14871-BHL040517-GBD14765_19034-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCCTTTACTTTATTTTTGGAGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGGTTATTCGAACAGAATTAGGACGACCCGGATCTTTCATAGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGTAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCCAGTTTTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609775 Chironomus sp. water mite diet isolate 14897-BHL040517-GBD6979_10679-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTTTATATTATTTTTGGGGCTTGATCCGGAATAGCGGGAACTTCATTATGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCGCTTACACTTCATCAATCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609776 Chironomus sp. water mite diet isolate 14942-BHL040517-GBD24455_20903-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTAGAGCAGAATTCGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTGATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTTTTTCCCCCCTCACTAACTCTACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609777 Chironomus sp. water mite diet isolate 14966-BHL040517-GBD12913_19785-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCCTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCTCTCTTACTCTTCTTCTATCTAGTTTATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609778 Chironomus sp. water mite diet isolate 14985-BHL040517-GBD23885_8040-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTTTACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATTCTTATTCGAGCAGAATTAGGACGTCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTCGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTGTTACCCCCCTCACTAACTCTACTACTATCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609779 Chironomus sp. water mite diet isolate 15055-BHL040517-GBD4293_15918-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCTGGAATAGTTGGAACTTCATTTAGAATGCTTATTCGAGCAGAATTATGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTACTTCTTTCCAGTGCTGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609780 Chironomus sp. water mite diet isolate 15058-BHL040517-GBD7832_11795-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGATCTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTTTACCCCTAATACTTGGAGCACCTGACATAGCTTCTCCTCGAATAAATAATATAAGATTCTGACTATTACCCCCCTCTCTTACTCTACTACTTTCAAGAACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609781 Chironomus sp. water mite diet isolate 15091-BHL040517-GBD12507_27301-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTTACTCTACTTCTTTCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609782 Chironomus sp. water mite diet isolate 15156-BHL040517-GBD28015_12359-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCTGGTATAGTGGGAACTTCTTTAAGAATGCTTATTCGAGCAGAACTAGGACGACCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCTCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609783 Chironomus sp. water mite diet isolate 15170-BHL040517-GBD11627_16710-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCCGGGATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTAACTGCACATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCCCTTACTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609784 Chironomus sp. water mite diet isolate 15190-BHL040517-GBD24093_11770-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGCATGCTTATTCGAGTAGAATTAGGACGCCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTGACTGCACATGCTTTTATTATAATTTTGTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609785 Chironomus sp. water mite diet isolate 15200-BHL040517-GBD22769_25663-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTTGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAGCTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCTTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609786 Chironomus sp. water mite diet isolate 15223-BHL040517-GBD23462_3996-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGCACTTCATTAAGAATGCTTATTCGAGTAGAATT AGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTT TATAGTGATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCC TCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCACTTACTCTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCT GGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609787 Chironomus sp. water mite diet isolate 15225-BHL040517-GBD21708_8058-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATATTTTATTTTTGGGGCTTGATCCGGAATAGTTGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTA TGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTT ATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCA CGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTACTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTG GAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609788 Chironomus sp. water mite diet isolate 2814-BHL032417-GBD13978_13155-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTTTTTTGGAACTTGATCAGGAACGGTAGGGACTTCTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACT TTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATGCCAATTT TAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGATATATCTTTCCCCCGAATAAATAATATAA GTTTCTGATTACTTCCCCCATCACTTACATTATTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID MF708877, identified in GenBank as Chironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609789 Chydoridae sp. water mite diet isolate 8533-BHL101416-GBD14654_28117-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCA CCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTT ATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCT TAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAA CAGG	Using NCBI BLASTN in June 2018, this sequence was 89.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609790 Chydoridae sp. water mite diet isolate 8550-BHL101416-GBD7005_15516-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGG TACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCC ATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAA TTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609791 Chydoridae sp. water mite diet isolate 8691-BHL101416-GBD25520_13141-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATACGAGCAGAATTAGGAC AAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAG TTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGA ATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATC- GTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID MG449896, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609792 Chydoridae sp. water mite diet isolate 9620-BHL032417-GBD14827_26464-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTGTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGAACTGCTCTTAGCCTGGTAATTCGAGCAGAATTAGGAC AAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCGCATGCTTTTGTTATAATCTTTTTTATAG TTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCTTTTCCGCGA ATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGA ACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609793 Chydoridae sp. water mite diet isolate 12172-BHL040517-GBD14654_28117-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCA CCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTT ATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCT TAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAA CAGG	Using NCBI BLASTN in June 2018, this sequence was 89.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609794 Chydoridae sp. water mite diet isolate 12189-BHL040517-GBD7005_15516-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGG TACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCC ATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAA TTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609795 Chydoridae sp. water mite diet isolate 12330-BHL040517-GBD25520_13141-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATACGAGCAGAATTAGGAC AAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAG TTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGA ATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATC- GTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID MG449896, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609796 Chydorus brevilabris water mite diet isolate 464-BHL040517-GBD8874_17939-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATTTCCTATTTGGAATTTGAGGTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATAAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCGTAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTTGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609797 Chydorus brevilabris water mite diet isolate 5153-BHL032417-GBD22756_19850-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAACCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609798 Chydorus brevilabris water mite diet isolate 5720-BHL032417-GBD5857_16841-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGAGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609799 Chydorus brevilabris water mite diet isolate 5946-BHL032417-GBD24329_4444-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCTCAGCTTTAACCCTTCTTTTAGTAGAGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609800 Chydorus brevilabris water mite diet isolate 8399-BHL101416-GBD8874_17939-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATTTCCTATTTGGAATTTGAGGTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATAAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCGTAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTTGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609801 Chydorus brevilabris water mite diet isolate 8465-BHL101416-GBD9385_11440-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTCCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGGGGGACCCTTATTGGAGATGATAAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTCCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTT	Using NCBI BLASTN in June 2018, this sequence was 98.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609802 Chydorus brevilabris water mite diet isolate 8638-BHL101416-GBD19689_4739-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGAGCAACGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGAGGGTTTGGAAAATGACTTGTCCCCCTAATATTAGGAGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609803 Chydorus brevilabris water mite diet isolate 8668-BHL101416-GBD13682_13891-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGTGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCCTAATTGGGGGTTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTAAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTATCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609804 Chydorus brevilabris water mite diet isolate 8735-BHL101416-GBD20121_3717-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTATATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCATGTTAATTCGAGCAGAATTAGGACAAAGAGGTACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCCTTTGTTATAATATTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAACCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGCGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609805 Chydorus brevilabris water mite diet isolate 8760-BHL101416-GBD13033_3536-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAAATAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTGTTGTCACTGCACATGCCTTTGTTATAATATTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCACGTCTTAATAATTTAAGTTTCTGGATTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGAGGGGGCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609806 Chydorus brevilabris water mite diet isolate 8833-BHL101416-GBD9246_10570-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGATCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTTACTGCTCATGCTTTTATTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTTGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609807 Chydorus brevilabris water mite diet isolate 8846-BHL101416-GBD5493_12123-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCTGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTAGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCGCGTCTTAACAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTACTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609808 Chydorus brevilabris water mite diet isolate 9544-BHL032417-GBD28094_13172-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGTCTGTTAATTCGAGCAGAATTAGGACAAAAAGGGACACTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATTATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAAATTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609809 Chydorus brevilabris water mite diet isolate 9548-BHL032417-GBD28835_14240-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGCATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATAGTAGGGGCACCTGATATAGCCGTCCCTCGGCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCGTCTTTGAGGAGGGGGGGCAGTAGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609810 Chydorus brevilabris water mite diet isolate 9553-BHL032417-GBD8348_13629-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTTTTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTATTTCGAGCAGAATTGGGACAAAGAGGTACCCTTATTGGAGATGATCAGATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGGAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609811 Chydorus brevilabris water mite diet isolate 9556-BHL032417-GBD22621_19438-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACACTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGTGGTTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATATAAGATTCTGGCTTCTGCCCCCAGCTTTAACCCTACTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609812 Chydorus brevilabris water mite diet isolate 9565-BHL032417-GBD19508_4258-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTATTTTTGGAGTTTGAGCTGGAATAGTGGGCACTGCTTTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCACATGCTTTTGTTATAGTCTTTTTTATAGTTATACCCATCTTAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609813 Chydorus brevilabris water mite diet isolate 9578-BHL032417-GBD18927_6037-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAAAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCCTTTGTTATAGTTTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCAGATATAGCCTTCCCTCGGCTAAATAATTTAAGTTTCTGGCTTCTACCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG449896, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609814 Chydorus brevilabris water mite diet isolate 9579-BHL032417-GBD13654_4020-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTCTATTTGGAATTTGAGCGGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGATATTGTCACTGCACATGCTTTTGTTATAATGTTTTTTATAGTTATACCCATCCTAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCATCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609815 Chydorus brevilabris water mite diet isolate 9584-BHL032417-GBD11770_27702-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACCGCACATGCTTTTGTTATAATCTTTTTTATAGTTATGCCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGACTAAATAATTTAAGTTTCTGGCTACTTCCCCCAGCTTTGACCCTTCTTTTAGCAGGGGGAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609816 Chydorus brevilabris water mite diet isolate 9590-BHL032417-GBD17925_5561-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATATTTTTTATAGGTAGACCCATCATAATTGGGGGGTTTCGAACCTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGCAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609817 Chydorus brevilabris water mite diet isolate 9591-BHL032417-GBD16956_4445-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTGTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCCTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATATTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGGAACTGACTTGTCCCCCTAATATTAGGGTCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGTGGGGGCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609818 Chydorus brevilabris water mite diet isolate 9608-BHL032417-GBD27505_16238-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTCTTTGGAATTTGAGCTGGAATAGTGGGCACTGCTATTAGCCTGTTAATTCGAGCAGAATTAGGTCAACGAGGGACCCTTATTGGAGATGATCAAGTTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGATTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609819 Chydorus brevilabris water mite diet isolate 9610-BHL032417-GBD5831_22296-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAGTTTGAGCTGGAATAGTGGGAACTGCTCTCAGCATGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGTGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGGTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609820 Chydorus brevilabris water mite diet isolate 9613-BHL032417-GBD23395_7786-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCTTTATTGGAGATGATCAAATTTACAATGTCATTGTTACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCGGATATAACCTTCCCTCGACTAAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTACTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609821 Chydorus brevilabris water mite diet isolate 9614-BHL032417-GBD13739_2649-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAAGTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAAGTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGGTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGCGCTGGAGCAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609822 Chydorus brevilabris water mite diet isolate 9621-BHL032417-GBD16327_10526-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCTGAATTAGGACAACCAGGAACCTTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTCATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609823 Chydorus brevilabris water mite diet isolate 9629-BHL032417-GBD25436_5772-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTTTTTGGAATTTGAGATGGAATAGTGGGAACTGCTTTTAGACTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCTTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGTGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609824 Chydorus brevilabris water mite diet isolate 9632-BHL032417-GBD14430_15474-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTTTTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGTACCTTTATCGGAGATGATCAAATTTACAATGTTATTGTCACTGTACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCTTAATTGGGGGGTTTGGAAACCGACTTGTCCCCCTAATATTAGGGGCCCCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609825 Chydorus brevilabris water mite diet isolate 9636-BHL032417-GBD27724_11844-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCTCTGCTCTTAGACTGTTAATTCGAGTAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACGTGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGTGGGTTTGGAACCTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGACTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609826 Chydorus brevilabris water mite diet isolate 9639-BHL032417-GBD10492_23675-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTTTATTTTCTATTTGGAGTTTGAGCTGGAATAGTGGGCACTGCTTTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATCTAAGTTTCTGGCTACTTCCCCCAGCTTTAACCCTTCTTTTAGAAAGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609827 Chydorus brevilabris water mite diet isolate 9642-BHL032417-GBD7035_17361-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTTTTAGCCTGTTAATTCGAGCAGAATTAGGACAAGGAGGGTCACTTATTGGAGATGGTCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGAGCACCTGATATAGCCTTCCCTCGTCTTAATAATATAAGTTTCTGGCTTCTTCCCCCGGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609828 Chydorus brevilabris water mite diet isolate 9645-BHL032417-GBD23516_16483-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTTTTAGCCTGTTAATTCGAGCAGAATTAGGTCAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCCTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTACACTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609829 Chydorus brevilabris water mite diet isolate 9650-BHL032417-GBD11187_18953-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTATATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGACTGTTAATTCGAGCAGAATTAGGACAAAGAGGAACACTTATTGGAGGTGATCAAATTTACAATGTTCTTGTCACTGCACATGCATTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609830 Chydorus brevilabris water mite diet isolate 9652-BHL032417-GBD27601_13028-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTTTTTGGACTTTGAGCTGGAATAGTGGGCACTGCTCTTAGACTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCTTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCCCATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATTTTAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609831 Chydorus brevilabris water mite diet isolate 9656-BHL032417-GBD13739_3760-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTGTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAATAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACGGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCCTAATTGGGGGGTTTGGAACCTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTCAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609832 Chydorus brevilabris water mite diet isolate 9659-BHL032417-GBD29422_13232-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGAACCTTTATTGGAGATGATCAAATTTACAATGTTGTTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATGGCCTTCCCTCGACTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTCTAACCCTTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID GU680595, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609833 Chydorus brevilabris water mite diet isolate 9664-BHL032417-GBD24814_22045-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGATCTGGTATCGTGGGCACTTCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAACGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGTGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGACTTAATAATGTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609834 Chydorus brevilabris water mite diet isolate 9669-BHL032417-GBD17901_4246-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGAGCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATGTTTTTTATAGTTATACCCATCCTAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACATGATATAGCCTTCCCTCGTCTTAATAATTTACGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGAGGGGGCAGTCGAAAATGGCGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609835 Chydorus brevilabris water mite diet isolate 9672-BHL032417-GBD5156_21562-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGTGGTTTGGAACCTGGCTTGTCCCCCTAATATTAGGGGCACCTGATATCGCCTTCCCTCGCCTTAATAATTTAAGTTTCTGGCTTCTGCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609836 Chydorus brevilabris water mite diet isolate 9673-BHL032417-GBD15512_6174-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCTTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCTTAATTGGGGGATTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGATTCTGGCTTCTTCCCCCATCTTTAACCCTTCTTTTATTATGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG449232, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609837 Chydorus brevilabris water mite diet isolate 9675-BHL032417-GBD22413_3276-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGACTTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGCATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTTTAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTGAATAAATTAAGTTTCTGGCTTCGTCCCCCAGCTTTAACCCGACTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609838 Chydorus brevilabris water mite diet isolate 9677-BHL032417-GBD10097_5713-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAACAATTTCCGTTTCTGGCTTCGTGCCTCAGCTATAACCCTGCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609839 Chydorus brevilabris water mite diet isolate 9678-BHL032417-GBD21564_4873-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAGTTTGATCTGGAATATTGGGCACTTCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGTACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTATAGTTATGCCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCGTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609840 Chydorus brevilabris water mite diet isolate 9679-BHL032417-GBD26683_7372-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGGATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAACAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTGTGGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATTATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCGTCGTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609841 Chydorus brevilabris water mite diet isolate 9680-BHL032417-GBD24512_16242-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTGTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTGGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAACCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGCCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTACATTTAGCAGGGGGGGCAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609842 Chydorus brevilabris water mite diet isolate 9683-BHL032417-GBD13697_5138-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATCCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAAGTTACAATGGTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCCTAATTGGAGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCCCCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609843 Chydorus brevilabris water mite diet isolate 9685-BHL032417-GBD16125_3757-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGTACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATGTTTTTTATAGTTATACACATCATAAGTGGGGGGTTTGGAAACTGGCTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCTAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609844 Chydorus brevilabris water mite diet isolate 9686-BHL032417-GBD3396_15380-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTTTATTTTCTCTTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCATGTTAATTCGAGTAGAATTAGGACAAAGAGGGACACTTATTGGAAATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTTTCCCCCTAATATTAGGGGCACCCGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG449232, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609845 Chydorus brevilabris water mite diet isolate 9694-BHL032417-GBD12973_2070-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGTACCCTTATTGGTGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTATCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCGACGTTGAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609846 Chydorus brevilabris water mite diet isolate 9699-BHL032417-GBD29011_14374-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTCTTTATTTTCTCTTTGGACTTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAAGTTAAGTTTCTGGCTACTTCCCCCAGCTTTAACCCTTCATTTAGAAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609847 Chydorus brevilabris water mite diet isolate 9709-BHL032417-GBD24464_9211-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAAAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCGAATTTACAATGTTATCGTCACTGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAAAATAAGTTTCTGGCTTCGTCCCCCAGCTTTAACCCTTCGTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609848 Chydorus brevilabris water mite diet isolate 9711-BHL032417-GBD23877_21031-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTCTTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTTATTCGAGCAGAATTAGGACAAAGATGGACCGTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGACTAAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGTAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609849 Chydorus brevilabris water mite diet isolate 9761-BHL040517-GBD27236_13313-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAATGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGTACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTATATTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTTCCCTTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGATTCTGGCTTCTTCCCCCCGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609850 Chydorus brevilabris water mite diet isolate 9818-BHL040517-GBD14634_4725-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTATATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACATAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACAGCACATGCATTTGTTATAATTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCCCCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGACAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609851 Chydorus brevilabris water mite diet isolate 12104-BHL040517-GBD9385_11440-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTCCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGGGGGACCCTTATTGGAGATGATAAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTCCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTT	Using NCBI BLASTN in June 2018, this sequence was 98.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609852 Chydorus brevilabris water mite diet isolate 12277-BHL040517-GBD19689_4739-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGAGCAACGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCCATCATAATTGGAGGGTTTGGAAAATGACTTGTCCCCCTAATATTAGGAGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609853 Chydorus brevilabris water mite diet isolate 12307-BHL040517-GBD13682_13891-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGTGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCCATCCTAATTGGGGGTTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTAAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTATCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609854 Chydorus brevilabris water mite diet isolate 12374-BHL040517-GBD20121_3717-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTATATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCATGTTAATTCGAGCAGAATTAGGACAAAGAGGTACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCCTTTGTTATAATATTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAACCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGCGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609855 Chydorus brevilabris water mite diet isolate 12399-BHL040517-GBD13033_3536-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAAATAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTGTTGTCACTGCACATGCCTTTGTTATAATATTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCACGTCTTAATAATTTAAGTTTCTGGATTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGAGGGGGCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609856 Chydorus brevilabris water mite diet isolate 12472-BHL040517-GBD9246_10570-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGATCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTTACTGCTCATGCTTTTATTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTTGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609857 Chydorus brevilabris water mite diet isolate 12485-BHL040517-GBD5493_12123-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCTGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTAGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCGCGTCTTAACAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTACTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609858 Chydorus sp. water mite diet isolate 8497-BHL101416-GBD7385_9235-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGTTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATAAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGACTAAATAATATAAGATTCTGACTACTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609859 Chydorus sp. water mite diet isolate 8513-BHL101416-GBD19833_5792-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCATTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAACGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGGAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATC-GTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609860 Chydorus sp. water mite diet isolate 8534-BHL101416-GBD11529_9276-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGTGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTC-GTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609861 Chydorus sp. water mite diet isolate 8627-BHL101416-GBD6218_20719-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGCGGGACCTTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGAGGGTTTGGAAACTGACTTGTCCCCCTAATATTTGGGGCACCTGATATAGCCTTCCCTCGTATTAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGTACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609862 Chydorus sp. water mite diet isolate 8648-BHL101416-GBD25729_23798-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTATCCCCCTAATATTAGGGGCACCTGATATAACCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCTTCATTAAC---TCTTTTACTTTCAAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609863 Chydorus sp. water mite diet isolate 8675-BHL101416-GBD17775_6615-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAAAATTAGGACAAAGAGGGACCCTTATTGGAGATGATAAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGCTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTC-GTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID EU702113, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609864 Chydorus sp. water mite diet isolate 8763-BHL101416-GBD10082_13037-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGGAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTGTTGTTATACCCATCATAATTGGAGGATTTGGAAACTGACTTGTCCCCTTAATATTAGGGGCACCTGATATAGCCTTCCCTCGACTAAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTACTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609865 Chydorus sp. water mite diet isolate 8770-BHL101416-GBD6494_9490-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGTGGGACCCTTATTGGAGATGATCAAATTTACAACGTTATTGTCACTGCACTTGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATATTTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTAAATAATATAAGTTTCTGGCTACTTCCCCCAGCTTTAACCCTACTTTTAGTAGGGGGAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609866 Chydorus sp. water mite diet isolate 8798-BHL101416-GBD17443_9978-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGCCTCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATACTGTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCATAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGGCAGTAGAAAATCGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG449232, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609867 Chydorus sp. water mite diet isolate 8811-BHL101416-GBD22063_4427-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGTGATGACCAAATTTACAATGTTATTGTCACTGCACATGCCTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCCGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609868 Chydorus sp. water mite diet isolate 9539-BHL032417-GBD4749_9100-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGATTCTGGCGACTTCACCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609869 Chydorus sp. water mite diet isolate 9546-BHL032417-GBD6108_7308-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTTTTGGCCTGTTAATTCGAGCAGAATTAGGACAAAAAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTCATAGTTATACCCATTATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTATTAGGGGGGGCAGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609870 Chydorus sp. water mite diet isolate 9554-BHL032417-GBD25232_19544-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTTTTAATTCGAGCAGAATTAGGACAAATAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATATCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGACTTAATAATATAAGTTTCTGGCTACTTCCCCCAGCATTAACCCTACTTTTAGCAGGGGGGGCAGTAGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609871 Chydorus sp. water mite diet isolate 9563-BHL032417-GBD17654_17570-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGAAATAGCCTTCCCTCGGCCTAAAAAATTAAGGTTCCGGGCTCCTCCCCCAGCCTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609872 Chydorus sp. water mite diet isolate 9564-BHL032417-GBD19463_28210-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTTTATTTTCTTTTTGGAATTTGAGCTGGAATAGTGGGCACTGCTTTTAGCCTGTTTATTCGAGCAGAATTAGGACAAAAAGGGACTTTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGAGCACCTGATATAGCCTTCCCTCGTCTAAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCGTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609873 Chydorus sp. water mite diet isolate 9566-BHL032417-GBD26848_16748-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTTTTTGGAATTTGAGCTGGAATAGTGGGCGCTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGACTTAATAATATAAGTTTCTGGCTACTTCCCCCAGCTTTAACCCTTCTAATAGCAGGGAGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609874 Chydorus sp. water mite diet isolate 9567-BHL032417-GBD19537_13908-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGACTAGTTCCCTTAATATTAGGAGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCTTTAACTCTTCTTTTA	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID MG449896, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609875 Chydorus sp. water mite diet isolate 9568-BHL032417-GBD8827_18028-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAGTTTGAGCTGGAATAGTGGGCACTGCTTTTAGACTGTTAATTCGAGCAGAATTAGGACAACGAGGGACCTTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGAGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTAAATAATATAAGATTCTGGCTACTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609876 Chydorus sp. water mite diet isolate 9570-BHL032417-GBD6888_5716-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTCTTTGGAGTTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACACTTATTGGAGATGATCAAATTTATAATGTTATTGTTACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCACTAATATTAGGAGCACCTGATATAGCCTTCCCTCGTCTAAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609877 Chydorus sp. water mite diet isolate 9574-BHL032417-GBD27137_22591-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTTTTAGCATGTTAATTCGAGCAGAATTAGGACAAAGGGGGACCTTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTAGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTATCAGGGGGAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609878 Chydorus sp. water mite diet isolate 9575-BHL032417-GBD17812_19539-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACTCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATTTTAATTGGGGGGTTTGGAAACTGACTTGTTCCCCTAATATTAGGAGCACCTGATATAGCCTTCCCTCGTATAAATAATATAAGATTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609879 Chydorus sp. water mite diet isolate 9576-BHL032417-GBD4152_8491-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGATCTGGAATAGTGGGCACTGCTCTTAGCCAGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGTGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTATAAATAATATAAGTTCCTGACTACTTCCCCCAGCTTTAACCCTACTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609880 Chydorus sp. water mite diet isolate 9580-BHL032417-GBD15041_13270-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGATCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCTTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCTCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTATAAATAATATAAGATTCTGGCTACTACCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609881 Chydorus sp. water mite diet isolate 9582-BHL032417-GBD13685_11411-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTATATTTGGAGTTTGATCTGGAATAGTGGGCACTGCTTTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCTTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATTTTAATTGGGGGGTTTGGAAACTGACTAGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGACTAAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609882 Chydorus sp. water mite diet isolate 9586-BHL032417-GBD20169_11802-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAGTTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGTCAAAGAGGAACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGTGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATATAAGTTTCTGGCTACTTCCCCCAGCTTTAACCCTTCTTTTGGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609883 Chydorus sp. water mite diet isolate 9588-BHL032417-GBD6346_25682-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTTTATTTTCTTTTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGTCTGTTAATTCGAGCAGAGTTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGAGCACCTGATATAGCCTTCCCTCGTCTAAATAATATAAGTTTCTGACTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609884 Chydorus sp. water mite diet isolate 9594-BHL032417-GBD4648_23742-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTATATTTTCTTTTTGGACTTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGGGGGACACTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGAGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTACTTCCCCCAGCTTTAACCCTACTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609885 Chydorus sp. water mite diet isolate 9597-BHL032417-GBD3911_22734-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTTTATTTTCTTTTTGGAATTTGAGCTGGAATAGTGGGCACTGCTTTTAGCATGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTTATTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGAGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCGTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609886 Chydorus sp. water mite diet isolate 9598-BHL032417-GBD20100_13866-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGAACTGCTTTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGTGGGACCTTTATTGGAGATGATCAAATTTACAATGTTATTGTTACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTTTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGACTAAATAATATAAGATTCTGACTTCTTCCCCCAGCTTTAACCCTACTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609887 Chydorus sp. water mite diet isolate 9599-BHL032417-GBD24674_20818-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTTTTTGGAATTTGAGCTGGAATAGTGGGCACTGCTTTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTTACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGTTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCTCCTGATATAGCCTTCCCTCGTCTAAATAGTTTAAGTTTCTGGCTACTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609888 Chydorus sp. water mite diet isolate 9600-BHL032417-GBD7310_11333-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTCTTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCCTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGAGGCACCTGATATAGACGCCCCTCGTCTTAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTGCTTTTAGAAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609889 Chydorus sp. water mite diet isolate 9601-BHL032417-GBD22687_7721-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTTTTAGTCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACTCTTATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCTTAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATACAGCCTTCCCTCGTCTAAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGCGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609890 Chydorus sp. water mite diet isolate 9604-BHL032417-GBD25106_6151-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTTTTTGGAATTTGAGCTGGAATAGTGGGCACTGCTTTTAGCATGTTAATTCGAGCAGAATTAGGACAAAGAGGGACTCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGAGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGACTAAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTACTTTTAGTAGGGGGGGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609891 Chydorus sp. water mite diet isolate 9605-BHL032417-GBD23064_5092-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTCTTTATTTTCTTTTTGGAGTTTGAGCTGGAGTAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCTTTATTGGAGATGATCAAATTTATAATGTTATTTTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGGCTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTAAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609892 Chydorus sp. water mite diet isolate 9606-BHL032417-GBD16963_1877-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGCATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGTGGGACCTTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGGCTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCAACTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609893 Chydorus sp. water mite diet isolate 9607-BHL032417-GBD27322_14345-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTCTTTGGAGTTTGAGCTGGAATAGTGGGCACTGCTCTTAGCTTGTTAATTCGAGCAAAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCTTAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTACTATTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609894 Chydorus sp. water mite diet isolate 9609-BHL032417-GBD28435_12502-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTATTTTTGGAGTTTGAGCTGGAATAGTGGGCACTGCTCTTAGTATGTTAATTCGAGCAGAATTAGGACAAAGAGGAACCTTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATTATAATTGGGGGGTTTGGAAACTGACTTGTCCCTCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTAAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609895 Chydorus sp. water mite diet isolate 9612-BHL032417-GBD21165_11548-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATCGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATATAAGTTTCTGGCGGCTTGGCCCAGCTATAAACCTGCGTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609896 Chydorus sp. water mite diet isolate 9615-BHL032417-GBD18241_9153-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCTGAATTAGGACAAAGAGGGTCCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCCATCATAATTGGGGGATTTGGAAACTGACTTGTCCCCCTAATATTAGGAGCACCTGATATAGCCTTCCCTCGTCTGAATAATTTAAGTTTCTGGCTTCGTCCCCCAGCTTTAACCCTACTTCTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609897 Chydorus sp. water mite diet isolate 9617-BHL032417-GBD24797_11806-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGCGGGACACTTATTGGAGATGATCAAATTTACAATGTTATCGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGTGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGCATAAATAATATAAGTTTATGGCTTCTTCCCCCAGCTTTAACCCTACTTTTAGTAGGGGCGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609898 Chydorus sp. water mite diet isolate 9619-BHL032417-GBD26927_16675-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTCTTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAATGAGGGATCCTTATTGGAGATGATCAAATCTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATAATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTGAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTACTATTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609899 Chydorus sp. water mite diet isolate 9622-BHL032417-GBD27085_10547-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTTTATTTTCTATTTGGAGTTTGAGCTGGAATAGTGGGCATTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAGTTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCTTAATTGGGGGGTTTGGAAATTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTAAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCCTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609900 Chydorus sp. water mite diet isolate 9626-BHL032417-GBD9565_18887-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTTTTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAAAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTCATAGTTATACCCATTATAATTGGAGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCCGATATAGCCTTCCCTCGACTAAATAATATAAGATTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609901 Chydorus sp. water mite diet isolate 9627-BHL032417-GBD23605_22908-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGATTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCCCCTGATATAGCCTTCCCTCGACTTAATAATATAAGTTTCTGGCTTCTACCCCCAGCTTTAACCCTACTGTTAGTAGGGAGAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609902 Chydorus sp. water mite diet isolate 9628-BHL032417-GBD26674_19768-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTTCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATTTTAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGACTTAATAATTTAAGTTTCTGGCTATTACCCCCAGCTTTAACCCTACTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609903 Chydorus sp. water mite diet isolate 9630-BHL032417-GBD16478_7885-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTCATAATTTTTTTTATAGTTATACCCATCATAATTGGAGGGTTTGGAAACTGACTAGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCGCGTATAAATAATATAAGATTCTGGCTACTACCCCCAGCATTAACCCTACTTTTAGTAAGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609904 Chydorus sp. water mite diet isolate 9631-BHL032417-GBD20037_20424-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGATCTGGAATAGTGGGCACTGCTTTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGTACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTAATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCGCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGACTAAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTACTATTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609905 Chydorus sp. water mite diet isolate 9633-BHL032417-GBD19783_3606-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTATATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGTGGGTTTGGAAACTGACTAGTCCCCCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGTCTTAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTACTTTTAGTAGGGGGAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609906 Chydorus sp. water mite diet isolate 9634-BHL032417-GBD28633_20566-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTTTTTGGATTTTGAGCTGGAATAGTGGGCACTGCTCTTAGTCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTAAATAATTTAAGTTTCTGACTTCTGCCCCCAGCTTTAACCCTACTATTAGCAAGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609907 Chydorus sp. water mite diet isolate 9635-BHL032417-GBD10614_19401-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTATGACAAAGAGGGACCCTTCTTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTGTAATTTTTTTTATAGTTATACCCATCTTAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAAAAAATTAAGATTCTGGCTTCTTCCCCCAGCTTTAACCCCACTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609908 Chydorus sp. water mite diet isolate 9637-BHL032417-GBD12613_5127-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGCATTTGAGCTGGGATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGACTTAGGACAAAGCGGGACCTTTATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGAGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGAGCACCTGATATAGCCTTCCCTCGTCTAAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609909 Chydorus sp. water mite diet isolate 9638-BHL032417-GBD25375_7972-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGGGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGAGGGTTTGGAAACTGGCTTGTCCCCCTAATATTAGGAGCACCTGATATAGCCTTCCCACGTCTAAATAATATAAGATTCTGACTACTACCACCAGCTTTAACCCTACTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609910 Chydorus sp. water mite diet isolate 9641-BHL032417-GBD22967_11632-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTACTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCGCCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCGTCGGGCCCCAGCTATAAACCGGCTTTTAGAAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609911 Chydorus sp. water mite diet isolate 9644-BHL032417-GBD16294_21214-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTTTTTGGAGTTTGATCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGGAGAATTAGGTCAAAGAGGGACTTTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACACGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCGCCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609912 Chydorus sp. water mite diet isolate 9647-BHL032417-GBD24612_21932-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGCATAGTGGGCACTGCTTTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGTACCCTTATTGGAGAGGATCAAATTTACAATGTTATTGTTACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATTATAATTGGGGGATTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGACTTAATAATTTAAGTTTCTGGCTACTTCCCCCAGCTTTAACCCTACTATTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609913 Chydorus sp. water mite diet isolate 9648-BHL032417-GBD14458_9927-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTTTTTGGAGTTTGATCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACATTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTCGTTATAATCTTTTTTATAGTTATACCCATTATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGACTTAATAATTTAAGATTCTGGCTACTTCCCCCAGCTTTAACCCTACTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609914 Chydorus sp. water mite diet isolate 9653-BHL032417-GBD9882_22484-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGTGCACCTGATATAGCCTTCCCTCGTCCTAATAATATAAGTTTGTGGGTTCGTCCCCCAGCTTTAAACCGGCGTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609915 Chydorus sp. water mite diet isolate 9654-BHL032417-GBD27472_18280-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTACTTTATTTTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGCTAATTCGAGCAGAATTAGGACAACGAGGGACTCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATTATAATTGGAGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGAGCACCTGATATAGCCTTCCCTCGACTAAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609916 Chydorus sp. water mite diet isolate 9660-BHL032417-GBD20831_27344-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTGTATTTTCTTTTTGGAATTTGAGCTGGAATAGTGGGAACTGCTCTTAGCATGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGAGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAACCTTCCCTCGACTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609917 Chydorus sp. water mite diet isolate 9662-BHL032417-GBD27126_22573-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATATTGGGCACTGCTCTTAGTCTGTTAATTCGAGCAGAATTAGGACAACGGGGGACTCTTATTGGAGATGATCAAATTTACAATGTTATTGTAACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGACTTAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609918 Chydorus sp. water mite diet isolate 9663-BHL032417-GBD26667_13101-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTTAGCTGGAATAGTGGGCACTTCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCCATTATAATTGGTGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCCCCTGATATAGCCTTCCCTCGACTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609919 Chydorus sp. water mite diet isolate 9665-BHL032417-GBD28889_19268-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTTTTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGTCTGTTAATTCGAGCAGAATTAGGACAAAGTGGGACCGTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTCATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGACACCTGATATAGCCTTCCCTCGTCTTAATAATGTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609920 Chydorus sp. water mite diet isolate 9666-BHL032417-GBD24105_16385-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTATATTTGGAATTTGAGCTGGAATAGTGGGAACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCACATGCTTTTGTTATAATTCTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGAGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTCTAGCAGGGGGAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609921 Chydorus sp. water mite diet isolate 9667-BHL032417-GBD20014_26429-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCTCTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAACAGGGACCCTTATTGGAGATGACCAAATTTATAATGTTATTGTTACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATTATAATTGGAGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGAGCACCTGATATAGCCTTCCCTCGTCTTAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609922 Chydorus sp. water mite diet isolate 9668-BHL032417-GBD7286_21176-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTTTATTTTCTTTTTGGAATCTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCTTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAATTATACCCATCTTAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGAGCACCTGATATAGCCTTCCCTCGTCTTAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTACTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609923 Chydorus sp. water mite diet isolate 9670-BHL032417-GBD12454_25426-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGAACTGCTTTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGCGGGACCCTTATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGATTTGGAAACTGACTTGTCCCCCTAATATTAGGTGCACCTGATATAGCCTTCCCTCGTCTAAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAAGGGCGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609924 Chydorus sp. water mite diet isolate 9671-BHL032417-GBD19754_8122-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGATCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAATCTGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTAAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609925 Chydorus sp. water mite diet isolate 9674-BHL032417-GBD26405_18812-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTCTTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGTACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGAGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGACTAAATAACATAAGTTTCTGGCTACTTCCCCCAGCTTTAACCCGACTTTTAGCAGGGGGGGCAGGAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609926 Chydorus sp. water mite diet isolate 9676-BHL032417-GBD11056_21558-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCATGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCCATCTTAATTGGGGGGTTTGGAAACTGACTTGTCCCCTTAATATTAGGGGCACCTGATATAGCCTTCCCCCGTCTTAATAATTTAAGTTTCTGACTTCTTCCCCCAGCTTTAACCCTTCTTTTATCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609927 Chydorus sp. water mite diet isolate 9681-BHL032417-GBD28895_14415-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTCTTTGGAATTTGCGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATGATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCGTCCCTCGTCTTAATAATTTAAGGGTCTGGCTTCTTCCCCCAGCTGTAACCCAGCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609928 Chydorus sp. water mite diet isolate 9684-BHL032417-GBD22653_6120-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTTCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGTACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCCATCATAATTGGTGGGTTTGGAAACTGACTTGTCCCACTAATATTAGGGGCACCTGATATAGCATTCCCTCGACTAAATAATATAAGATTCTGGCTACTTCCCCCAGCTTTAACCCTTCTTTTAGGAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609929 Chydorus sp. water mite diet isolate 9691-BHL032417-GBD28205_12386-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTTTTTGGAGTTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGTCCTTTATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAACATTAGGTGCACCTGATATAGCCTTCCCTCGACTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTACTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609930 Chydorus sp. water mite diet isolate 9692-BHL032417-GBD16628_13886-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAGTTTGAGCTGGAATAGTGGGCACTGCTTTTAGCATGTTAATTCGAGTAGAATTAGGACAAAGAGGCACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTCTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTGGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTACTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609931 Chydorus sp. water mite diet isolate 9693-BHL032417-GBD25099_12307-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTTTTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGAACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTATAGTAATACCCATCATAATTGGAGGGTTTGGAAACTGACTTGTACCCCTAATATTAGGGGCACCTGATATAGCCTTCCCACGACTAAATAATTTAAGATTCTGGCTACTACCCCCAGCTTTAACCCTACTATTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609932 Chydorus sp. water mite diet isolate 9695-BHL032417-GBD15399_23455-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTTTTTGGAATTTGATCTGGTATAGTGGGCACTGCTCTTAGTCTGTTTATTCGAGCAGAATTAGGACAAAGTGGGATCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTAAATAATTTAAGGTTCTGGCTACTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609933 Chydorus sp. water mite diet isolate 9696-BHL032417-GBD19131_5506-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCTTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCTCATGCTTTTATTATAATTTTTTTATGGTTATACCCATTATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATATAAGCTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTGGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609934 Chydorus sp. water mite diet isolate 9697-BHL032417-GBD13497_22575-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCCCATGCTTTTGTTATAATTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTAAATAATATAAGATTCTGACTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGAGAACAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609935 Chydorus sp. water mite diet isolate 9700-BHL032417-GBD8913_12801-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAGTTTGAGCCGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCTTTATTGGAGATGATCAAATTTACAATGTTACTGTTACTGCACATGCTTTTGTAATAATTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGTGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609936 Chydorus sp. water mite diet isolate 9701-BHL032417-GBD19901_25470-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTTTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTTACTGCTCATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGAGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGACTTAATAATATAAGTTTCTGGCTACGTCCCCCAGCTTTAACCCTACTATTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609937 Chydorus sp. water mite diet isolate 9705-BHL032417-GBD27993_10759-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTTTTTGGAATTTGAGCTGGAATAGTGGGCACTTCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGTCTCTTATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCATTCCCTCGTCTAAATAATATAAGTTTCTGGCTTCTTCCCCCAGCATTAACCCTACTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609938 Chydorus sp. water mite diet isolate 9706-BHL032417-GBD23346_25313-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTTTTTGGAATTTGAGCTGGAATAGTGGGTACTTCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACTCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGAGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGAGGCACCTGATATAGCCTTCCCTCGACTAAATAATATAAGTTTCTGACTTCTTCCCCCAGCTTTAACCCTTCTATTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609939 Chydorus sp. water mite diet isolate 9707-BHL032417-GBD19826_7630-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTTTTTGGAATTTGATCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAAAATTAGGACAAAGCGGGACCATTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGTGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTAAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTATTAGCAGGGGCGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609940 Chydorus sp. water mite diet isolate 12136-BHL040517-GBD7385_9235-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGTTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATAAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGACTAAATAATATAAGATTCTGACTACTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609941 Chydorus sp. water mite diet isolate 12152-BHL040517-GBD19833_5792-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCATTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAACGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGGAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATC-GTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609942 Chydorus sp. water mite diet isolate 12173-BHL040517-GBD11529_9276-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGTGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTC-GTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609943 Chydorus sp. water mite diet isolate 12266-BHL040517-GBD6218_20719-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGCGGGACCTTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGAGGGTTTGGAAACTGACTTGTCCCCCTAATATTTGGGGCACCTGATATAGCCTTCCCTCGTATTAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGTACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609944 Chydorus sp. water mite diet isolate 12287-BHL040517-GBD25729_23798-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTATCCCCCTAATATTAGGGGCACCTGATATAACCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCTTCATTAAC---TCTTTTACTTTCAAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609945 Chydorus sp. water mite diet isolate 12314-BHL040517-GBD17775_6615-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAAAATTAGGACAAAGAGGGACCCTTATTGGAGATGATAAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTCCTCGAATAAATAATATAAGCTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTC-GTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID EU702113, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609946 Chydorus sp. water mite diet isolate 12402-BHL040517-GBD10082_13037-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGGAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTGTTGTTATACCCATCATAATTGGAGGATTTGGAAACTGACTTGTCCCCTTAATATTAGGGGCACCTGATATAGCCTTCCCTCGACTAAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTACTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609947 Chydorus sp. water mite diet isolate 12409-BHL040517-GBD6494_9490-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGTGGGACCCTTATTGGAGATGATCAAATTTACAACGTTATTGTCACTGCACTTGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATATTTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTAAATAATATAAGTTTCTGGCTACTTCCCCCAGCTTTAACCCTACTTTTAGTAGGGGGAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609948 Chydorus sp. water mite diet isolate 12437-BHL040517-GBD17443_9978-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGCCTCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATACTGTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCATAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATCGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG449232, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609949 Chydorus sp. water mite diet isolate 12450-BHL040517-GBD22063_4427-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGTGATGACCAAATTTACAATGTTATTGTCACTGCACATGCCTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCCGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609950 Chymomyza sp. water mite diet isolate 5229-BHL032417-GBD6059_18968-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAACAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTATTTCCTTTAATATTAGGAGCACCTGATATAGCTTTGCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID EU493571, identified in GenBank as Chymomyza procnemis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609951 Chymomyza sp. water mite diet isolate 13728-BHL040517-GBD26033_7603-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGATCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID EU493571, identified in GenBank as Chymomyza procnemis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609952 Coelotanypus sp. water mite diet isolate 2051-BHL022317-GBD18312_15461-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTCATCTTTGGAGCTTGAGCTGGTATAGTAGGTACCTCCCTTAGTATCTTAGTACGAGCTGAATTAGGTCATCCTGGTGCTCTAATTGGTGATGATCAAATTCATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTCTTTATAGTTATACCTATTTTAATTGGAGGATTCGGGAATTGACTAGTTCCTTTAATATTAGGTGCCCCTGATATAGCCTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTTCTTCTT-TCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR085247, identified in GenBank as Coelotanypus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609953 Copepoda sp. water mite diet isolate 604-BHL072216-GBD16028_25235-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTAATTGCAGGTGCTTGGGCAGGATTAATTGGTACAGGTTTAAGTTTAATTATTCACCTTGAGTTAGGACAACCAGGATCTCTTCTACAAGATGACCAAATTTATAATGTAGTAGTAACTGCGCATGCCTTTATTATAATTTTTTTTATGGTAATACCAATTTTAATTGGGGGTTTTGGTAATTGACTTGTGCCTTTAATATTAGGATCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTCTGATTTCTGAGTCCCGCTTTAATTATACTTTTATTTAGATCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID MG449281, identified in GenBank as Cyclopidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609954 Cricotopus sp. water mite diet isolate 766-BHL040916-GBD26918_15740-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTCTAAGAATTTTAATTCGAGCAGAATTAGGACATGCTGGCTCATTAATTGGTGATGATCAAATTTATAATGTGATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTACCCCCTTCTCTTACATTATTACTATCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM995443, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609955 Cricotopus sp. water mite diet isolate 768-BHL040916-GBD10339_13780-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACATCTTTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTCATTAATTGGTGATGATCAAATTTATAATGTGATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTTATAATTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTTACATTATTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM995443, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609956 Cricotopus sp. water mite diet isolate 771-BHL040916-GBD22969_26182-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCATGATCAGGAATAGTAGGGACTTCTTTAAGAATTTTAATTCGGGCCGAATTAGGACATTCTGGTTCTTTAATTGGTGATGATCAAATTTATAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCCAACATTATTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR629900, identified in GenBank as Cricotopus trifasciatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609957 Cricotopus sp. water mite diet isolate 774-BHL040916-GBD21960_3651-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACATCTTTAAGAATTTTAATTCGAGCCGAATTAGGACATCCTGGCTCATTAATTGGTGATGATCAAATTTATAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCATCTCTTACGTTATTACTATCAAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM933933, identified in GenBank as Cricotopus trifasciatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609958 Cricotopus sp. water mite diet isolate 776-BHL040916-GBD8495_10888-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCATGATCGGGAATAGTAGGGACTTCTCTAAGAATTTTAATTCGAGTCGAATTAGGACATGCTGGCTCATTAATTGGAGATGATCAAATTTATAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTCTAATATTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTCTTACATTATTTCTATCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR695870, identified in GenBank as Cricotopus trifasciatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609959 Cricotopus sp. water mite diet isolate 779-BHL040916-GBD20770_22937-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTTGGAGCATGATCAGGAATAGTAGGGACTTCTCTAAGAATTTTAATTCGAGCCGAATTAGGACATCCTGGCTCATTAATTGGTGATGGTCAAATTTATAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTACCCCCTTCTCTAACATTATTACTATCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM933933, identified in GenBank as Cricotopus trifasciatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609960 Cricotopus sp. water mite diet isolate 780-BHL040916-GBD16105_23652-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGGACTTCTCTAAGAATTTTAATTCGGGCCGAATTAGGACATGCTGGCTCATTAATTGGTGATGATCAAATTTATAATGTGATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGTGCTCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCTTCTCTAACATTACTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM933933, identified in GenBank as Cricotopus trifasciatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609961 Cricotopus sp. water mite diet isolate 782-BHL040916-GBD25247_13467-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGGACATCTTTAAGAATTTTAATCCGGGCCGAATTAGGACACGCTGGCTCTTTAATTGGTGATGATCAAATTTATAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCACTAACATTATTACTATCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM933933, identified in GenBank as Cricotopus trifasciatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609962 Cricotopus sp. water mite diet isolate 783-BHL040916-GBD19672_2556-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCATGATCAGGAATAGTAGGGACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGACATCCTGGCACATTAATTGGTGATGATCAAATTTATAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCAATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCACTAATATTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTCTTACATTATTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM933933, identified in GenBank as Cricotopus trifasciatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609963 Cricotopus sp. water mite diet isolate 784-BHL040916-GBD24958_20524-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGGACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGACATGCTGGGTCATTAATTGGGGATGATCAAATTTATAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAAATGATTAGTTCCTCTAATATTAAGTGCTCCTGATATAACTTTCCCTCGAATAAATAAAATAAATTTTTGACTTCTTCCCCCTTCTCTAACATTATTACTTTCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR695870, identified in GenBank as Cricotopus trifasciatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609964 Cricotopus sp. water mite diet isolate 785-BHL040916-GBD22526_20787-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCATGATCAGGAATAGTAGGGACATCTCTAAGAATTTTAATTCGGGCTGAATTAGGACATCCTGGCTCATTAATTGGAGATGATCAAATTTATAATGTGATTGTTACAGCACATGCATTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGTGCTCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTCTAACATTATTACTTTCAAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM995443, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609965 Cricotopus sp. water mite diet isolate 788-BHL040916-GBD10576_10993-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGGACTTCTTTAAGAATTTTAATTCGGGCCGAATTCGGACACGCTGGTTCTTTAATTGGTGATGATCAAATTTATAATGTGATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTTACATTATTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM995443, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609966 Cricotopus sp. water mite diet isolate 791-BHL040916-GBD7369_16139-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTTGGAGCATGATCAGGAATAGTAGGGACTTCTTTAAGAATTTTAATTCGGGCCGAATTAGGACACGCTGGCTCATTAATCGGAGATGATCAAATTTATAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCACTAACATTATTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR695870, identified in GenBank as Cricotopus trifasciatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609967 Cricotopus sp. water mite diet isolate 819-BHL100916-GBD10501_5006-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCTTTAATACTTGGGGCACCAGATACAGCCTTTCCCCGGATAAATAACATAAGTTTTTGACTTCTACCCCCATCATTAACTCTTTTGCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR670938, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609968 Cricotopus sp. water mite diet isolate 826-BHL100916-GBD21274_18089-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGATTTAGGTCAGGCCGGCTCATTAATTGGTGACGATCAAATTTATAATGTACTTGTTACAGCCCATGCTTTCGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCATTAATATTTGGGGCACCAGATATAGCCTTTCCCCGGATAAATAACATAAGTTTTTGACTTCTACCCCCATCATTAACTCTTTTGCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR670938, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609969 Cricotopus sp. water mite diet isolate 827-BHL100916-GBD23181_3592-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCCTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTCGGTCATGCTGGTTCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCGTCTCTCACCTTACTACTATCAAGGTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609970 Cricotopus sp. water mite diet isolate 836-BHL100916-GBD11342_11269-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACCTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTCATAGTTATACCTATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609971 Cricotopus sp. water mite diet isolate 837-BHL100916-GBD27244_11034-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTTGGGGCTTGGTCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGTCATGACGGATCATTAATTGGAGATGATGGAATTTATAACGTTATTGTTACAGTTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609972 Cricotopus sp. water mite diet isolate 838-BHL100916-GBD20873_20512-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGACATGCCGGATCATTTATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTAACCTTACTTCTTTCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609973 Cricotopus sp. water mite diet isolate 839-BHL100916-GBD17371_8339-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCATTAACTCTTTTGCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609974 Cricotopus sp. water mite diet isolate 841-BHL100916-GBD12192_27993-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGAGATTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGCCACCCAGGCTCATTAATCGGATACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGAGTTGGAAACTGATTAGTTCCTTTAATGTTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGAGTATTACCCCCTGCTCTCACCTTACTTCTTTCAGGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609975 Cricotopus sp. water mite diet isolate 860-BHL100916-GBD8956_11791-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTGCTTTAGAATCTTAATTCGAGCTGAATTATGTCATGCCGGATCATTAATTGGAGATGATCAACTTTATAACGTTATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTCACCTTACTACTTTCAAGTGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609976 Cricotopus sp. water mite diet isolate 870-BHL100916-GBD9217_3152-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACCTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTGAGAATTTTAATTCGAGCAGAACTCGGTCATGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTCACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTCCCGTTAATATTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTCTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609977 Cricotopus sp. water mite diet isolate 873-BHL100916-GBD15790_16897-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGTGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCACGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609978 Cricotopus sp. water mite diet isolate 881-BHL100916-GBD22679_4184-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAAAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCTTTAATACTTGGGGCACCAGATATAGCCTTTCCCCGGATAAATAACATAAGTTTTTGACTTCTACCCCCATCATTAACTCTTTTGCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR670938, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609979 Cricotopus sp. water mite diet isolate 892-BHL100916-GBD24247_17179-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGCACTTCTTTGAGAATTTTTATTCGAGCAGAACTAGGTCATGCCGGTTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609980 Cricotopus sp. water mite diet isolate 893-BHL100916-GBD13448_9128-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATTTTAATTCGAGCTGAATTCGGTCACGCTGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTATCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609981 Cricotopus sp. water mite diet isolate 898-BHL100916-GBD28200_9791-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTCGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATCCCGGATCATTAATTGGAGATGATCAAATCTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCCTACTTCTATCAAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609982 Cricotopus sp. water mite diet isolate 900-BHL100916-GBD9664_17045-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTGAGAATCTTTATTCGAGCTGAATTAGGACATGCCGGATCATTCATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTCCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATCGTAGAAAATGGAGCCGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609983 Cricotopus sp. water mite diet isolate 913-BHL100916-GBD21375_6702-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCGTCCCGGATCTTTTATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609984 Cricotopus sp. water mite diet isolate 919-BHL100916-GBD23548_3916-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGGACTTCATTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTCATTGGAGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTTGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609985 Cricotopus sp. water mite diet isolate 921-BHL100916-GBD12593_28493-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCGGGAATGGTAGGGACTTCCTTTAGAATCTTAATTCGACCTGAATTAGGTCATGCAGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTAACCTTACTTCTATCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609986 Cricotopus sp. water mite diet isolate 930-BHL100916-GBD16573_4292-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAAGTAGGTCATGCCTGATCATTAATTGGAGATGATCTAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609987 Cricotopus sp. water mite diet isolate 938-BHL100916-GBD11120_25004-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGAACATTCATTGGAGATGATCAAATTTATAACGTTATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCACCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTCACCTTACTTCGTTCAAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609988 Cricotopus sp. water mite diet isolate 939-BHL100916-GBD23644_20140-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTCGGAGCTTGATCAGGTATAGTAGGGACTTCCTTTAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTAATGTTAGGGGCGCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCGTCTCTAACCTTACTACTATCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609989 Cricotopus sp. water mite diet isolate 940-BHL100916-GBD29316_16938-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTACTTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCGCTCACCGGACGGCGGGCAAGGGCAAGGGGGGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609990 Cricotopus sp. water mite diet isolate 950-BHL100916-GBD9757_3404-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTTTATTTTATTTTTGGGGCTTGGTCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGTCATGCCGGCTCATTAATTGGTGACGATCAATTTTATAATGTAATTGTTACAGCCCATGCTTTCGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCTTTAATACTTGGGGCACCAGATATAGCCTTTCCCCGGATAAATAAAATAAGTTTTTGACTTCTACCCCCATCATTAACACTTTTGCAATCTAGCTCAATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR670938, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609991 Cricotopus sp. water mite diet isolate 953-BHL100916-GBD17577_22181-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGCTCATTAATTGGAGATGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGGGCTCCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTATTACCCCCATCACTCACCTTACTACTATCAAGTTCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609992 Cricotopus sp. water mite diet isolate 956-BHL100916-GBD20810_3815-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAGTTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAGTTTATAACGTTCTTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGAGATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCCAACCGTACTTCTGTCAAGTTCTATCGTTGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609993 Cricotopus sp. water mite diet isolate 969-BHL100916-GBD12114_6480-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGCATAGTAGGCACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCGTCACTAACCTTACTACTATCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609994 Cricotopus sp. water mite diet isolate 971-BHL100916-GBD26799_18408-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCTCGATCAGGAATAGTAGGGACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCACTCACCTTACTACTATCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609995 Cricotopus sp. water mite diet isolate 973-BHL100916-GBD14757_21571-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATATTAATTCGAGTTGAATTAGGACATGCCGGATCATTAATTGGAGATGATCAAATTTATAACATTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATATTAATTGGAGGATTTGGAAACTGGTTAGTACCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAACTGCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW609996 Cricotopus sp. water mite diet isolate 980-BHL100916-GBD24663_20942-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGTATAGTAGGTACTTCCTTGAGAATCTTAATTCGAGCTGAATTCGGTCATGCTGGTTCTTTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTAACCTTACTACTATCAAGCTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609997 Cricotopus sp. water mite diet isolate 981-BHL100916-GBD2834_17932-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTGGGAACTTCCTTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTACCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCCCCTTCTCTCACCTTACTTCTTCCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609998 Cricotopus sp. water mite diet isolate 983-BHL100916-GBD19389_2211-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCCTTGAGTATCTTAATTCGAGCTGAATTAGGGCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGTGCTCCTGATATAGCTTTCCCCCGAATAAATAACATAAGTTTTTGATTATTACCCCCTTCTCTAACCCTACTTCTATCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW609999 Cricotopus sp. water mite diet isolate 985-BHL100916-GBD21846_7833-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTTATTCGAGCTGAATTAGGTCATCCCGGATCTTTAATTGGAGATGATCAAATTTATAATGTTATCGTTACTGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTCCCTTTAATGTTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCCTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610000 Cricotopus sp. water mite diet isolate 986-BHL100916-GBD27442_19575-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGTTCATTAATTGGAGATGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTAACCTTACTATTATCTAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610001 Cricotopus sp. water mite diet isolate 994-BHL100916-GBD20253_4090-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCCCCTTCTCTAACCTCACTTCTATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610002 Cricotopus sp. water mite diet isolate 995-BHL100916-GBD7009_17780-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGGCACGCAGGATCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCCCCTTCTCTCACCTTACTTCTATCAAGTTCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610003 Cricotopus sp. water mite diet isolate 1001-BHL100916-GBD28731_16520-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGTGACGAGCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCTTTAATACTTGGGGCACCAGATATAGCCTTTCCCCGAATAAATAACATAAGATTTTGACTTCTACCCCCATCATTAACTCTATTGCTTTCTAGCACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR670938, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610004 Cricotopus sp. water mite diet isolate 1004-BHL100916-GBD7234_12462-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCAAGTTGAATTAGGTCATGCCGGCTCATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCTTTAATATTTGGGGCACCAGATATAGCCTTTCCCCGGATAAATAACATAAGTTTTTGACTTCTACCCCCATCATTAACTCTTTTGCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.0% identical to accession ID KR670938, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610005 Cricotopus sp. water mite diet isolate 1013-BHL100916-GBD20259_23382-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCTTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCTTTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCACTAACCTTACTACTATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610006 Cricotopus sp. water mite diet isolate 1014-BHL100916-GBD28010_14461-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGCACATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCACTCACCTTACTTCTATCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610007 Cricotopus sp. water mite diet isolate 1020-BHL100916-GBD25327_8855-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTGGGGACTTCTTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGTTCTTTAATTGGAGATGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTCTCACCTTACTACTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610008 Cricotopus sp. water mite diet isolate 1021-BHL100916-GBD6778_14489-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGTTGAATTATCACATCCCGGATCATTATTTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTGCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610009 Cricotopus sp. water mite diet isolate 1023-BHL100916-GBD4318_17439-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGGGCTTGATCAGGAATAGTAGGAACTTCCTTGAGAATCTTTATTCGAGCTGAATTAGGACATGCCGGATCATTCATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCACATGCTTTTATAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGAAAACTGATTAGTTCCTTTAATGTTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCCTCTCTCACCTTACTTCCTTCAAGTTCAATCGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610010 Cricotopus sp. water mite diet isolate 1027-BHL100916-GBD6678_9653-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTAAGAATCTTAATTCGAGCTGAATTCGGTCATGCCGGATCTTTAATTGGAGATGATCAAATTTATAACGTTATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTTGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTACTATCTAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610011 Cricotopus sp. water mite diet isolate 1034-BHL100916-GBD9791_11729-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCCTTTAGAATCTTAATTCGAGCTGAATTTGGTCATGCAGGATCTTTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTATAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610012 Cricotopus sp. water mite diet isolate 1039-BHL100916-GBD6643_17084-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGCAGGGACTTCCTTGAGAATCTTTATTCGAGCTGAATTAGGTCAAGCCGGATCTTTCATTGGAGATGATCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATCGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610013 Cricotopus sp. water mite diet isolate 1041-BHL100916-GBD13263_7017-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCCTTGAGAATTTTAATTCGAGCTGAATTAGGACATGCCGGATCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATGTTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACCTTACTACTATCAAGTTCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610014 Cricotopus sp. water mite diet isolate 1042-BHL100916-GBD18994_3247-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGGGCTTGGTCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAACTAGGTCATGCCGGCTCATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAACTGATTAGTTCCTTTAATATTTGGAGCACCAGATATAGCCTTTCCCCGAATAAATAACATAAGTTTTTGACTTCTACCCCCATCATTAACTCTTTTGCTTTCAAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR670938, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610015 Cricotopus sp. water mite diet isolate 1051-BHL100916-GBD28564_14735-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGAGCTTGATCAGGCATAGTAGGGACTTCCTTGAGAATTTTAATTCGAGCTGAATTAGGTCAAGCCGGATCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCTAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610016 Cricotopus sp. water mite diet isolate 1053-BHL100916-GBD13620_15104-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTTGGGGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGTCATGCCGGCACATTAATTGGTGATGATCAAATTTATAATGTAATTGTTACAGCCCATGCTTTCGTTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCTTTAATACTTGGGGCACCAGATATAGCCTTTCCCCGGATAAATAACATAAGATCTTGACTTCTACCCCCATCATTAACTCTTTTGCTCTCTAGCACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR670938, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610017 Cricotopus sp. water mite diet isolate 1059-BHL100916-GBD24913_6989-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTTGGGGCTTGGTCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGTCACGCCGGATCATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCTTTAATACTTGGAGCACCAGATATAGCCTTCCCCCGAATAAATAACATAAGTTTTTGACTACTACCCCCATCATTAACTCTATTGCTATCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR670938, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610018 Cricotopus sp. water mite diet isolate 1070-BHL100916-GBD25860_20241-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGAACATTTATTGGAGATGACCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTAACCTTACTTCTATCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610019 Cricotopus sp. water mite diet isolate 1074-BHL100916-GBD28543_11383-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCTTGGTCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGACATGCCGGCACATTAATTGGTGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTTGTCCCTTTAATATTAGGGGCACCAGATATAGCCTTTCCCCGAATAAATAACATAAGTTTTTGACTTCTACCCCCATCATTAACTCTTTTGCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR670938, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610020 Cricotopus sp. water mite diet isolate 1075-BHL100916-GBD13872_20803-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGTAGAATTAGGACATGCCGGATCATTAATCGGAGATGATCAAATTTATAACGTTATTGTTACAGCACATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTCACCTTACTTCTATCAAGATCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610021 Cricotopus sp. water mite diet isolate 1076-BHL100916-GBD25131_19741-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGGTCAGGAATAGTAGGAACTTCCTTAAGAATCTTAATTCGAGCTGAATTAGGGCATCCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCCCGAATAAATAACATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610022 Cricotopus sp. water mite diet isolate 1077-BHL100916-GBD26772_20570-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTCGGAGCTTGATCAGGTATAGTAGGGACTTCCTTGAGAATATTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTTGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCCCCTTCTCTCACCTTACTACTATCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610023 Cricotopus sp. water mite diet isolate 1078-BHL100916-GBD25029_21200-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTTTGAGAATCTTAATTCGAGTTGAATTAGGTCATGCCGGATCATTAATCGGAGATGGTCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCACTCACCTTACTTCTATCGAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610024 Cricotopus sp. water mite diet isolate 1079-BHL100916-GBD22107_23942-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTTAGAATCTTAATTCGAGTTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTAACCTTACAACTTTCAAGTGCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610025 Cricotopus sp. water mite diet isolate 1083-BHL100916-GBD27554_14493-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGGACTTCCTTAAGAATTTTAATTCGAGCTGAACTCGGTCATGCTGGATCTTTAATTGGAGATGATCAAATTTATAACGTTATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCACTCACCTTACTACTATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610026 Cricotopus sp. water mite diet isolate 1091-BHL100916-GBD27534_13394-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATCATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGGACTTCCTTGAGAATATTAATTCGAGCTGAATTAGGTCATGCCGGATCATTTATTGGAGATGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCCCCTTCTCTCACCTTACTTCTTTCAAGTACAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610027 Cricotopus sp. water mite diet isolate 1094-BHL100916-GBD28094_21815-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCCTTTAGAATCTTAATTCGAGCTGAATTAGGTCATCCCGGATCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATATTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTCACCTTACTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610028 Cricotopus sp. water mite diet isolate 1095-BHL100916-GBD20240_15438-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATATTTTATTTTTGGAGCTTGGTCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGTCATCCCGGCTCATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCCCATGCTTTCGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATACTTGGGGCACCTGATATAGCCTTTCCCCGGATAAATAACATAAGATTTTGACTACTACCCCCATCATTAACCCTATTGCTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR670938, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610029 Cricotopus sp. water mite diet isolate 1097-BHL100916-GBD24449_24397-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATCTTAATTCGAGCTGAATTAGGACATGCAGGATCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGTGCTCCTGATATAGCTTCCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTAACCTTACTACTATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610030 Cricotopus sp. water mite diet isolate 1099-BHL100916-GBD22219_15136-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGGGCTTGGTCAGGAATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCTGAATTGGGTCATGCCGGCTCATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTTGGGGCACCAGATATAGCCTTTCCCCGGATAAATAACATAAGTTTTTGACTTCTACCCCCATCATTAACTCTATTACGATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR670938, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610031 Cricotopus sp. water mite diet isolate 1104-BHL100916-GBD23802_24538-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGGGCTTGGTCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGTCATGCCGGCTCATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCCCATGCTTTCGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATACTTGGGGCACCAGATATAGCATTCCCCCGGATAAATAACATAAGATTTTGACTACTACCCCCATCACTAACTCTATTGCTTGCTAGCGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR670938, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610032 Cricotopus sp. water mite diet isolate 1696-BHL110116-GBD11338_9981-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAAATGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610033 Cricotopus sp. water mite diet isolate 1715-BHL110116-GBD4767_20569-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATGTGCAGGAATAATTGGAACAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAAATGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610034 Cricotopus sp. water mite diet isolate 1734-BHL110116-GBD13589_16894-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTCGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATCCCGGAACATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAAATGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAACATAAGTTTTTGATTATTACCCCCTTCTCTAACCTTACTTCTATCAAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610035 Cricotopus sp. water mite diet isolate 1735-BHL110116-GBD20135_16544-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAAATGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610036 Cricotopus sp. water mite diet isolate 1775-BHL110116-GBD16054_25341-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTTGGGGCTTGGTCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGCGACGATCAAATTTATAATGTAATTGTTACAGCCCATGCTTTCGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCTTTAATATTAGGTGCACCAGATATAGCCTTTCCCCGGATAAATAACGTAAGTTTTTGACTTCTACCCCCATCATTAACTCTTTTGCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR670938, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610037 Cricotopus sp. water mite diet isolate 1850-BHL072216-GBD13441_15108-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTTGGGGCTTGGTCAGGAATAGTAGGAACTTCTCTAAGAATTTTAATTCGAGCTGAATTCGGTCATGCCGGCTCATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCCCATGCTTTCGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCTTCAATACTTGGGGCACCAGATATAGCATTCCCTCGGATAAATAACATAAGTTTTTGACTTCTACCCCCATCATTAACTCTTTTGCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR670938, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610038 Cricotopus sp. water mite diet isolate 2415-BHL072216-GBD19819_15275-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR960636, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610039 Cricotopus sp. water mite diet isolate 2521-BHL072216-GBD8745_22355-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAAGTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTGTGATTATTACCCCCTTCCCTCACCTTACTAGTATCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610040 Cricotopus sp. water mite diet isolate 3481-BHL032417-GBD14577_23971-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATCTTCGGAGCATGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAACCCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACAGCACATGCTTTTGTTATATTTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGTTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCTTCCTCCTTCTCTTACATTACTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610041 Cricotopus sp. water mite diet isolate 3499-BHL032417-GBD14802_7457-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATCTTCGGAGCATGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTTTTATAGTTATACCTATTTTAATTGGGGAATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCTTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR621135, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610042 Cricotopus sp. water mite diet isolate 3557-BHL032417-GBD12068_8143-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATCCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTTACATTACTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610043 Cricotopus sp. water mite diet isolate 3622-BHL032417-GBD10597_18455-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGACCATCTCTAGGAATTTTAATCCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATGGTTACAGCACATGCTCTTGTTATAATTTTTTTTATAGTTATACCTATTTTAGTTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCTCTTACATTACTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610044 Cricotopus sp. water mite diet isolate 3641-BHL032417-GBD4059_21127-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTCGGAGCATGATCAGGACTAGTAGGAACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACAATCAAATTTACAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGGTTTTGACTTCTTCCTCCTTCTCTTACATTACTACTTTCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610045 Cricotopus sp. water mite diet isolate 3677-BHL032417-GBD13937_28119-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTGTATTCGGAGCCTGATCAGGAATAGTAGGTACTTCCCTTAGTAATCTAGTACGAGCTGAATTAGGACACCCCGGGGCATTAATTGGAGACGATCAAATTTATAACGTAATGGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCTCTTACATTACTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610046 Cricotopus sp. water mite diet isolate 3689-BHL032417-GBD17229_28971-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATCCGGGCCGACTTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACAGCACATGCTTTTGTTTTAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTTCCACTAATATTAGGTGCACCAGATATAGCTTTCCCTCGAATAAATAATATATGCTTTTGATTATTACCCCCATCTTTAACATTACTATTAGCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR621135, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610047 Cricotopus sp. water mite diet isolate 3726-BHL032417-GBD6153_13275-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCCTGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGAATTTGGAAATTGATTAGTCCCTCTTATGCTGGGAGCTCCTGATAAGGCTTTCCCCCGAATAAATAATATAAATTCTTGGCTTCTCCCTCCTTCTTTAACTCTTCTTCTTTCTAGTTCAATGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID KR621135, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610048 Cricotopus sp. water mite diet isolate 3776-BHL032417-GBD5229_12895-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCTTGATCAAGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCTCTTACATTACTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.1% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610049 Cricotopus sp. water mite diet isolate 3807-BHL032417-GBD24242_24567-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCATGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATCCGGGCCGAATTAGGACATGCTGGATCATTAATTGGTGACGATCAAATTTATAATGTGATTGTTACGGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCTCCTTCTCTTACATTACTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR629900, identified in GenBank as Cricotopus trifasciatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610050 Cricotopus sp. water mite diet isolate 3825-BHL032417-GBD11499_2859-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAAGAACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTATTACAGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGCGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCACCTTCTCTTACATTACTACTTTCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610051 Cricotopus sp. water mite diet isolate 3849-BHL032417-GBD18244_27234-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATCCGGGCAGAATTAGGACATGCCGGATCTTTAATTGGTGACGACCAAATTTACAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTCTAACATTACTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610052 Cricotopus sp. water mite diet isolate 3869-BHL032417-GBD4155_20730-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCAGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAACTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTCTTGACTTCTTCCCCCTTCTTCGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610053 Cricotopus sp. water mite diet isolate 3908-BHL032417-GBD25961_12324-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGTGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCTCTTACATTACTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR629900, identified in GenBank as Cricotopus trifasciatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610054 Cricotopus sp. water mite diet isolate 3924-BHL032417-GBD16017_13494-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACATACATTACTCCGTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610055 Cricotopus sp. water mite diet isolate 3938-BHL032417-GBD11195_6234-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCCTGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATCCGAGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCACTTACTCTACTACTTTCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610056 Cricotopus sp. water mite diet isolate 3943-BHL032417-GBD7854_4035-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGTCATGCCGGATCATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTGATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCTCTTACATTACTACTATCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610057 Cricotopus sp. water mite diet isolate 4019-BHL032417-GBD27141_11008-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTTGGAGCATGATCAGGAATAGTAGGAACATCTTTAAGAATTTTTATCCGGGCCAAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTATAATGTGATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCTATTACATTACTACTTTCAAGTCCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610058 Cricotopus sp. water mite diet isolate 4318-BHL032417-GBD5616_18036-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGAACATCCCTAAGAATTTTAATCCGGACCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTATAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTCTTCCTCCTTCTCTTGCATTACTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610059 Cricotopus sp. water mite diet isolate 4450-BHL032417-GBD22294_22983-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAACTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610060 Cricotopus sp. water mite diet isolate 4909-BHL032417-GBD21241_15404-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATTCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTATAATGTGATTGCTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTCTAACATTACTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610061 Cricotopus sp. water mite diet isolate 5040-BHL032417-GBD15558_5182-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610062 Cricotopus sp. water mite diet isolate 5050-BHL032417-GBD15362_11754-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCATGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610063 Cricotopus sp. water mite diet isolate 5059-BHL032417-GBD4675_13710-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTAATGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCATCACTAACTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610064 Cricotopus sp. water mite diet isolate 5092-BHL032417-GBD27640_12010-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCTTGATCTGGAATGGTGGGAACCTCTCTTAGATTTTTATTTCGAGCGGATTTGGGTCACGCGGGTTCTTTATTTGTAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATATTTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATATGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAAATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610065 Cricotopus sp. water mite diet isolate 5121-BHL032417-GBD26511_17201-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGCACTTCTTTTAGAATTTTAATTCGAGTAGAATTAGGTCATGCAGGTTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGTGCCCCAGATATAGCATTCCCGCGAATAAATAACATAAGATTTTGATTATTACCACCTTCATTAACATTATTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610066 Cricotopus sp. water mite diet isolate 5151-BHL032417-GBD14141_2171-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAAAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCCTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610067 Cricotopus sp. water mite diet isolate 5159-BHL032417-GBD15802_20324-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCTGGAATAGTGGGAACTTCTCTTAGAATTTTAATTCGAGCTGAATTAGGTCATGCGGGATCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610068 Cricotopus sp. water mite diet isolate 5175-BHL032417-GBD9305_8286-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCTGGAATAGTGGGTACCTCTTTTAGAATTTTAATTCGAGCAGAACTCGGTCATGCTGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTATTAATTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTACTACCACCGTCATTAACATTATTATTATCAAGATCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610069 Cricotopus sp. water mite diet isolate 5177-BHL032417-GBD28193_10812-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCTGGAATAGTGGGAACTTCTTTTAGAATTTTAATTCGAGCAGAACTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGACATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTTCCCCCTTCATTAACATTACTATTATCAAGATCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610070 Cricotopus sp. water mite diet isolate 5214-BHL032417-GBD15980_11423-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGTTTTAGGTCATGCGGGATCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTTATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCGGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610071 Cricotopus sp. water mite diet isolate 5236-BHL032417-GBD29559_17379-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTATTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGTATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTGTATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCGGTAACAGGAGGAGGAGCAAGAGCGAGGGGAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610072 Cricotopus sp. water mite diet isolate 5243-BHL032417-GBD12063_18214-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATCCGGGTTCTTTTATTGGAGATGATCAATTTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATACTAGGAGCCCCAGATATAGCATTCCCACGAATAAAAAACATAAGATTTTGATTATTACCACCATCTTTAACATTATTACTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610073 Cricotopus sp. water mite diet isolate 5254-BHL032417-GBD16209_17979-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610074 Cricotopus sp. water mite diet isolate 5279-BHL032417-GBD19884_12176-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACCTCTTTTAGAATTTTAATTCGAGCAGAATTCGGTCATGCTGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCCTTTGTAATAATTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCATTAACATTATTATTATCAAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610075 Cricotopus sp. water mite diet isolate 5281-BHL032417-GBD24557_11319-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCTGGTATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTCGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATACTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCATTAACATTATTATTATCAAGATCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610076 Cricotopus sp. water mite diet isolate 5282-BHL032417-GBD8138_18884-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTTAGAATTTTAATTCGAGCAGAACTCGGTCATGCTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGAGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610077 Cricotopus sp. water mite diet isolate 5309-BHL032417-GBD2309_12785-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTCGGTGCCCGATCAGGAATAGTGGGAACTTTCCTAAGAATATTAATTCGAGCTGAACTAGGACATCACGGAACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610078 Cricotopus sp. water mite diet isolate 5319-BHL032417-GBD23838_16812-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCATAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAAATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610079 Cricotopus sp. water mite diet isolate 5345-BHL032417-GBD9811_11415-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGATATAGTAGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTCGGTCATGCTGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGGTTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTACTACCACCGTCATTAACATTACTATTATCAAGATCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610080 Cricotopus sp. water mite diet isolate 5356-BHL032417-GBD25253_15752-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGATTTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610081 Cricotopus sp. water mite diet isolate 5389-BHL032417-GBD10817_14272-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATACTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCCCCGTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610082 Cricotopus sp. water mite diet isolate 5403-BHL032417-GBD23422_21131-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCTGGCATAGTGGGAACTTCTTTTAGAATTTTAATTCGAGCAGAATTCGGTCATGCGGGTTCCTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCTCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCGTCCTTAACATTATTATTATCAAGATCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610083 Cricotopus sp. water mite diet isolate 5408-BHL032417-GBD9346_27469-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTTAATAATATAAGATTTTGACTATTACCCCCATCACTAACTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610084 Cricotopus sp. water mite diet isolate 5431-BHL032417-GBD12237_8343-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTCGGTGCCCGATCAGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATCTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCATTTCTAATTGGGGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610085 Cricotopus sp. water mite diet isolate 5438-BHL032417-GBD6860_4601-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATATTATTTTTGGTGCTTGATCCGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAAAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATAGTTACAGCACACGCATTTATTATAATTTTCTTTATAGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAGCATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610086 Cricotopus sp. water mite diet isolate 5444-BHL032417-GBD14430_6553-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCATGCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACATTATTATTATCTAGCTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610087 Cricotopus sp. water mite diet isolate 5456-BHL032417-GBD14058_5432-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTGTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATTCGTTTTCTTTAATTGTAGATTATCAAATTTACAATGTAATGGTTACTTCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCAAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGCGCTGGATCAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610088 Cricotopus sp. water mite diet isolate 5468-BHL032417-GBD21753_13138-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCTGGTATAGTGGGAACTTCTTTTAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTTTAATTGAAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCGTCTTTAACATTATTATTATCAAGATCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610089 Cricotopus sp. water mite diet isolate 5471-BHL032417-GBD18087_11099-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGTGGGTTCTTTAATTGGAGGTGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAACTGATTAGTCCCTTTAATACTAGGGGCCCCAGATATAGCATTCCCTCGAATAAAAAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610090 Cricotopus sp. water mite diet isolate 5473-BHL032417-GBD4700_13332-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTTTGAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610091 Cricotopus sp. water mite diet isolate 5501-BHL032417-GBD22428_4643-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAATAGGAACATCTTTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCTGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCACCTTCTTTAACATTATTATTATCTAGATCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610092 Cricotopus sp. water mite diet isolate 5514-BHL032417-GBD26475_21583-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCTTGATCCGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCTGGTTCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTATTACCACCTTCTTTAACATTATTATTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610093 Cricotopus sp. water mite diet isolate 5523-BHL032417-GBD22795_24451-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATCTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATACGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610094 Cricotopus sp. water mite diet isolate 5527-BHL032417-GBD28250_19457-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCTTTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCCGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGACTAGTCCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610095 Cricotopus sp. water mite diet isolate 5534-BHL032417-GBD15033_7571-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGTGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGATCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTATAGTAATACCAATTCTAATTAGAGGATTTGGAAACTGATTAGTCCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGACTATTACCCCCTTCTTTAACATTATTACTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610096 Cricotopus sp. water mite diet isolate 5537-BHL032417-GBD27275_12198-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACTTCTTTTAGAATTTTAATTCGAGCAGAATTAGGACATGCGGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCACGAATAAATAACATAAGATTTTGATTATTGCCCCCTTCATTAACATTATTATTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610097 Cricotopus sp. water mite diet isolate 5557-BHL032417-GBD15599_16336-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACTTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATCCTGGATCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTATTATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAAATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610098 Cricotopus sp. water mite diet isolate 5975-BHL032417-GBD28974_13313-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCATGCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACATTATTATTATCAAGCTCTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR445258, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610099 Cricotopus sp. water mite diet isolate 7699-BHL040517-GBD9981_21627-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTAGAATAGTGGGAACCTTTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTCAGACTATTACCTCCTTCTCTAACCCTTCTTCTT-TCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610100 Cricotopus sp. water mite diet isolate 7754-BHL040517-GBD19191_8418-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTTGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610101 Cricotopus sp. water mite diet isolate 7757-BHL040517-GBD24075_10110-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCTTTCTCTTTCTCTTTTACTTTCTAGTTCAATTATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610102 Cricotopus sp. water mite diet isolate 7896-BHL040517-GBD17432_15348-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGATTAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTCTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610103 Cricotopus sp. water mite diet isolate 7967-BHL040517-GBD4830_24020-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGACGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610104 Cricotopus sp. water mite diet isolate 7975-BHL040517-GBD7598_8293-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCTAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610105 Cricotopus sp. water mite diet isolate 8079-BHL040517-GBD12380_20315-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCCTTTGTAATAATTTTTTTATTGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTGCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610106 Cricotopus sp. water mite diet isolate 8083-BHL040517-GBD9854_15279-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAGTTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610107 Cricotopus sp. water mite diet isolate 8096-BHL040517-GBD19134_6143-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTGGTCCCTTTGATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTT-TCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610108 Cricotopus sp. water mite diet isolate 8231-BHL040517-GBD26900_16760-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACATCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGGTCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610109 Cricotopus sp. water mite diet isolate 8618-BHL101416-GBD22244_16176-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTCGGAAATTGATTAGTTCCTCTAACATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCTCTTACATTACTCCTTTCAAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610110 Cricotopus sp. water mite diet isolate 10705-BHL101516-GBD14764_4110-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KT708452, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610111 Cricotopus sp. water mite diet isolate 10725-BHL101516-GBD15731_11263-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCGTAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTCCCACCGTCTCTTTCTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610112 Cricotopus sp. water mite diet isolate 10829-BHL101516-GBD28103_9245-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTGGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCGTCTCTAACCTTACTACTATCAAGTTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610113 Cricotopus sp. water mite diet isolate 10833-BHL101516-GBD9583_4149-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCCCCGTCACTAACCTTACTATTATCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610114 Cricotopus sp. water mite diet isolate 10853-BHL101516-GBD5474_9887-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATGTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCGATTTTAATTGGGGGTTTCGAAAATTGATTAGTTCCTTTAATGTTAGAGGCCCCTGATATAGCCTTCCCGCGAATAAATAATATAAGATTTTGACTTCTCCCACCGTCTCTTTCTCTTCTTCTTTCTAGTGCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KT708452, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610115 Cricotopus sp. water mite diet isolate 10858-BHL101516-GBD6326_21388-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATTTTAATTCGAGTAAAATTAGGACATCCAGGATCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTACCTTTAATATTAGGGGCTCCTGATATAGCTTTCCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCACTCACCTTACTTCTATCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610116 Cricotopus sp. water mite diet isolate 10859-BHL101516-GBD21387_24495-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCAGGATCATTAATTGGTGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTACCTTTAATGTTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTCACCTTACTACTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610117 Cricotopus sp. water mite diet isolate 10878-BHL101516-GBD6566_14460-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATGATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCCCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610118 Cricotopus sp. water mite diet isolate 10908-BHL101516-GBD4679_21922-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTTCCCCCTTCTCTAACCCTACTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610119 Cricotopus sp. water mite diet isolate 11469-BHL101516-GBD17646_2602-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTGTTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCCTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTATTACCCCCTTCTCTTCCCCTACTTCTTTCTAGTTCTTTCGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610120 Cricotopus sp. water mite diet isolate 11503-BHL101516-GBD13550_27187-Lq80 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTATTACCCCCTTCATTCACCTTACTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610121 Cricotopus sp. water mite diet isolate 11504-BHL101516-GBD21993_8726-Lq80 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGTGCTCCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTATTACCCCCATCACTAACCTTACTACTAGCAAGTTCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610122 Cricotopus sp. water mite diet isolate 11507-BHL101516-GBD9704_27887-Lq80 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCGTCACTCACCTTACTACTATCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610123 Cricotopus sp. water mite diet isolate 11508-BHL101516-GBD27191_12690-Lq80 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTACTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAACATAAGATTCTGGTTACTACCTCCGTCTATTTCTTTGCTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KT708452, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610124 Cricotopus sp. water mite diet isolate 11756-BHL101516-GBD27699_9745-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTCGGGACTTCCTTGAGAATATTAATTCGAGCTGAATTAGGACATGCTGGATCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCGTAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCCCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610125 Cricotopus sp. water mite diet isolate 11765-BHL101516-GBD5405_9883-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGCTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATAGCTGTCCCTCGAATAAATAATATAAGTTTTTGACTATTACCCCCTTCACTAACCTTACTTCTTTCAAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610126 Cricotopus sp. water mite diet isolate 11775-BHL101516-GBD14383_1955-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGCATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCACGCACCTTACAACTATCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610127 Cricotopus sp. water mite diet isolate 11780-BHL101516-GBD27206_16309-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATATTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTCACCTTATTACTTTCAAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610128 Cricotopus sp. water mite diet isolate 11790-BHL101516-GBD15274_4137-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGAGCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATTTAAGATTCTGACTACTCCCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610129 Cricotopus sp. water mite diet isolate 11805-BHL101516-GBD4535_11429-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGTTCTTTAATTGTAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCGTCACTAACCTTACTACTATCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610130 Cricotopus sp. water mite diet isolate 11815-BHL101516-GBD18838_7475-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGTATAGTAGGAACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCCTTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTCACCTTACTACCAACAAGTACAATTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610131 Cricotopus sp. water mite diet isolate 11830-BHL101516-GBD20222_23164-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTGGGAACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCTTTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTAACCTTACTACTTTCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610132 Cricotopus sp. water mite diet isolate 11831-BHL101516-GBD13499_28208-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTCACCCTACTTCTATCAAGTACAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610133 Cricotopus sp. water mite diet isolate 11832-BHL101516-GBD9757_17861-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCACGCCGGATCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCCCCGTCTTTCACCTTACTACTATCAAGTTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610134 Cricotopus sp. water mite diet isolate 11839-BHL101516-GBD18196_17043-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTACTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGAACATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610135 Cricotopus sp. water mite diet isolate 11843-BHL101516-GBD27521_17420-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATAGAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTACAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610136 Cricotopus sp. water mite diet isolate 11849-BHL101516-GBD28678_17532-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATCCCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGAGGCTCCTGATAAAGCTTTCCCTCGAAAAAATAATAAAAATTTTGGATTATTACCCCCTACTCACACCTTACTGCTTTCAAGTTCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610137 Cricotopus sp. water mite diet isolate 11858-BHL101516-GBD23846_20812-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTCGGAGCTGGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTCGGTCATGCCGGATCTTTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTCGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCGTCGCTCACCTTACTACTATCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610138 Cricotopus sp. water mite diet isolate 11873-BHL101516-GBD16112_13553-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGACATCCAGGCTCATTAATCGGAGATGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGGGCTCCTGATATAGCTTTCCCGCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCACTCACCTTACTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610139 Cricotopus sp. water mite diet isolate 11884-BHL101516-GBD8376_17834-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCAAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTATTGAATATTACCCCCGTCTCTCGACTGACATCTGTCAAGTGCAATAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610140 Cricotopus sp. water mite diet isolate 11893-BHL101516-GBD18936_6498-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGTACTTCCTTGAGTATCTTAATTCGAGCTGAATTTGGTCATGCCGGTTCATTTATTGGTGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTGATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610141 Cricotopus sp. water mite diet isolate 11894-BHL101516-GBD13436_27642-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATCCCGGCTCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGCAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCACTAACCTTACTTCTATCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610142 Cricotopus sp. water mite diet isolate 11903-BHL101516-GBD14017_5236-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTGGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCTTATCATTAATTGGAGATGATCAAATTTATAACTTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAACCTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCCCCTTCTCTCACCTTACTTCTTTCAAGTTCACTTGTTGAAACTGGAGCTGGCTCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610143 Cricotopus sp. water mite diet isolate 11907-BHL101516-GBD23049_21924-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAACTAGGTCATGCCGGATCTTTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTATTACCCCCTTCTCTAACCTTACTACTTTCAAGTAGAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610144 Cricotopus sp. water mite diet isolate 11920-BHL101516-GBD26378_15349-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGGGCTTGATCCGGAATAGTAGGAACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTCATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGACATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTCACCCTACTTCTTTCAAGTTCAATCGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610145 Cricotopus sp. water mite diet isolate 11921-BHL101516-GBD11883_17141-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTAACTCTTCTACTATCTAGTTCTTTCACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610146 Cricotopus sp. water mite diet isolate 11922-BHL101516-GBD21058_24326-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGTATCTTAATTCGAGCTGAATTAGGTCATCCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTAACCTTACTTCTTTCAAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610147 Cricotopus sp. water mite diet isolate 11923-BHL101516-GBD11696_17500-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCTGAGCTTGATCGGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGACATCCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAACAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCACTAACCTTACTTCTATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610148 Cricotopus sp. water mite diet isolate 11924-BHL101516-GBD8782_24633-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAGCATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGCATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTACCTTTAATATTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTCACCTTACTACTTTCAAGTGCAATAGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610149 Cricotopus sp. water mite diet isolate 11927-BHL101516-GBD11332_9212-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGCATAGTAGGCACTTCCTTGAGAATCTTAATTCGAGCTGAATTCGGTCATGCCGGATCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCGTCTCTCACCTTACTTCTATCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610150 Cricotopus sp. water mite diet isolate 11935-BHL101516-GBD26704_12637-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTAAGAATCTTTATTCGAGCTGAATTAGGACATTCCGGATCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTAATATTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610151 Cricotopus sp. water mite diet isolate 11939-BHL101516-GBD7904_16147-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGCGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATGTTTAATTGGAGATTATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTAGTAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCTGATATAGCGTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610152 Cricotopus sp. water mite diet isolate 11941-BHL101516-GBD10589_23968-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGCATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCCTTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCGTCACTCACCTTACTATTATCTAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610153 Cricotopus sp. water mite diet isolate 11942-BHL101516-GBD24755_5761-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGCATAGTAGGCACTTCCTTGAGAATCTTAATTCGAGCAGAATTAGGTCATGCCGGATCCTTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGAAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTATTATCAAGCTCACTTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610154 Cricotopus sp. water mite diet isolate 11954-BHL101516-GBD28818_15514-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGTATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGACGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGTGCTCCAGATATAGCTTTCCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCATCCCTCACCTTACGTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610155 Cricotopus sp. water mite diet isolate 11955-BHL101516-GBD16041_24840-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATCCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGTGCTCCTGATATAGCTTTCCCACGAATAAATAATATAAGATTTTGATTATTACCACCTTCTCTCACCTTACTACTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610156 Cricotopus sp. water mite diet isolate 11956-BHL101516-GBD26753_9297-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCAAGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTAATGCTTTTGTAATAATTTTTTTCATAGTTAACCCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGACTCCTGATATAGCTTTCCCTCGGATAAATAATACAAAGTTTTGATTATTTCCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610157 Cricotopus sp. water mite diet isolate 11957-BHL101516-GBD29136_18093-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTACACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCGTCATTAACCTTACTATTATCAAGTTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610158 Cricotopus sp. water mite diet isolate 11960-BHL101516-GBD10785_17741-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCCTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAACTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAGCTGATTATTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTTCCCCCTTCTCTCACCTTACTTCTTTCAAGTACAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610159 Cricotopus sp. water mite diet isolate 11972-BHL101516-GBD23243_19302-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGAGCTTGATCTGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGCTCCTTTAATGTTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTCTCACCTTACTACTATCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610160 Cricotopus sp. water mite diet isolate 11973-BHL101516-GBD11910_5845-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACCTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGTTCTTTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCCCCTTCTCTAACCTTACTTCTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610161 Cricotopus sp. water mite diet isolate 11977-BHL101516-GBD17825_13924-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTGAGAATTTTAATTCGAGTAGAATTAGGACATGCAGGATCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCACTCACCTTACTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610162 Cricotopus sp. water mite diet isolate 11987-BHL101516-GBD7099_19403-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGTTCATTAATTGGAGACGATCAAATTTATAACGTTATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATAAAAGTTTTTGATTATTACCCCCTTCATTAACCTTACTACTATCAAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610163 Cricotopus sp. water mite diet isolate 11991-BHL101516-GBD20231_18044-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTGTGAATCTTAATTCGAGCTGAATTAGGTCATGCCAGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGAGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTGCTACTTTCAAATACATTTGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610164 Cricotopus sp. water mite diet isolate 12001-BHL101516-GBD19861_19970-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGACATCCCGGAACTTTAATTGGTGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATGATTACCCCCTTCTCTCACCTTACTTCTATCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610165 Cricotopus sp. water mite diet isolate 12002-BHL101516-GBD6676_19576-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTATTACCCCCTTCTCTCACCCTACTTCTGTCAAGTTCAATCGGAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610166 Cricotopus sp. water mite diet isolate 12007-BHL101516-GBD16007_15453-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATCCCGGATCTTTAATTGGAGATGATCAAATTTATAACGTTATTGTTACTGCTCATGCTTTTATAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCCTACTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610167 Cricotopus sp. water mite diet isolate 12009-BHL101516-GBD28803_16260-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTAGTTCCCCCTTCACTAACCTTACTACTATCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610168 Cricotopus sp. water mite diet isolate 12017-BHL101516-GBD24326_24724-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGTTGAATTAGGACATACCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATCTTGACTATTACCCCCTTCTCTCACCTTACTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610169 Cricotopus sp. water mite diet isolate 12028-BHL101516-GBD12762_14280-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGCACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGACATGCCGGATCATTAATTGGAGAGGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCGATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTCACCTTACTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610170 Cricotopus sp. water mite diet isolate 12029-BHL101516-GBD26329_22489-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGTGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCATTCCCTCGAATAAATAATACAAGATTTTGATGATTACCCCCTTCTCTAACCTTACTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610171 Cricotopus sp. water mite diet isolate 12030-BHL101516-GBD25843_23309-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCCTTTAGAATCTTAATTCGAGCTGAATTATGTCATCCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTTTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTACCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTCTGACTATTACCCCCTTCTCTAACCTTACTACTTTCAAGTGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610172 Cricotopus sp. water mite diet isolate 12034-BHL101516-GBD7098_14148-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCCGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGGCAGGCCGGAACATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATGCCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAACAATATAAGGTTTTGATTATTACCCCCTTCTCTCACCCTACTTCTGGCAAGTACAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610173 Cricotopus sp. water mite diet isolate 12036-BHL101516-GBD26508_22944-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGCGCTTGATCAGGAATAGTAGGGACTTCCTTTAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGAACATTAATTGGTGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATAACTATTTTAATTGGAGGATTTGGAAAATGATTAGTTCCTTTAAGGTTAGGTGCTCCTGATATAGCTTTCCCACGAATAAATAATAAAAGTTTTTGATTATTACCCCCGTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610174 Cricotopus sp. water mite diet isolate 12037-BHL101516-GBD24001_5148-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGACTCCTGATAGAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCGCTCACCTTACATCAATCAAGTGCAATAGTTGAAGATGGAGCTGGAGCAG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610175 Cricotopus sp. water mite diet isolate 12257-BHL040517-GBD22244_16176-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTCGGAAATTGATTAGTTCCTCTAACATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCTCTTACATTACTCCTTTCAAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610176 Cricotopus sp. water mite diet isolate 13343-BHL040517-GBD8628_22465-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610177 Cricotopus sp. water mite diet isolate 13381-BHL040517-GBD22022_22179-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCCCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610178 Cricotopus sp. water mite diet isolate 13474-BHL040517-GBD17787_21402-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCCCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCCAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR960636, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610179 Cricotopus sp. water mite diet isolate 13478-BHL040517-GBD4999_11934-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCCCTAAGAATCTTAATTTGAGCTGAATTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAATTGATTAGTCCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610180 Cricotopus sp. water mite diet isolate 13583-BHL040517-GBD14035_7864-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCCCTAAGAATCGTAATTCGAGCTGAATTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTT-CTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610181 Cricotopus sp. water mite diet isolate 13592-BHL040517-GBD18248_14893-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATGAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR961044, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610182 Cricotopus sp. water mite diet isolate 13613-BHL040517-GBD13853_3477-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCCCTAAGAATCTTAATTCGAGCTAAATTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTGCTATTATCTAGCTCTCAAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 93.4% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610183 Cricotopus sp. water mite diet isolate 13635-BHL040517-GBD18901_25327-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTTATTCGGGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATATATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KR961044, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610184 Cricotopus sp. water mite diet isolate 13646-BHL040517-GBD18509_15813-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCCCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCCCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.7% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610185 Cricotopus sp. water mite diet isolate 13665-BHL040517-GBD13570_29011-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCCTTAAGAATCTTTATTCGAGCTGAATTAGGACATGCCGGGTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTTCTTTCAAATTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610186 Cricotopus sp. water mite diet isolate 13692-BHL040517-GBD6806_14013-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCTTTAAGAATCTTAATTCGAGCTGAATTCGGTCATGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACCATCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610187 Cricotopus sp. water mite diet isolate 13698-BHL040517-GBD25406_19393-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGTAACTTCCCTAAAAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCAAATAAATAATATAAGTTTTTGATTATTACTTCCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID KR960636, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610188 Cricotopus sp. water mite diet isolate 13702-BHL040517-GBD12568_25405-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGCACATTATATTTTATTTTCGGGGCCTGATCAGGGATAGTAGGTACTTCCCTAAGAATCTTAATTCGAGCTGAATTAGATCATGCCGGGACATTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAAGAATTTTTTTCATAGTTATACCTATTTTAATTGGTGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGGGCTCCTGATATAGCCTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTGGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610189 Cricotopus sp. water mite diet isolate 13718-BHL040517-GBD22273_10951-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACTTTATATTTTATTTTCGGGGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGATCATGCTGGTTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCTCCTTCTCTTACCTTATTACTATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610190 Cricotopus sp. water mite diet isolate 13726-BHL040517-GBD18347_10646-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCCCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGAACATTGATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTATTACCTCCTTCTCTAACCTTATTACTTTCAAGTACAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR960636, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610191 Cricotopus sp. water mite diet isolate 13766-BHL040517-GBD8998_6032-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610192 Cricotopus sp. water mite diet isolate 13818-BHL040517-GBD27659_10283-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCCCTAAGAATCTTAATTCGAGCTAAATTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAATTATACCTATTTTAATTGGGGGGTTCGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTATTACCTCCTTCTCTAACCTTATTACTTTCAAGTACAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610193 Cricotopus sp. water mite diet isolate 13831-BHL040517-GBD10037_21690-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGAACTTCCCTAAGAATCTTAATTCGAGCTGAATTAGGACATGCCGGATCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCTCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCTCCTTCTCTTACCTTATTACTTTCAAGTACAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KX535221, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610194 Cricotopus sp. water mite diet isolate 13881-BHL040517-GBD24276_14070-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCCTGATCAGGGATAGTAGGTACTTCCTTAAGAATTTTAATTCGAGCTGAACTAGGTCATGCTGGGTCATTAATCGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACTATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610195 Cricotopus sp. water mite diet isolate 13910-BHL040517-GBD3566_8451-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTTGTGGCCTGATCAGGGATAGTAGGTACTTCTCTAAGAATTTTAATTCGAGCTGAACTCGGTCATGCCGGGTCTTTAATCGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610196 Cricotopus sp. water mite diet isolate 13912-BHL040517-GBD19861_24129-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCCCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTGATAGTTATACCTATTTTAATTGGGGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGGGCACCTGATATAGCTTTCCCACGAATAAATAATATAAGATTTTGATTATTACCTCCTTCTCTTACCTTATTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610197 Cricotopus sp. water mite diet isolate 13914-BHL040517-GBD18605_28091-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGCACTTCTTTCAGAATTTTAATTCGAGTTGAATTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAATTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCGCGAATAAATAATATAAGATTTTGATTATTACCTCCTTCTCTTACCTTATTACGATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610198 Cricotopus sp. water mite diet isolate 14159-BHL040517-GBD6170_11794-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCTGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGGCCCAGATATAGCATTCCCTCGAATAAATAGTATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610199 Cricotopus sp. water mite diet isolate 14200-BHL040517-GBD10182_7217-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGCACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610200 Cricotopus sp. water mite diet isolate 14207-BHL040517-GBD10397_22154-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATCTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGATTTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610201 Cricotopus sp. water mite diet isolate 14301-BHL040517-GBD23511_10195-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCATTAATGTTAGAAGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610202 Cricotopus sp. water mite diet isolate 14344-BHL040517-GBD19717_7604-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTCGGATCTTGATCAGGAATAATCGGAACTTCCTTAAGTATATTTATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTTATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCACTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610203 Cricotopus sp. water mite diet isolate 14347-BHL040517-GBD22228_9064-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTCTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATCGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATCGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCATTAACTCTTCTTCTT-TCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610204 Cricotopus sp. water mite diet isolate 14360-BHL040517-GBD26249_14759-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTCGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGTATTCTAATTCGAGCAGAATTAGGTCATCCGGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCATCTTTAACATTATTATTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610205 Cricotopus sp. water mite diet isolate 14410-BHL040517-GBD23550_14102-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGGTCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTTATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCCTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGTGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610206 Cricotopus sp. water mite diet isolate 14411-BHL040517-GBD10565_14989-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGATCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTAGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTATCTCTTCTTCTT-TCTAGCTCAATTGTAGAAAATGGAGCTGGAAAAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610207 Cricotopus sp. water mite diet isolate 14412-BHL040517-GBD2829_12679-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTGGGAACTTCTTTTAGAATTTTAATTCGAGCAGAATTAGGTCATCCGGGTTCTTTAATTGGAGATGATCAAATTTGCAATGTAATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATAATAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610208 Cricotopus sp. water mite diet isolate 14460-BHL040517-GBD17381_9739-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGATTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGGTTACTTCCCCCTTCTTTATCTCTTCTTCTT-TCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610209 Cricotopus sp. water mite diet isolate 14466-BHL040517-GBD14284_24967-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTGGGTACTTCTTTTAGAATTTTAATTCGAGCAGAACTCGGTCACGCGGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCAATTCTAATTGGAGGTTTTGGAAATTGATTAGTCCCTTTAATATTGGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCGTCATTAACATTATTATTATCAAGATCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KP039729, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610210 Cricotopus sp. water mite diet isolate 14474-BHL040517-GBD26136_7306-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATACTGGGAACCTCTCTTAGAATTTTTATTCGAGCTGAATTCGGTCATCCGGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTAACAAGAACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610211 Cricotopus sp. water mite diet isolate 14477-BHL040517-GBD20192_5087-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACTTCTTTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTCATAGTAATACCAATTTTAATTGGAGGATTTGGAAATCGATTAGTCCCTTTAATACTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCCCCTTCTCTAACATTACTACTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610212 Cricotopus sp. water mite diet isolate 14488-BHL040517-GBD2602_14646-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCTTTTAGAATTTTTATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTTATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTCATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGACTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCCCCTTCTTTAACATTATTATTATCAAGATCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610213 Cricotopus sp. water mite diet isolate 14506-BHL040517-GBD18599_22381-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGGGCCCCTGACATAGCATTCCCCCGAATAAATAATATAAGTTTCTGATTACATCCCCCATCACTTACATTACTCCTATCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610214 Cricotopus sp. water mite diet isolate 14552-BHL040517-GBD7107_9210-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTTGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGACATCCGGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCATTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTCTGATTACTACCACCTTCTTTAACATTACTATTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610215 Cricotopus sp. water mite diet isolate 15214-BHL040517-GBD18815_5522-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTAGATTTTATTGTTGGGGCTTGGTCAGGAATAGGAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGTCATGCCGGCTCATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTCGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAATTGATTAGTTACTTTAATACTTGGGGCACCAGAAATAGCCTTTCCCCGAATAAATAACATAAGTTTTTGACTTCTACCCCCATCATTAACTCTGTTGCTTTCTAGCTCAATGGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR670938, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610216 Cricotopus sp. water mite diet isolate 537-BHL040517-GBD21614_25950-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTTTATAGTAATACCAATACTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610217 Cricotopus sp. water mite diet isolate 754-BHL040916-GBD26742_11846-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610218 Cricotopus sp. water mite diet isolate 759-BHL040916-GBD17191_13853-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCCCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCACAGATATAGCTTTCCCTCGAATAAATAACAAAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGGTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610219 Cricotopus sp. water mite diet isolate 816-BHL100916-GBD7795_5452-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGTATAGTAGGGACTTCCTTTAGAATCTTAATTCGAGCTGATTTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGAGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTATTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAACTGTTGAAAATAGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610220 Cricotopus sp. water mite diet isolate 820-BHL100916-GBD9432_15822-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATCGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCGTCTCTCACCTTACTTCTATCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610221 Cricotopus sp. water mite diet isolate 834-BHL100916-GBD10498_5701-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCTTTTATAGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTAACCTTACTTCTTTCAAGTACAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610222 Cricotopus sp. water mite diet isolate 835-BHL100916-GBD23495_12981-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTCCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTCCTTTCAAGTTCAATTGTTGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610223 Cricotopus sp. water mite diet isolate 840-BHL100916-GBD16009_21496-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGCTCATTAATTGGAGATGATCAAATTTATAACGGTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATGTGGAAACTGATTAGTTCCTTGACTGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTGACTTCTTTCAAGTTCAATTGTTGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610224 Cricotopus sp. water mite diet isolate 844-BHL100916-GBD25595_10957-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGTATCTTAATTCGAGCTGAATTAGGACATGCCGGATCTTTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGTGGCTCCTGATATAGCTTGCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610225 Cricotopus sp. water mite diet isolate 848-BHL100916-GBD24115_4673-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCCTGATCAGGAATAGTAGGAACTTCCTTAAGTATATTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTAACCTTACTTCTTTCAAGCTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610226 Cricotopus sp. water mite diet isolate 857-BHL100916-GBD14718_20377-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTTGGACATGCCGGATCATTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTTGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610227 Cricotopus sp. water mite diet isolate 861-BHL100916-GBD27635_16372-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATATTAATTCGAGCTGAATTAGGTCATGCAGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTATAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGATTACTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610228 Cricotopus sp. water mite diet isolate 867-BHL100916-GBD22998_7450-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATACTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATCCCGGACCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCACCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTCACCTTACTTCTTTCAAGTACAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610229 Cricotopus sp. water mite diet isolate 868-BHL100916-GBD24215_6822-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGAACATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCCCCCTCTCTAACCTTCCTACTTTCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610230 Cricotopus sp. water mite diet isolate 869-BHL100916-GBD3444_10954-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCGGAATTAGGCAATGCCGGATCATTAATTGGAGATGATCAAATTTTTAACGTTATTGTTACAGCTCATGCTTTTGTAAAAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610231 Cricotopus sp. water mite diet isolate 876-BHL100916-GBD13357_26234-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAAGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGACTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGGTTTTGATTATTACCCCCTTCTCTCAACTTACTTCGTACCAGTCCAATTGGTGAAAAAGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610232 Cricotopus sp. water mite diet isolate 879-BHL100916-GBD13009_28261-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGAGCAGGAATAGTAGGGACTTCCTTTAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACATTCTTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAACAATATAAGATTTTGATTATTACCCCCTTCTCTAACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610233 Cricotopus sp. water mite diet isolate 880-BHL100916-GBD27710_18818-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGTATCTTAATTCGAGCTGAATTAGGTCATGCCGGATGATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGCTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCACTCACCTTACTTCTGTCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610234 Cricotopus sp. water mite diet isolate 884-BHL100916-GBD28262_18368-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCTGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATTCTTTTGTAATAATTTTTTTCATAGTTTTACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGATCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTACTCTAACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGATGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610235 Cricotopus sp. water mite diet isolate 885-BHL100916-GBD9017_13943-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTAGGAGCTTGATCAGGAATAGTATGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGGGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGTGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTGCTGTCAAGTTCAATAGTTGAAAATGGAGGTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610236 Cricotopus sp. water mite diet isolate 888-BHL100916-GBD24505_17795-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGGACTTCTTTGAGTATATTAATTCGAGCTGAACTAGGTCATGCTGGATCATTTATTGGTGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610237 Cricotopus sp. water mite diet isolate 894-BHL100916-GBD14561_6659-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCCTTGAGAATCTTAATTCGAGCTGAATTATGTCATGCCGGATCATTCATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTTTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTCACCTTACTACTTTCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610238 Cricotopus sp. water mite diet isolate 897-BHL100916-GBD28536_10070-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGACGGATCCTTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCATTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGTCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCACACCTTACTTCTATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610239 Cricotopus sp. water mite diet isolate 899-BHL100916-GBD24715_11193-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAAGAAATAATAAAAGTTTTGGATTATTACCCCCTTCGCTCACCTTACTTCTTTCAAGTTCAATAGTTGAAAATGGAGCTGAAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610240 Cricotopus sp. water mite diet isolate 902-BHL100916-GBD3790_10684-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGGACTTCCTTTAGAATCTTAATTCGAGCTGAATTATGTCATCCCGGATCATTCATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCACATGCTTTTGTAATAATTTTTTTCCTAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTCTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAACGGAGCTGGATCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610241 Cricotopus sp. water mite diet isolate 909-BHL100916-GBD12172_8141-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGATATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAACGTTAGTAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610242 Cricotopus sp. water mite diet isolate 911-BHL100916-GBD24902_9945-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTACTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAAAGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGTGATCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTACTATCAAGCTCAATTGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610243 Cricotopus sp. water mite diet isolate 914-BHL100916-GBD25174_17145-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTATGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCACCTTCTCGCACCTTACTTCAATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610244 Cricotopus sp. water mite diet isolate 915-BHL100916-GBD27680_21926-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATCTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCAGGCCGGATCATTAATTGGAGATGATCAAATTTATAATGTTATTGTGACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCGCTCACCTTACTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610245 Cricotopus sp. water mite diet isolate 923-BHL100916-GBD23866_5294-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATCCCGGATCATTTATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTATAATAATTTTTTTCATAGGTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTGACCTTACTTCTTTCAAGTTCAATTGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610246 Cricotopus sp. water mite diet isolate 929-BHL100916-GBD18332_18505-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATCATTACCCCCTTCTCTAACCTTACTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610247 Cricotopus sp. water mite diet isolate 936-BHL100916-GBD14715_19418-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAACTCGAGCTGAATTAGGTCATCCCGGATCACTAATTGGAGATGATCAAACTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGATTAGTTCCTTTAATATTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610248 Cricotopus sp. water mite diet isolate 942-BHL100916-GBD12873_15094-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCCTAAGAATCTTAATTCGAGCTGAACTAGGTCATCCTGGATCATTTATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTAACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610249 Cricotopus sp. water mite diet isolate 943-BHL100916-GBD26872_19131-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTCGGTGCTTGATCAGGAATAGTAGGTACTTCCTTTAGAATCTTAATTCGAGCTGAATTAGGTCATGCAGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCGCTCACCTTACTTCCTTCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610250 Cricotopus sp. water mite diet isolate 948-BHL100916-GBD5658_6906-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTAGGAGCTTGAGCAGGAATAGTAGGGACTTCGTTGAGAATATTAATTCGAGCTGAATTAGGTCAAGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGACTAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610251 Cricotopus sp. water mite diet isolate 949-BHL100916-GBD21824_8328-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTTATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATAGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTTGGGGCACCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTTCTTCTTTCAAGTTCAATCGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610252 Cricotopus sp. water mite diet isolate 952-BHL100916-GBD26201_10798-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGATCTTGATCAGGAGTAGTAGTTATTTCCTTGAGAATCTTCATTCGAACTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610253 Cricotopus sp. water mite diet isolate 958-BHL100916-GBD6554_6189-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GACCATTATATTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGTCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTGTCAAGTTCAATGGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610254 Cricotopus sp. water mite diet isolate 959-BHL100916-GBD4602_17673-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTTGTTCCTTTAATGTTAAGGGCTCCTGATATAGGTTTTCCCCCAATAAATAAAAAAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610255 Cricotopus sp. water mite diet isolate 968-BHL100916-GBD20988_25760-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTTATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTCACCTTACTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610256 Cricotopus sp. water mite diet isolate 970-BHL100916-GBD19233_2963-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGTTGAATTAGGTCATCCCGGGTCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCCAATAAATAATATAAGGTTTTGAATATTACCCCCTTCTCTCACCTTACTTCTATCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610257 Cricotopus sp. water mite diet isolate 977-BHL100916-GBD25836_23577-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGACCAGGAATAGTAGGTACTTCCTTTAGAATCTTAATTCGAGCTGAATTAGGTCATGCCAGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGTGTCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGGTTATTACCCCCTTCTCTCACCTTACGTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610258 Cricotopus sp. water mite diet isolate 982-BHL100916-GBD8095_20161-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGTGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCCCGAATAAATAACATAAGTTTTTGACTATTACCCCCTTCTCTCACCTTACTCCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610259 Cricotopus sp. water mite diet isolate 984-BHL100916-GBD26785_9350-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTGAGAATCTTAATTCGAGCTGAATTAGGACATTCCGGATCATTTATTGGTGATGATCAAATTTATAACGTTATTGTTACATCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610260 Cricotopus sp. water mite diet isolate 987-BHL100916-GBD26139_20791-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCCGGAATAGTAGGAACTTCCTTAAGAATCTTAATTCGAGCTGAATTAGGTCATCCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTGTTGTTACTGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTAACCTTACTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610261 Cricotopus sp. water mite diet isolate 993-BHL100916-GBD24711_14630-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGTTGAATTAGGTCATGCCGGATCATTATTTGGAGATGATCAACTTTATAACGTTTTTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCCTAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTACTCTCACCTTACTTCGTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610262 Cricotopus sp. water mite diet isolate 997-BHL100916-GBD26749_15821-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGACATGCCGGATCACTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTTGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTATTACCCCCTTCTCTCACCTTACATCTTTCAAGTTCAATCGTTGAAAATGGAGCTGGGACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610263 Cricotopus sp. water mite diet isolate 998-BHL100916-GBD22796_13846-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCATTGAGAATCTTAATTCGAGCTGAATTATGTCATGCCGGATCATTACTAGGAGATGATCAAATTTATAACATTCTTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATCGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610264 Cricotopus sp. water mite diet isolate 1002-BHL100916-GBD15701_4269-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCAGAATTAGGACAAGCCGTATCATTAATTGGAGATGATCAAATTTATAACGTTATAGGTACAGCACATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTTCTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610265 Cricotopus sp. water mite diet isolate 1006-BHL100916-GBD4266_10306-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGCATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATAGAAGTTTTTGATTATTACCCCCTTCTCTCACCATACTTCAACCAAGTGCAATAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610266 Cricotopus sp. water mite diet isolate 1008-BHL100916-GBD6964_11374-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCCGGAATAGTTGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATGATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGGTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610267 Cricotopus sp. water mite diet isolate 1009-BHL100916-GBD25630_22064-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGACAATCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTATTGATTATTACCCCCTTCTCTCACCTTACTTCTTGCAAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610268 Cricotopus sp. water mite diet isolate 1012-BHL100916-GBD19488_27584-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCTTTTAGAATTTTAATTCGAGCTGAATTAGGTCATGCCGGTTCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610269 Cricotopus sp. water mite diet isolate 1016-BHL100916-GBD6352_5459-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGGTCATTTATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATGACCCCCTTCTCTAACCTTACTTCTTTCAAGTTCAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610270 Cricotopus sp. water mite diet isolate 1022-BHL100916-GBD2062_18401-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTACTTCGAGCTGAATTAGGTCATTCCGGATCATTAATTGTAGATGATCATATTTATAACGTTATTGTTACAGCTCATGCTTTTGGAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGTGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCGCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610271 Cricotopus sp. water mite diet isolate 1024-BHL100916-GBD6294_11501-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGTCTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCACATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTACCTTTAGTGTTAGGGGCACCTGATATAGCTTTCCCTCGAATAAACAATATAAGATTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATCGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610272 Cricotopus sp. water mite diet isolate 1026-BHL100916-GBD13766_26253-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCATATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAGCTGATTAGTTCCTTTAATGTTAGAGGCTACTGATATAGCTTTCCCTCGAATAAATAATATAAGTTATTGATTATTACCCCCTTCTCTCACCGTACTTCTTTCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610273 Cricotopus sp. water mite diet isolate 1030-BHL100916-GBD5272_13739-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCGGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATACCGGATCATTAATTGGTGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610274 Cricotopus sp. water mite diet isolate 1031-BHL100916-GBD20742_10080-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCCTGATCAGGAATAGTAGGAACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGATCATGCTTTCGTAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTGCTCTCACCTTACCTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610275 Cricotopus sp. water mite diet isolate 1032-BHL100916-GBD10105_11461-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTACTTGGAGATGATCAAATTTATAACGTTATCGTTACAGCTCATGCTTTAGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCACGAATAAATAATATAAGATTTTGATTATTACCCCCTTCACTCACCTTACTTCTTTCAAATTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610276 Cricotopus sp. water mite diet isolate 1035-BHL100916-GBD16870_3060-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAAAATTATATTTCATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCTGATCATTAATTGGAGATGATCGAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTCTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACCGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610277 Cricotopus sp. water mite diet isolate 1038-BHL100916-GBD22561_8914-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTGAGTATCATAATTCGAGCTGAATTAGGTCATGCCGGATCATTGATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCATTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610278 Cricotopus sp. water mite diet isolate 1044-BHL100916-GBD19813_18413-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTGTATTTTATTTTCGGAGCTTGATCATGAATAGTAGGTACTTCCTTGTGAATCTTAATTCGAGCTGATTTCGGTCATGCCAGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGTGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610279 Cricotopus sp. water mite diet isolate 1045-BHL100916-GBD9761_17427-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCCGGAATAGTAGGGACTTCCTTGTGAATCTTAATTCTAGCTGCATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATCATTACCCCCTTCTCTCACCTTACTTCATTCAAGTGCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610280 Cricotopus sp. water mite diet isolate 1047-BHL100916-GBD18242_15514-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAACGGAATTAGGTCATGCTGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTCCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATCGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610281 Cricotopus sp. water mite diet isolate 1048-BHL100916-GBD4023_13467-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGAACATTAATTGGAGATGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTCGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCCCCTTCTCTCACCTTACGTTTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610282 Cricotopus sp. water mite diet isolate 1050-BHL100916-GBD3712_16110-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTAAGAATTTTAATTCGAGCAGAATTAGGTCACCCCGGATCATTAATTGGAGATGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610283 Cricotopus sp. water mite diet isolate 1052-BHL100916-GBD13262_5169-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCAAGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTCATAGTTATACCTATATTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTATTACCCCCTTCTCTCACCTTACTTGTTTCAAGTTCAATCGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610284 Cricotopus sp. water mite diet isolate 1056-BHL100916-GBD20836_10557-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGACTAGTAGGGACTTCCTTGAGAATCTTTATTCGAGCTGAATTAGGTCATGCCGGATCTTTAATTGGAGATGATCAAATTTATAACGCTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGTTATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAACTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610285 Cricotopus sp. water mite diet isolate 1057-BHL100916-GBD16634_26713-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTAATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTTATATTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTGTTACCCCCTTCTCTCACCTTACTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610286 Cricotopus sp. water mite diet isolate 1060-BHL100916-GBD23582_26056-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGACTAGTAGGGACTTCCTTTTGACTCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGACTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTAGTACCCCCTTCTCTCACCTTACGTCTTACAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610287 Cricotopus sp. water mite diet isolate 1061-BHL100916-GBD5855_21412-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAAGGGCTCCTGATATAGCTCTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCCCCTTCTCTCACCTCACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610288 Cricotopus sp. water mite diet isolate 1064-BHL100916-GBD8451_21223-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTATGTCATGCCGGATCATTAATAGGAGGTGATCAAATTTATGACGTTATTGTTACAGCCCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTCCTTTCAAGTGCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610289 Cricotopus sp. water mite diet isolate 1065-BHL100916-GBD4832_17344-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTTATTCGAGCTGAATTAGGTCGTGCCGGAACATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACACCCTTCTCTCACCCTACTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610290 Cricotopus sp. water mite diet isolate 1066-BHL100916-GBD26670_19108-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATAAAGCTTTCCCTCCAATAAAAAATAAAGATTTTTGATTATTTCCCCCTTCTCTCGCCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610291 Cricotopus sp. water mite diet isolate 1067-BHL100916-GBD25332_14301-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCCGGAATAGTAGGGACTTCATTGAGAATCTTTATTCGAGCTGAATTAGGTCATCCCGGATCATTCATTGGAGATGACCAAATTTATAACGTTATTGTTACGGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610292 Cricotopus sp. water mite diet isolate 1072-BHL100916-GBD22967_24003-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGTGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTATTTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTACATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGTGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCGCTTCTCTCACCTTACTACTTGCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610293 Cricotopus sp. water mite diet isolate 1088-BHL100916-GBD22191_5989-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTGAGTATCTTAATTCGAGCTGAATTTGGTCATGCTGGATCATTTATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGTGCTCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCACTCACCCTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610294 Cricotopus sp. water mite diet isolate 1089-BHL100916-GBD16956_8670-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCGTAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCGATCCCTCGAATAAATAATATAAGTTCTTGATTATTACCCCCTTCGCTCACCTTACTTCTTTCAAATTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610295 Cricotopus sp. water mite diet isolate 1098-BHL100916-GBD23348_20804-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGTATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTACTTCCCTTAATGTTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAACATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610296 Cricotopus sp. water mite diet isolate 1102-BHL100916-GBD16950_2587-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTAGATTTTATTATCGGAGCTTGATCAGGAATAGGAGGGACTTCCTTGAGAATCTGAATTCGAGCTGAATTAGGTCATTCCTGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGGAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCCCCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610297 Cricotopus sp. water mite diet isolate 1205-BHL110116-GBD6974_7115-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAAATGATTAGTTCCTTTAATGTTAGTGGCTCCTGATATAGCTTTCCCTCGGATAAACAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTGGCAAGTACAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610298 Cricotopus sp. water mite diet isolate 1444-BHL110116-GBD10059_16162-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAAATGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAACAAATAATATAAGTTTTTGACTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610299 Cricotopus sp. water mite diet isolate 1769-BHL110116-GBD17015_15990-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCTTTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610300 Cricotopus sp. water mite diet isolate 1770-BHL110116-GBD25375_13046-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTACTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610301 Cricotopus sp. water mite diet isolate 1784-BHL110116-GBD20064_9530-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGCACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCCCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAATGTTATCGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610302 Cricotopus sp. water mite diet isolate 1816-BHL011116-GBD23290_15113-Ldc73 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610303 Cricotopus sp. water mite diet isolate 1836-BHL072216-GBD19474_22452-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610304 Cricotopus sp. water mite diet isolate 1843-BHL072216-GBD7715_8817-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTCGGTCAGGCGGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGGTTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTACTACCACCGTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610305 Cricotopus sp. water mite diet isolate 1862-BHL072216-GBD19313_22486-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCCCTAAGAATCTTAATTCGAACTGAATTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACCATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610306 Cricotopus sp. water mite diet isolate 2216-BHL072216-GBD17555_12837-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGGATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAAATGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTGCCACCTTCTCTCACCTTATTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610307 Cricotopus sp. water mite diet isolate 2343-BHL072216-GBD13717_6637-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGGGCTTGGTCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGTCATGCCGGCTCATTAACTGGTGACGATCAAATTTATAATGTAATTGTTACAGCCCATGCTTTCGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCTTTAATACTTGGGGCACCAGATATAGCCTCTCCCCGGATAAATAACATAAGTTTTTGACTACTACCCCCATCATTAACTCGTTTGCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR670938, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610308 Cricotopus sp. water mite diet isolate 2402-BHL072216-GBD20079_19331-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGCATTAGGTCATGCCGGACCATTAATTGGAGATGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTGTAATCATTTTTTTCATAGTTATTCCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610309 Cricotopus sp. water mite diet isolate 2550-BHL072216-GBD9673_4007-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCTTTGAGAATCTTAATTCGAGTTGAATTAGGTCATCCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCGCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTATCAAGGTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610310 Cricotopus sp. water mite diet isolate 3271-BHL032417-GBD10881_2659-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATCTTCGGAGCATGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCTCTTACATTACTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610311 Cricotopus sp. water mite diet isolate 5792-BHL032417-GBD21557_11003-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAAATTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTGTTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610312 Cricotopus sp. water mite diet isolate 6088-BHL032417-GBD22713_8890-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTATAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATAATAGGAACCCCTGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATGATTAGTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610313 Cricotopus sp. water mite diet isolate 6165-BHL032417-GBD4603_10748-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTTTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGATCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACAAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610314 Cricotopus sp. water mite diet isolate 7262-BHL032417-GBD12714_13756-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATCTTAGGAGCATGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAAAGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATGAATAATATAAGTTTTTGACTTCTTCCTCCTTCTCTTACATTACTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610315 Cricotopus sp. water mite diet isolate 7784-BHL040517-GBD8516_6292-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGGGCTTGTTCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGTCATGCCGGCTCATTAATTGGTGACGATCAAATTTATAATGTAATCGTTACAGCCCATGCTTTCGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCTTTAATACTTGGGGCACCAGATATAGCCTTTCCCCGGATAAATAACATAAGTTTTTGACTTCTACCCACATCATTAACTCTTTTGCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR670938, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610316 Cricotopus sp. water mite diet isolate 8659-BHL101416-GBD6042_11710-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCCTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATCCCGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAAATGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610317 Cricotopus sp. water mite diet isolate 9227-BHL032417-GBD8753_15496-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAAATGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCACTCGAATAAATAATATAAGTTTTTGATTATTGACGCCTTCTCTCACCTTACTCCTGTCAAGTTCAATAGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610318 Cricotopus sp. water mite diet isolate 10840-BHL101516-GBD18835_3183-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGCGCTTGATCAGGAATAGTAGGGACTTCCTTGAGCATCTTAATTCGAGCTGGATTAGGTCATGCCGGTTCATTAATTGGAGATGATCAAATTTATACCGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAAGTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTCTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAACGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610319 Cricotopus sp. water mite diet isolate 10915-BHL101516-GBD27653_9661-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAGTTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATCACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610320 Cricotopus sp. water mite diet isolate 11001-BHL110116-GBD16959_6402-Lq74 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCAGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAGTGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610321 Cricotopus sp. water mite diet isolate 11012-BHL110116-GBD13231_8453-Lq75 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610322 Cricotopus sp. water mite diet isolate 11026-BHL110116-GBD20288_5918-Lq76 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGATCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTGTGATTATGACCCCCTTCTCCCACCTTACTTCTTTCAAGTTCAATAGTTGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610323 Cricotopus sp. water mite diet isolate 11028-BHL110116-GBD6363_14663-Lq76 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTATTACCCCCCTCTCTAACCTTACTTCTTTCAAGTACAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610324 Cricotopus sp. water mite diet isolate 11120-BHL110116-GBD20300_19094-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTAACCCCTTCTCTCACCTTACTTCTTTCAAGATCAATTGGAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610325 Cricotopus sp. water mite diet isolate 11139-BHL110116-GBD21969_19450-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGAGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCCGACGTCTTTCAAGTTCAATCGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610326 Cricotopus sp. water mite diet isolate 11400-BHL101516-GBD7048_15016-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTCATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610327 Cricotopus sp. water mite diet isolate 11447-BHL101516-GBD21196_5702-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATCGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATCCCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCATACTTCTTGCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610328 Cricotopus sp. water mite diet isolate 11526-BHL101516-GBD15528_13408-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610329 Cricotopus sp. water mite diet isolate 11741-BHL101516-GBD2222_11683-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGTATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGTGCTCCTGATATAGCTTTCCCACGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTCACCTTACTTCTATCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610330 Cricotopus sp. water mite diet isolate 11742-BHL101516-GBD17035_2012-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTCGATCAGGAATAGTAGGGACTTCCTTGAGCATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGACCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCGATCAAGTACAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610331 Cricotopus sp. water mite diet isolate 11743-BHL101516-GBD10135_5243-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTCGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGAGTATTACCCCCTTCTCTCACCTTACGTCAAGCAAGTGCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610332 Cricotopus sp. water mite diet isolate 11745-BHL101516-GBD27689_9762-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGTGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTGTTTGATTATTACCCCCTTCTCTCACCAAACTTCTTTCAAGTACATTATTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610333 Cricotopus sp. water mite diet isolate 11747-BHL101516-GBD24768_8889-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGACTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTCTTTGATTATTACCCCCTTCTCCCACCTTACTTCATACAAGTTCAATTGTTGAAAATGGAGCTGAAACA	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610334 Cricotopus sp. water mite diet isolate 11748-BHL101516-GBD3574_13798-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTCGGCGCTTGATCAGGAATAGTAGGGACTTCCTTGAGTATCTTAATTCGAGCTGAATTAGGTCATGCGTGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGTCTCCTGATATAGCTTTCCCTCGAATAAATAATATAATTTTTTGATTATTACCCCCTTCTCTCACCTTGCTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610335 Cricotopus sp. water mite diet isolate 11749-BHL101516-GBD6161_15021-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGTGCGCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTAGTACCCCCTTCTCTCACCTTACTGCTTTCAAGTGCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610336 Cricotopus sp. water mite diet isolate 11752-BHL101516-GBD25553_13837-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGTGCTTGATCAGGAATAGTAGGGACTTCCTTTAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCGTTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTCGTCCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610337 Cricotopus sp. water mite diet isolate 11753-BHL101516-GBD13931_17160-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAGTAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGACATAGCCTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTACTATCAAGTTCAATAGTTAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610338 Cricotopus sp. water mite diet isolate 11754-BHL101516-GBD13649_5137-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAACTAGGACATGCCGTATCATTAATTGGAGATGACCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTCTCACCTTTCTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610339 Cricotopus sp. water mite diet isolate 11755-BHL101516-GBD24207_22832-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGTTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAACAATATAAGTTTTTGAATATTACCCCCTTCTCTAACCTTACTTCGTGCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610340 Cricotopus sp. water mite diet isolate 11757-BHL101516-GBD24090_19234-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGTTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCCTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTTTAACCTTACTTCCATCAAGTTCAATAGTTGAAAATGGAGCTGGAACTGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610341 Cricotopus sp. water mite diet isolate 11758-BHL101516-GBD18445_14404-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAGCATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGACATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTGATATTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTACTATCAAGTTCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610342 Cricotopus sp. water mite diet isolate 11759-BHL101516-GBD8104_20175-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAGTTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTTTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAAATGATTAATTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACTCTACTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610343 Cricotopus sp. water mite diet isolate 11760-BHL101516-GBD17291_11287-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCGGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGATCATGCTTTTGTAATTATTTTTTTCATAGTTAAACCTATTTTAATTGGAGGATTTGGAAACTTATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGGTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610344 Cricotopus sp. water mite diet isolate 11762-BHL101516-GBD26798_7497-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGGTCCTGATATAGCATTCCCTCGAATAAATAAAAAAAGTTTTGGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTGCAATTGTTGAAAATAGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610345 Cricotopus sp. water mite diet isolate 11764-BHL101516-GBD27789_10511-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCCTTGAGAATCTTAATTCGAGCTGAACTAGGTCATGCCGGTTCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGTTCTCCTGATATAGCGTTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCCCCTTCTCTCACCTTGCTTCTTTCAAGTTCAATTGTTGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610346 Cricotopus sp. water mite diet isolate 11769-BHL101516-GBD27052_19523-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGGGCTTGATCCGGAATAGTAGGGACTTCATTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCCTTAATGTTAGGAGCTCCTGATATAGCTTTCCCCCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCACACCTTACCTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610347 Cricotopus sp. water mite diet isolate 11770-BHL101516-GBD2183_14295-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGTATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTGCCCTCGAAGAAATAATATAAGTTTTTGATTATTACCCCCTTCGCGCGCCTGACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610348 Cricotopus sp. water mite diet isolate 11772-BHL101516-GBD8319_10712-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTCGGGACTTCCTTGAGAATCTTAATTCGAGCTGAGTTCGTTCATGCCGGTTCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCAGAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTATCAAGTGCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610349 Cricotopus sp. water mite diet isolate 11777-BHL101516-GBD16835_15294-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGTATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCCCGAATAAATAACATAAGTTTTTGATTATTACCCCCTCCTCTCACCTTACTTCTATCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610350 Cricotopus sp. water mite diet isolate 11779-BHL101516-GBD12558_16992-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTTATTCGAGCTGAATTAGGTCATCCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTATAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTTACCTTACATCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610351 Cricotopus sp. water mite diet isolate 11781-BHL101516-GBD16707_5664-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCTGAGCATTAATTGTAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCCCCTTCCTTCTTTCAAGTTCACTTGTTGAAAATGGAGCTGGACCAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610352 Cricotopus sp. water mite diet isolate 11783-BHL101516-GBD12312_26399-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGACATTCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTTCCCCCTTCTCTAACTTTACTTCTTTCAAGTACAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610353 Cricotopus sp. water mite diet isolate 11784-BHL101516-GBD3251_9831-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCAGTATCATTAATTGGATATGATCAAATTTATAACGTTATTGTTACAGCACATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGAGTCTCCTGATATAGCTTTCCCTCGACTAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610354 Cricotopus sp. water mite diet isolate 11786-BHL101516-GBD20391_20097-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTGGGACATCCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTCCATAGTGATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTATCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610355 Cricotopus sp. water mite diet isolate 11787-BHL101516-GBD18893_4117-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATCGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCCTGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTCTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTGTGATTATTACCCCCTTCTCGCACCGTACCTCGTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610356 Cricotopus sp. water mite diet isolate 11788-BHL101516-GBD16306_21208-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATCTTCGGAGCTTGATCAGGTATAGTAGGTACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGAAACTGATTAGTTTCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCGTCTCTCACCTTACTTCTGTCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610357 Cricotopus sp. water mite diet isolate 11789-BHL101516-GBD13643_5449-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTGGATCAGGAATAGAAGGGACTTCCTGGAGAATCTTAATTCGAGCGGAATTAGGTCATGCCGTATCATTAATGGGATATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610358 Cricotopus sp. water mite diet isolate 11791-BHL101516-GBD24479_20582-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTCTTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCCTTGAGAATCTTAATTCGAGCTGCATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATACCGTTATTGTTACATCTCATGCTTTTGTAATAATTTTTTTCATAGCTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTTGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610359 Cricotopus sp. water mite diet isolate 11792-BHL101516-GBD25442_19253-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATATTAGGGACTTCCTTGAGAATCTTAATTCGAGCCGAATTAGGTCATGCCGGATCATTAATTGGAGAAGATCAAATTTATAACGTTCTTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTGTATTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTCACCTTACTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610360 Cricotopus sp. water mite diet isolate 11794-BHL101516-GBD15577_4760-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATCTTCGGAGCTTGATCAGGAATAGGAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATTCCGGATCATTAATTGGAGATGATCAAATTTATAACGGTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCACCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTCCCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610361 Cricotopus sp. water mite diet isolate 11795-BHL101516-GBD11318_2784-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATGGTTATACCCATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTCTCCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610362 Cricotopus sp. water mite diet isolate 11796-BHL101516-GBD24367_24265-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGACCAGGAATAGTAGTTACTTCCTTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATCCCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGTGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTAACCTGACTTCGTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610363 Cricotopus sp. water mite diet isolate 11797-BHL101516-GBD27567_20491-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTGTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGACTCTTAATTCGAGCTGTATGAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTGATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTTTTGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610364 Cricotopus sp. water mite diet isolate 11800-BHL101516-GBD23720_13712-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCTGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAGTTCGGTCATGCCGGCTCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTAATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATGTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTGCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610365 Cricotopus sp. water mite diet isolate 11802-BHL101516-GBD28924_14205-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGCGCATCTTAATTCGAGCTGAATTAGGTCATGCCGTTTCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATGTGGAAACTGATTAGTTTCTTTAATGTTAGCGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCGTACTTCTATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610366 Cricotopus sp. water mite diet isolate 11803-BHL101516-GBD7954_24544-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTTCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGGTCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCCCCTTCTCTCACCTTACTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610367 Cricotopus sp. water mite diet isolate 11806-BHL101516-GBD17790_28366-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTCTATTTTATTTTCGGAGCTTGATCAGGCATAGTAGGGACTTCCTTGAGTATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTACTAATTTTTTTCATAGTTATCCCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGTGCTCCTGATATAGCTTTCCCTCGAAGAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610368 Cricotopus sp. water mite diet isolate 11807-BHL101516-GBD10108_25272-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCCTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTGCCCCCTTCACTCACCTTACTTCTATCAAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610369 Cricotopus sp. water mite diet isolate 11809-BHL101516-GBD8388_24362-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAACAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTTATGCTTTTTTAATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGGTTCTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610370 Cricotopus sp. water mite diet isolate 11812-BHL101516-GBD18851_7020-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTCATTGGAGACGATCAAATTTATAACGTTCTTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTATTTCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610371 Cricotopus sp. water mite diet isolate 11814-BHL101516-GBD22649_25655-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTACTTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTATAATTGGAGGATTTGGAAACTGATGAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTGCCCTCGAATAAATAATATAAGTTTTTGATTATGACCCCCTTCTCTCACCTTACTTCTATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610372 Cricotopus sp. water mite diet isolate 11816-BHL101516-GBD17235_11472-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGTTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTCGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATGACACCCTTCTCTCACCTTACCACTTTCAAGTTCAATAGTTGAAAATGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610373 Cricotopus sp. water mite diet isolate 11819-BHL101516-GBD23594_22938-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGTGGCTCCTGATATAGCTTTCCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCACACCTTACTTCTTTCAAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610374 Cricotopus sp. water mite diet isolate 11822-BHL101516-GBD26071_19941-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACCTTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGAGTATTACCCCCCTCTCTAACCTTACTACGTTCAAGGACAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610375 Cricotopus sp. water mite diet isolate 11823-BHL101516-GBD11801_8524-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGGATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTACTTGGAGATGATCAAATTTATAACTTTATTGTTACAGCTCATGCTTTTGTAATAACTTTTTTCATAGTTATACCTCTTTTAATTGGAGGATTTGGAAACTGATTAGTACCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTGCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610376 Cricotopus sp. water mite diet isolate 11824-BHL101516-GBD26789_22813-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAGTAGTAGGGACTTCCTTGAGTATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCGCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTAACCTTACTTCTATCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610377 Cricotopus sp. water mite diet isolate 11825-BHL101516-GBD28233_17699-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGACGGCTCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCCTAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGACTCCTGATATAGCTTTCCCTCGAATAAATAAGATAAGTTTTTGATTATTACCCCCTTCTCTCACCTGACGTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610378 Cricotopus sp. water mite diet isolate 11827-BHL101516-GBD17514_26927-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAACTTGATCAGGAATAGTAGGTACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGAATCATTAATTGGAGCTGATCAAATTTATAACGTTATTGTTACAGCTCATGCTCTTGTAATAATTTTTTTCATAGTTATTCCTATTTTAATTGGAGGATTTGGAAACTGAGTAGTTCCTTTAATGTTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610379 Cricotopus sp. water mite diet isolate 11828-BHL101516-GBD22829_14234-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGCATAGTAGGGACTTCCTTGAGAATCTTACTTCGAGCTGAATTAGGTCATGCCGGATCTTTACTTGGAGATGATCTAATTTATAACGTTATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610380 Cricotopus sp. water mite diet isolate 11833-BHL101516-GBD10703_3722-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGCCATACCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTAACCTTACTACTTGCAAGTGCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610381 Cricotopus sp. water mite diet isolate 11835-BHL101516-GBD24302_9878-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTAATGCTGGATCATTAATTGGAGATGATCAAATTTATAACTTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGTAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCCCCTTCTCTCACCCTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610382 Cricotopus sp. water mite diet isolate 11837-BHL101516-GBD27601_22366-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATACCGGATCATTTATTGGTGATGATCAAATTTATAACGTTATTGTTATAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTCGTTCCTCTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTGACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610383 Cricotopus sp. water mite diet isolate 11838-BHL101516-GBD7950_6959-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTAGGAGCTTGATCAGGAATAGTTGGAACTTCCTTGAGAATATTAATTCGAGCTGAATTATGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCACATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610384 Cricotopus sp. water mite diet isolate 11841-BHL101516-GBD10470_8706-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GACCATTATATTTTATTTTCGGATCTTGATCAGTAATAGTAGGTACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGTGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGGTTTTGATTATTACCCCCTTCGCTCACCTTACCTCTTTCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610385 Cricotopus sp. water mite diet isolate 11844-BHL101516-GBD23279_18177-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGAAAATTATTTGGAGATTATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCATTTAATGTTAGGGGCTCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610386 Cricotopus sp. water mite diet isolate 11847-BHL101516-GBD8723_5711-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTTATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGACTTAGGTCATGCCGGATCATCAATTGGAGATGTTCAAATTTATAACTTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGAGTTGGAAACTGATTAGTTCCTTTAATGTTCGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGGTTTTGATTATTACCCCCTCCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610387 Cricotopus sp. water mite diet isolate 11848-BHL101516-GBD25476_24150-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCAGGCCGGATTATTAATTGGAGGTGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCGTCTCGAACCTTACTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610388 Cricotopus sp. water mite diet isolate 11854-BHL101516-GBD15264_27873-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTGTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGTATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATGCCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTATCAAGTACAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610389 Cricotopus sp. water mite diet isolate 11856-BHL101516-GBD13987_2155-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTGAATTCGAGCTGAATTAGGTCATGCCGGATCTTTAATTGGAGATGATCAAATTTATGACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTTTTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGCGCTTGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610390 Cricotopus sp. water mite diet isolate 11857-BHL101516-GBD4796_10020-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATCTTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGATTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTCATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATGTGGAAACTGATTAGTTCCTTTAATGTTAGGGACTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTCCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610391 Cricotopus sp. water mite diet isolate 11860-BHL101516-GBD7092_18023-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTGAGAATCTTTATTCGAGCTGAATTAGGTCATACCGGATCATTTATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTATAATAATTTTTTTCATAGTTATACCTATTTTAATTGAAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610392 Cricotopus sp. water mite diet isolate 11863-BHL101516-GBD23874_23391-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGTAGCTTGACCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGACGGAGCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGTAAACTGATTAGTTCCTTTAATGTTAGTGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCACACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610393 Cricotopus sp. water mite diet isolate 11864-BHL101516-GBD3398_16402-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTAGGAGCTTGATCGGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGTGATTATCAAATTTATAACGTTATTGTTACAGCTCATGATTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCTCCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGAAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610394 Cricotopus sp. water mite diet isolate 11866-BHL101516-GBD19650_13151-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATTCCGGAACATTCATTGGAGATGATCAAATTTATAACGTGATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTGTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610395 Cricotopus sp. water mite diet isolate 11867-BHL101516-GBD24850_13531-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTATTAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTATCCCTCGAATAAATAATATAAGTTTTTGATTATTACCACCTACTCTAACCGTACTACATTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610396 Cricotopus sp. water mite diet isolate 11868-BHL101516-GBD25904_15241-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTCGGAGCTTGATCAGGAATAGTAGGGATTTCCTTGAGTATCTTAATTCGCGTTGAATTAGGTCATGCCGGATCATTAATTGGAAATGATCAAATTTATAACGTTATTGTTGCAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTACTTTCAAGTACAATTGTTGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610397 Cricotopus sp. water mite diet isolate 11870-BHL101516-GBD26789_15631-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGACGGTACCTTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTGATACCTATTTTAATTGTAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGTCGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610398 Cricotopus sp. water mite diet isolate 11871-BHL101516-GBD17067_5849-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATTATTAATTGGAGATGAGCAAATTTATAACGTTATTGTTACAGCGCATGCTTTTTTAAGAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATTTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610399 Cricotopus sp. water mite diet isolate 11874-BHL101516-GBD11141_24505-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTCGGAGCTTGATCAGGAATAATAGGGACTTCATTGAGTGTCTTAATTCGAGCTGAATTAGGTCATGCCGGATCTTTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTACTAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATGTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610400 Cricotopus sp. water mite diet isolate 11875-BHL101516-GBD7274_25403-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATCCCGGATCTTTTATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTAACCCTACTTCTTTCAAGTTCAATCGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610401 Cricotopus sp. water mite diet isolate 11876-BHL101516-GBD19350_17213-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCATTAATATTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCACCTTCTCTCACCTTATTTCTTTCAAGTAGAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610402 Cricotopus sp. water mite diet isolate 11878-BHL101516-GBD25081_13835-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTCGGAGCTTGATCAGGGATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAACTAGGTCATGCCGGCTCATTAATTGGAAATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATATTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610403 Cricotopus sp. water mite diet isolate 11880-BHL101516-GBD4615_18109-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGTATCTTAATTCGAGCTGAATTAGGTCATGCCGGTTCATTTATTGGAGATGACCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATGTTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCCTTCTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610404 Cricotopus sp. water mite diet isolate 11885-BHL101516-GBD23370_9465-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCCTAATTCGAGCTGTATTAGGTCACGCCGGATCATTAATTGGCGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCGTACAGCTTTCAAGTGCAATTGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610405 Cricotopus sp. water mite diet isolate 11888-BHL101516-GBD8098_21759-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAGCATTATATTTATTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTGAGAATCTTAATTCGAGTTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTCACCATACTTCTTTCAAGTACAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610406 Cricotopus sp. water mite diet isolate 11890-BHL101516-GBD13087_27161-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCACGCCGGATTATTAATTGGAGATGATCAATTTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCGCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610407 Cricotopus sp. water mite diet isolate 11892-BHL101516-GBD25730_16150-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAGTAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGAATCATTATTTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGCAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTCATTAGTTCCTTTAATGTTAGGAACTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610408 Cricotopus sp. water mite diet isolate 11895-BHL101516-GBD24560_20966-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGTTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCTGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGAGTTGGTAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCACCTTCTCACACCTTACTTATTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610409 Cricotopus sp. water mite diet isolate 11896-BHL101516-GBD10414_12036-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTCGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGTTGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTAAACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGTCTCCTGATATAGCTTTCCCTCGAATAAAAAATAAAAGGTTTTGATTATTTCCCCCTTCACTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610410 Cricotopus sp. water mite diet isolate 11898-BHL101516-GBD24670_24823-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGTTGAATTAGGCCATGCCGGATCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATATTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTCACCTTACTTCTATCAAGCTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610411 Cricotopus sp. water mite diet isolate 11902-BHL101516-GBD22670_23087-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGTTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACATCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACATATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTGTTTGATTATTACCCCCTTCTCTCACCTTACTTCATTCAAGTTCAATTGTTGAAAATGGAGCTGAAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610412 Cricotopus sp. water mite diet isolate 11904-BHL101516-GBD10041_15134-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATTCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTTTTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATAACTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAAAGTTAGGGACTCCTGATATAGCGTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCGTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610413 Cricotopus sp. water mite diet isolate 11906-BHL101516-GBD10443_25020-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTCTATTTTATTTTCGGAGCTTGATCAGGAATTGTAGGGCCTTCCTCGAGAATCTTAATTCGAGCTGAATTGGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTAACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTATCCCCTTCTCTCACCTTACTTCTCTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610414 Cricotopus sp. water mite diet isolate 11908-BHL101516-GBD6967_8517-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCACATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTTGTTCCCTTAATGTTTGGGGCTCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATGATTACCCCCTTCTCTCACCTTACTTCTTTCTAGTTCAATCGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610415 Cricotopus sp. water mite diet isolate 11909-BHL101516-GBD28738_17448-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTAGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGTATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATATTAATTGGAGGGTTTGGAATCTGATTAGTTCCTTTAATGTTAGGGACTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACATCTATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610416 Cricotopus sp. water mite diet isolate 11910-BHL101516-GBD12055_13614-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGTGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGGTTAGTTCCTTTAATGTTAGGGGCTCCTGATATGGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610417 Cricotopus sp. water mite diet isolate 11914-BHL101516-GBD22921_15506-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGACATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATCCCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCCCCTTCCCTCACCTTACTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610418 Cricotopus sp. water mite diet isolate 11917-BHL101516-GBD9493_14885-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATCTTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGATAATCTTAATTCGAGCTGAGTTAGGTCATGCCGGATCATTAATTGGTGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGGTTTTGATTATTACCCCCTTCTCTCACCTTACCTCTTTCAAGTACAATTGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610419 Cricotopus sp. water mite diet isolate 11918-BHL101516-GBD13279_27344-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCCTGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTAATTGTCACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTCCCCCCTTCTCTAACCTTACTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610420 Cricotopus sp. water mite diet isolate 11919-BHL101516-GBD13372_11794-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGACCTGAATTAGGTCATGCCGTATCATTAATTGGAGATGTTCAAATTTATATCGTTATTGTTACAGTTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTAACCTTACTACTTTCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610421 Cricotopus sp. water mite diet isolate 11925-BHL101516-GBD19653_6964-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATACTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGTGCATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCTTTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTACTTTCAAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610422 Cricotopus sp. water mite diet isolate 11928-BHL101516-GBD20531_7993-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGGATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCAGCTCTCACCTTACTTCTATCAAGGGCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610423 Cricotopus sp. water mite diet isolate 11930-BHL101516-GBD15625_2556-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATTCCTTATCATTAATTGGAGATGATCAAATTTATAACGTTATGGTTACAGCTCATGCATTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCTCTTCTCTCACCTTACTTCTTTCCAGTTCAATTGTTGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610424 Cricotopus sp. water mite diet isolate 11932-BHL101516-GBD5143_8576-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGTTCATTTATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTATTACCCCCTTCACTCACCCTACTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610425 Cricotopus sp. water mite diet isolate 11938-BHL101516-GBD27880_15922-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGATTTTGTCATAATTTTTTTCATAGTTATCCCTATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610426 Cricotopus sp. water mite diet isolate 11940-BHL101516-GBD9140_22862-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGCTCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTACTTTAATGTTAGTGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTGTTGATTATTACCCCCTTCTCGCACCTTACTTCTTGCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610427 Cricotopus sp. water mite diet isolate 11943-BHL101516-GBD23234_11725-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGACTTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACATTCTTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTATTACCACCTTCTCTCACCTTACTGCTTTCAAGTGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610428 Cricotopus sp. water mite diet isolate 11946-BHL101516-GBD3939_17601-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGAACATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTACCTTTAATGTTGGGAGCTCCTGATATAGCTTTCCCCCGAATAAATAATATAAGATTTTGACTATTACCCCCTTCCCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610429 Cricotopus sp. water mite diet isolate 11949-BHL101516-GBD13372_15184-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGCCATCCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCACATGCTTTTGTAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTTGTTCCTTTAATGTTAGGGGCACCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCCTACTTCTTTCAAGTTCAATGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610430 Cricotopus sp. water mite diet isolate 11950-BHL101516-GBD16962_6694-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTAAATTAGGTCATGCCGGATCATTTATTGGTGATGATCATATTTATAACGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATATCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCCTACTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610431 Cricotopus sp. water mite diet isolate 11951-BHL101516-GBD9178_3328-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCAGGATCATTAATTGGAGATGATCAAATTTATAACTTTATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTCCCGTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCGTCTCTCACCTTACTACTATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610432 Cricotopus sp. water mite diet isolate 11953-BHL101516-GBD20696_20510-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGTTACTTCCTTGTGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGTTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTGGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGGTTATTACCCCCATCTCTCACCTTACTACTTTCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610433 Cricotopus sp. water mite diet isolate 11958-BHL101516-GBD26392_11864-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGACATGCCGGACCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTGATAGTTATACCTATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCGGCTCTCACCTTACTTCTATCAAGTGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610434 Cricotopus sp. water mite diet isolate 11961-BHL101516-GBD19400_23018-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTAAATTAGGTCATGCTGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTACTTTCAAGTGCAGTTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610435 Cricotopus sp. water mite diet isolate 11967-BHL101516-GBD15868_3663-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGAAGGGACTTCCTTGAGAATCTTAATGCGAGCTGAATGAGGTCATGCCGGTTCATTAATTGGAGATGATCTAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCGTAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTCTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCCCCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610436 Cricotopus sp. water mite diet isolate 11970-BHL101516-GBD25225_19537-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACATTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGTGTCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATGATTACCCCCTTCTCTCACCTTACATCAATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610437 Cricotopus sp. water mite diet isolate 11971-BHL101516-GBD28773_18680-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATATATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTGTACCTATTTTAATTGGAGGATTTGGAAACTGATTAATTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTACTCTCACCTTACTTCTTTCAAGTGCAATCGTTGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610438 Cricotopus sp. water mite diet isolate 11974-BHL101516-GBD24599_11119-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTCTATTTTATTTTCGTAGCTTGATCAGGAATAGTATGGACTTCCTTGAGAATCTTACTTCGAGCTGAATTAGGTCCTGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATGGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGATGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTGTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610439 Cricotopus sp. water mite diet isolate 11976-BHL101516-GBD25913_10162-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAGTAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGCTCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACATCACATGCTTTTGTAATAATTTTTTCCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTAACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610440 Cricotopus sp. water mite diet isolate 11981-BHL101516-GBD27606_17366-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACCTTATATTTTATTTTCGGCGCTTGATCAGGAATAGTAGGTACTTCCTTGAGAATCTTAATTCGAACTGAATTAGGTCATGCCGGATCATTAATTGGAGATGCTCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCGTCTCTCACCTGACTTCAGTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610441 Cricotopus sp. water mite diet isolate 11989-BHL101516-GBD28359_15991-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGAATGGACTTCCTTTAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAAAGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAAATGGAGTATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTGTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTACAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610442 Cricotopus sp. water mite diet isolate 11992-BHL101516-GBD26437_24311-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGCTCAGGAACAGTAGGGACTTCCTTGAGCATCTTAATTCGCGCTGACTTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTGGGGGCTCCTGATATAGCTGGCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTGCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610443 Cricotopus sp. water mite diet isolate 11994-BHL101516-GBD28067_14638-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGACATGACGGATCATTAATTGGAGATGATCAACTTTATAACGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGTAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTACAATTGATGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610444 Cricotopus sp. water mite diet isolate 11995-BHL101516-GBD25336_21492-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGTTGAATTAGATCATGCAGGATCATTATTTGGAGATGATCAAATTTATAACTTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAAGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGACTAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAACTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610445 Cricotopus sp. water mite diet isolate 11996-BHL101516-GBD6654_17206-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGTATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGTGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGGGCACCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610446 Cricotopus sp. water mite diet isolate 11997-BHL101516-GBD29424_16024-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGTATAGTAGGGACTTCCTTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAACTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCACTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACCACTTTCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610447 Cricotopus sp. water mite diet isolate 11998-BHL101516-GBD9073_19962-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATCTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTGCTTGGAGATGATCAAATTTATAACATTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCCTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTGCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610448 Cricotopus sp. water mite diet isolate 12004-BHL101516-GBD24598_8919-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGACGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCACCTGATATAGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTACTACCCCCTGCTCTCACCTTACTTCTATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610449 Cricotopus sp. water mite diet isolate 12013-BHL101516-GBD8628_10692-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTCATTCGAGCTGTCTTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTAATGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAAGGTTGGGGACTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATGACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610450 Cricotopus sp. water mite diet isolate 12015-BHL101516-GBD24928_6364-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAGTAGTAGGGCCTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGCTATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTCTTGATTACTACCCCCTCCTCTCACCTTACTGCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610451 Cricotopus sp. water mite diet isolate 12019-BHL101516-GBD11359_13636-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGTATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCGTAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAACAATATAAGGTTTTGAGTATTACCCCCTTCTCTAACCTTACTTCTGTCAAGTACAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610452 Cricotopus sp. water mite diet isolate 12026-BHL101516-GBD22566_9138-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCAAGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGGTCATGCTTTTGTAATAATTTTTTTCATAATTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTACTTCTTTCAAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610453 Cricotopus sp. water mite diet isolate 12033-BHL101516-GBD23722_15987-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAGTTAGGTCATGCCGGATCATTAATTGGTAATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATCCCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGGTTTTGAATATTACCCCCTTCTCTCACCTTACTTCTGGCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610454 Cricotopus sp. water mite diet isolate 12038-BHL101516-GBD5081_9424-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATCTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTCGAGAATCTTAATTCGAGCTGAATTAGGTCATTCCGGATCATTAATTGGAGATGATCAAATTTATAACATTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTACCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTACCTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610455 Cricotopus sp. water mite diet isolate 12298-BHL040517-GBD6042_11710-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCCTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATCCCGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAAATGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610456 Cricotopus sp. water mite diet isolate 12844-BHL040517-GBD3847_15480-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCTCTTACATTACTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610457 Cricotopus sp. water mite diet isolate 13026-BHL040517-GBD15996_2910-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGTTCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGCATAAATAATATAAGTTTTTGATTGTTGCCCCCTTCTTTCACCTTACTCCTATCAAGTTCAATTGTTGAAAATGGAGCTGGATCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610458 Cricotopus sp. water mite diet isolate 13109-BHL040517-GBD12685_15072-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTCGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGTTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610459 Cricotopus sp. water mite diet isolate 13134-BHL040517-GBD19747_5862-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTCTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAACAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCGGACGTCGTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610460 Cricotopus sp. water mite diet isolate 13153-BHL040517-GBD8049_5637-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGGGCTTGGTCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGTCATGCCGGCTCATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCCCATGCTTTCGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCTTTAATACTTGGGGCACCAGATATAGCCTTTCCCCGGATAAATAACATAAGTTTTTGACTTCTACCCCCATCATTAACTCTTTTGCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR670938, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610461 Cricotopus sp. water mite diet isolate 13214-BHL040517-GBD14642_19414-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGGGCTTGGTCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGTCATGCCGGCTCATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCCCATGCTTTCGTAATAATTTTTTTATAGTAGTACCTATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCTTTAATACTTGGGGCACCAGATATAGCCTTTCCCCGGATAAATAACATAAGTTTTTGACTTCTACCCCCATCATTAACTCTTTTGCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR670938, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610462 Cricotopus sp. water mite diet isolate 13251-BHL040517-GBD24360_9888-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAAGAAATAACATAAGATTTTGATTAATTCCACCTTCATTAACATTATTATTATCAAGATCTCTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610463 Cricotopus sp. water mite diet isolate 13416-BHL040517-GBD5392_10112-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCCTTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGGTCGTTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTCCCCTCGAATAAATAATAAAAGTTTTTGATTATTACCCCCTTCTCTTACCTTAATACTTACAAGTTCAATTGTTGAAAATGAAGCTGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610464 Cricotopus sp. water mite diet isolate 13464-BHL040517-GBD10365_15910-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCTTGATCATGGATAGTAGGTACTTCCCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTTATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTTACCTTATTATTATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610465 Cricotopus sp. water mite diet isolate 13567-BHL040517-GBD11400_8597-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCGTGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610466 Cricotopus sp. water mite diet isolate 13672-BHL040517-GBD5246_17996-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGCACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTTGGTACTTCCCTTAGAATCTTAATTCGAGCTGAATTATGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGTGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGTGCTCCTGTTATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACTTTCAAGTGCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610467 Cricotopus sp. water mite diet isolate 13711-BHL040517-GBD13949_26056-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGAGCTTGATCAGGGATAGTAGGAACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATCCCGGATCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATCTTAATTGGTGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR960636, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610468 Cricotopus sp. water mite diet isolate 13744-BHL040517-GBD26133_18382-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGTTCATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCCCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGGACATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTAATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCTCCTTCTCTTACCTTATTACTTTCAAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610469 Cricotopus sp. water mite diet isolate 13828-BHL040517-GBD2287_18430-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACTTTATATTTTATTTTCGGGGCTTGATCAGCGATAGTAGGAACTTCCTTAAGAATCTTAATTCGAGCTGAACTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAATATTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTAACCTTATTACTATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610470 Cricotopus sp. water mite diet isolate 13853-BHL040517-GBD18085_3228-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCCCTAAGAATCTTAATTCGAGCCGAATTAGATCATTCCTTTTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTATCTTATTACTTTCAAATTCAATTGTTGAAAATGGAGCTGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610471 Cricotopus sp. water mite diet isolate 13875-BHL040517-GBD24132_15702-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGAACTTCCCTTAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGGTCATTATTTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATTCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTAACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610472 Cricotopus sp. water mite diet isolate 14002-BHL040517-GBD12227_27075-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCACCTTCTCTCAACTGACATCATTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610473 Cricotopus sp. water mite diet isolate 14034-BHL040517-GBD23080_7188-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTCGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAATTTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610474 Cricotopus sp. water mite diet isolate 14049-BHL040517-GBD24338_9097-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGGGCTTGGTCAGGAATAGTAGGAACTTCTCTAAGAATTTTAATTCGAGCTGAATTAGGTCATGCCGGCTCATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCCCATGCTTTCGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCTTTAATACTTGGGGCACCAGATATAGCCTTTCCCCGGATAAATAACATAAGTTTTTGACTTCTACCCCCACCATTAACTCTTTTGCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR670938, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610475 Cricotopus sp. water mite diet isolate 14229-BHL040517-GBD25049_14179-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGCCATGCCGGAACATTAATTGGAGATGATCAAGTTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTCCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610476 Cricotopus sp. water mite diet isolate 14231-BHL040517-GBD26931_19843-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACTTCTTTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCTGGTTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCACGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610477 Cricotopus sp. water mite diet isolate 14311-BHL040517-GBD21339_26927-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACTTCTCTTAGAATTTTAATTCGAGCTGAATTAGGTCATCCGGATTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGAACTACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610478 Cricotopus sp. water mite diet isolate 14312-BHL040517-GBD24809_23691-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACATCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTACTTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCCCGAATAAATAACATAAGATTTTGATCATTACCACCTTCGTTAACATTATTATTATCAAGATCGATTGTAGAAAAGGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610479 Cricotopus sp. water mite diet isolate 14326-BHL040517-GBD7968_25838-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGCATAGTGGGCACCTCTCTTAGAATTTTAATTCGAGCAGAATTCGGTCATGCCGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCTTCATTAACATTATTATTATCAAGATCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610480 Cricotopus sp. water mite diet isolate 14416-BHL040517-GBD21703_17460-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGTATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGTGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTTCCTCGAATAAATAATATAAGGTTTTGATTATTACCCCCTTCTCTCACCTTGCTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610481 Cricotopus sp. water mite diet isolate 14641-BHL040517-GBD22006_7244-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610482 Cricotopus sp. water mite diet isolate 14686-BHL040517-GBD11465_11940-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610483 Cricotopus sp. water mite diet isolate 14982-BHL040517-GBD24826_9835-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGGGCATGGCCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGTCATGCCGGCTCATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCCCATGCTTTCGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATACTTGGGGCACCAGATATAGCCTTTCCCCGGATAAATAACATAAGTTTTTGACTTCTACCCCCATCATTAACTCTTTTGCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR670938, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610484 Cricotopus trifasciatus water mite diet isolate 792-BHL040916-GBD26255_8526-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGCACTTCTCTAAGAATTTTAATCCGGGTCGAATTAGGACATGCTGGCTCATTAATTGGTGATGATCAAATTTATAATGTCATTGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCACTTACATTATTACTATCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM933933, identified in GenBank as Cricotopus trifasciatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610485 Cricotopus trifasciatus water mite diet isolate 908-BHL100916-GBD13261_26735-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGGACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGACATGCTGGCTCATTAATTGGTGATGATCAAATTTATAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGTGCTTCTGATATAGCGTTCCCTCGACTAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTTACATTATTACTTTCAAGTTCACTAGTAGAAAATGGAGCTGCAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KM933933, identified in GenBank as Cricotopus trifasciatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610486 Cricotopus trifasciatus water mite diet isolate 1855-BHL072216-GBD27250_11414-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGGACATCTCCAAGAATTTTAATCCGGGCCGAATTAGGACATGCTGGCTCATTAATTGGTGATGATCAAATTTATAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTCCTTCCCCCTTCTCTTACATTATTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KM933933, identified in GenBank as Cricotopus trifasciatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610487 Cricotopus trifasciatus water mite diet isolate 2310-BHL072216-GBD15987_12261-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTCATCTTCGGAGCATGATCAGGAATAGTAGGGACTTCTCTAAGAATTTTAATCCGGGCCGAATTAGGACATGCTGGCTCATTAATTGGTGATGATCAAATTTATAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGTGCTCCTGATATAGCTTTCCCGCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCTCTTACATTATTACTATCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KM933933, identified in GenBank as Cricotopus trifasciatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610488 Cricotopus trifasciatus water mite diet isolate 13060-BHL040517-GBD12190_21406-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGCACATCTCTAAGAATTTTAATCCGGGCCGAATTATGACATGCTGGCTCATTAATTGGTGATGATCAAATTTATAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTTACATTATTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KM933933, identified in GenBank as Cricotopus trifasciatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610489 Cricotopus trifasciatus water mite diet isolate 13392-BHL040517-GBD21770_3085-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGGACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGACATGCTGGCTCATTAATTGGTGATGATCAAATTTATAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTTACATTATTACTTTCAAGTTCAATTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KM933933, identified in GenBank as Cricotopus trifasciatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610490 Cricotopus trifasciatus water mite diet isolate 13858-BHL040517-GBD9920_24410-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGGACATCTCTAAGAATTTTAATCCGGGCCGAGTTAGGACATGCTGGCTCATTAATTGGTGATGATCAAATTTATAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTCTTGACTACTTCCCCCTTCTCTTACATTATTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KM933933, identified in GenBank as Cricotopus trifasciatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610491 Cricotopus trifasciatus water mite diet isolate 14054-BHL040517-GBD7751_18911-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGGACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGACATGCTGGCTCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTAACATTATTACTTTCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KM933933, identified in GenBank as Cricotopus trifasciatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610492 Cryptochironomus sp. water mite diet isolate 533-BHL040517-GBD3940_15691-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAATATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTCTTGGAGACAACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGCTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATACTGTGGGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGAGTTTGACTTTTACCACCAGCCTTGACTCTTCTTCTTTCAAAATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610493 Cryptochironomus sp. water mite diet isolate 6952-BHL032417-GBD25337_6260-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGATTTAGGACGATCAGGAACTTTTATTGGAGACGACCAATTTTTTAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610494 Cryptochironomus sp. water mite diet isolate 7093-BHL032417-GBD27290_14484-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACAACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCGTAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTATTACCCCCATCCTTAACTCTACTACTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610495 Cryptochironomus sp. water mite diet isolate 7132-BHL032417-GBD4044_12933-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACATTATTTTTGGGGCATGATCCGGAATAGTGGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAGTTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATACTGGGATCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610496 Cryptochironomus sp. water mite diet isolate 7177-BHL032417-GBD26944_9660-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACAACCTGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATACTAGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTCTACCCCCATCCTTAACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ445484, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610497 Cryptochironomus sp. water mite diet isolate 7209-BHL032417-GBD28208_15307-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTTGGAGCTTGATCAGGAATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACAACCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTAATACTAGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTATTACCCCCATCTTTGACCCTTCTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610498 Cryptochironomus sp. water mite diet isolate 7211-BHL032417-GBD24056_8573-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTCGGACGATCAGGATCTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTAACACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTATTACCCCCATCCTTGACTCTACTACTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610499 Cryptochironomus sp. water mite diet isolate 7220-BHL032417-GBD11573_27586-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACTTCTTTAAGCATATTAATTCGAGCAGAATTAGGACGTCCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATACTAGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTATTACCCCCATCCTTAACTCTACTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610500 Cryptochironomus sp. water mite diet isolate 7230-BHL032417-GBD9248_3789-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACCGAATTCGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTCGGAAATTGATTAGTACATCTTATACTGTGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610501 Cryptochironomus sp. water mite diet isolate 7269-BHL032417-GBD16527_14517-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGGAGGAATCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCAGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610502 Cryptochironomus sp. water mite diet isolate 7271-BHL032417-GBD25475_13953-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGTATATTAGGAACATCATTAAGTATATTAATTCGAGCAGAATTAGGACCACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATACTGAGAACCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTACTACTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610503 Cryptochironomus sp. water mite diet isolate 7285-BHL032417-GBD12548_23390-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTTATTCGAGCAGAATTAAGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACGGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610504 Cryptochironomus sp. water mite diet isolate 7287-BHL032417-GBD23446_13417-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGACCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTAATACTGGGAGCCCCAGATATAGCATTCCCCCGAATAAATAATATAAGATTTTGACTATTACCCCCATCCTTAACTCTACTACTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610505 Cryptochironomus sp. water mite diet isolate 7343-BHL032417-GBD13238_13672-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCCGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATACTAGGAGCCCCAGATATGGCATTTCCACGAATAAATAATATAAGATTTTGACTATTACCACCATCCTTGACTCTACTTCTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610506 Cryptochironomus sp. water mite diet isolate 7364-BHL032417-GBD27510_17099-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCTTTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTAACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAAATGATTAGTACCTCTTATACTAGGAGCTCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCTTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610507 Cryptochironomus sp. water mite diet isolate 7422-BHL032417-GBD12688_9911-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGAAAAAGCAATTCCCCGAAAAAAAAATAAAAGAATTTGACCTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610508 Cryptochironomus sp. water mite diet isolate 7489-BHL032417-GBD11392_24163-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGCATAGTAGGAACTTCTTTAAGTATATTAATTAGAGCAGAATTAGGATGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGGATGATTTGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATGTTGACTTTTACCCCCATCCTTAACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610509 Cryptochironomus sp. water mite diet isolate 7555-BHL040517-GBD4211_14183-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTAATGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATATCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGTCCCAGATATAGCATTTCCCCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCCCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610510 Cryptochironomus sp. water mite diet isolate 7680-BHL040517-GBD25217_14234-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATATCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGTCCCAGATATAGCATTTCCCCGAATAAAAAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610511 Cryptochironomus sp. water mite diet isolate 7683-BHL040517-GBD26947_13739-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATCTTAGGAACCTCATTAAGTATATTAATTCGAGCAGATTTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGCTATATCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGTCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610512 Cryptochironomus sp. water mite diet isolate 7688-BHL040517-GBD27719_10303-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTCCACTAAGAATATTAATTCGAGCTGAACTAGGACATCATGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTAGACCTATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGTCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610513 Cryptochironomus sp. water mite diet isolate 7706-BHL040517-GBD24731_7714-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATATCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGTCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610514 Cryptochironomus sp. water mite diet isolate 7731-BHL040517-GBD13356_8686-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCTAGCGGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGCAATTGTAACAGCTCATGCTTTTATTATGATTTTTTTCATGGTTATATCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGTCCCAGATATAGCATTTCCCCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610515 Cryptochironomus sp. water mite diet isolate 7761-BHL040517-GBD17394_15239-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATATCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGTCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCGTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610516 Cryptochironomus sp. water mite diet isolate 7845-BHL040517-GBD8693_12744-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGCATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATATCAATTTTAATTGGAGGATCCGGAAATTGATTAGTACCTCTTATACTGGGAGTCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCATCTCCTTTCTAGTTCTTTCGTAGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610517 Cryptochironomus sp. water mite diet isolate 7864-BHL040517-GBD12354_22090-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTCATGGTTATATCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGTCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610518 Cryptochironomus sp. water mite diet isolate 7955-BHL040517-GBD19979_5125-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATTTTAATTCGAGCAGAATTAGGACAACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTCTAATAATTTTTTTCATGGTTATATCAATTTTAATTGGAGGATTTGGAAATTGATTAGTATCTCTAATACTGGGAGTCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTACTTCTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610519 Cryptochironomus sp. water mite diet isolate 8068-BHL040517-GBD10076_23706-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGAAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCGTTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATATCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGTCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ445484, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610520 Cryptochironomus sp. water mite diet isolate 9899-BHL040517-GBD11923_4959-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610521 Cryptochironomus sp. water mite diet isolate 9943-BHL040517-GBD4496_11114-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ445484, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610522 Cryptochironomus sp. water mite diet isolate 10004-BHL040517-GBD22016_19277-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGTATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACACTTCTTCTTTCTAGTTCTTTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610523 Cryptochironomus sp. water mite diet isolate 10051-BHL040517-GBD21550_18048-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610524 Cryptochironomus sp. water mite diet isolate 10068-BHL040517-GBD8873_19679-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCGAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610525 Cryptochironomus sp. water mite diet isolate 10074-BHL040517-GBD18426_17435-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGGACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ207490, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610526 Cryptochironomus sp. water mite diet isolate 10101-BHL040517-GBD18949_23771-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGTGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCGAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR769864, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610527 Cryptochironomus sp. water mite diet isolate 10118-BHL040517-GBD13027_27082-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610528 Cryptochironomus sp. water mite diet isolate 10154-BHL040517-GBD8761_7174-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGATCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTGATAATGTTAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACCTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610529 Cryptochironomus sp. water mite diet isolate 10226-BHL040517-GBD17666_19347-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGGGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGTGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610530 Cryptochironomus sp. water mite diet isolate 10237-BHL040517-GBD13103_12408-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAGGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610531 Cryptochironomus sp. water mite diet isolate 10249-BHL040517-GBD8394_4652-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATACGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGACATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610532 Cryptochironomus sp. water mite diet isolate 10291-BHL040517-GBD6571_25926-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTGCCCGAATAAATAATATAAGATTTTGACTTTTGCCACCATCCTTGACTCTGCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610533 Cryptochironomus sp. water mite diet isolate 10392-BHL040517-GBD22957_6758-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCAAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAGTGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR085381, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610534 Cryptochironomus sp. water mite diet isolate 10466-BHL040517-GBD4873_16153-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTGGGAACTTCATTAAGAATGCTTATTTGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTGCCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KJ445484, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610535 Cryptochironomus sp. water mite diet isolate 10499-BHL040517-GBD15767_24478-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATTGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610536 Cryptochironomus sp. water mite diet isolate 10511-BHL040517-GBD20197_28040-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACATTATTTTTGGGGCTTGATCCGGAATATTGGTAACTTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGTGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGAACAATTGTAGAAAGTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610537 Cryptochironomus sp. water mite diet isolate 10638-BHL040517-GBD22801_5145-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGAATATTAGGAACTTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTAGTACCTCTAATACTGGGAGCACCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTGCCCCCATCATTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610538 Cryptochironomus sp. water mite diet isolate 10659-BHL040517-GBD8737_26052-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCTTGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.0% identical to accession ID KR085303, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610539 Cryptochironomus sp. water mite diet isolate 13973-BHL040517-GBD13932_7968-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACAACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGTGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610540 Cryptochironomus sp. water mite diet isolate 13988-BHL040517-GBD26548_6733-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGTATATTAGGAACCTCTTTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACAACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTAATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGAGTTTGACTTTTACCCCCATCATTGACTCTACTACTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610541 Cryptochironomus sp. water mite diet isolate 13989-BHL040517-GBD29422_14662-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACAACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610542 Cryptochironomus sp. water mite diet isolate 13991-BHL040517-GBD21314_9934-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGGACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACAACCAAATTTATAATGTAATTGTAACAGCTCTTGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCCTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGAGTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610543 Cryptochironomus sp. water mite diet isolate 13996-BHL040517-GBD27921_11610-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTTGGAGCTTGATCGGTAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGAGTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610544 Cryptochironomus sp. water mite diet isolate 14041-BHL040517-GBD6686_8918-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATACTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGACAACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTAATACTTGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGAGTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610545 Cryptochironomus sp. water mite diet isolate 14053-BHL040517-GBD29242_12577-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACAACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATACTTGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGAGTTTGACTATTACCCCCATCCTTGACTCTACTATTTTCAAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610546 Cryptochironomus sp. water mite diet isolate 14062-BHL040517-GBD25556_19798-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTCGGGAGCTGGATCAGGGATATTAGGACCCTCATTATGTATATTAATTCGAGCAGAATTAGGACTACCAGGAACTTTTATTGGAGACAACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGAGTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610547 Cryptochironomus sp. water mite diet isolate 14074-BHL040517-GBD24980_25644-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAACTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAAAATTAGGACGACCAGGAACTTTTACTGGAGACAACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATCATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGTCCCAGATATAGCATTTCCCCGAATAAATAATATAAGAGTTTGACTATTACCCCCATCCTTGACTCTTATTCTTTCAAGATCAAGTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610548 Cryptochironomus sp. water mite diet isolate 14076-BHL040517-GBD3737_16271-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACAACCAGGAACTTTTATTGGAGATAACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTAATACTGTGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGAGTTTGACTTTTATCCCCATCCTTGACTCTTCTTCTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610549 Cryptochironomus sp. water mite diet isolate 14090-BHL040517-GBD7074_16402-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAGGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACAACCAAATTTATAATGTAATTGTAACGGCTCATGTTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTAATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAACATAAGAGTTTGACTTTTACCCCCATCCTTGACCCTTCTTCTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610550 Cryptochironomus sp. water mite diet isolate 14097-BHL040517-GBD28405_14388-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTGATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACAACCAAATTTATAATATAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGATTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGAAATAGCATTTCCCCGAATAAAAAAAAATAAGAGTTTGACTTTTACCCCCATCCTTGACCCTTCTTCATTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610551 Cryptochironomus sp. water mite diet isolate 14138-BHL040517-GBD17684_24667-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACGACCAGGAACTTTTATTGGAGACAACCAAATTTATAATGTAATTGTAACAGCACATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGAGTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610552 Cryptochironomus sp. water mite diet isolate 775-BHL040916-GBD19296_24907-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAAAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATATCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGTCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610553 Cryptochironomus sp. water mite diet isolate 1780-BHL110116-GBD22307_6310-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTTATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGATTTTATTATAATTTTTTTCATGGTTATATCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGTAGTCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610554 Cryptochironomus sp. water mite diet isolate 2346-BHL072216-GBD7993_13575-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGTTTTTATCATAATTTTTTTCATGGTTATATCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGTCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610555 Cryptochironomus sp. water mite diet isolate 2892-BHL032417-GBD24833_25328-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGTGATATTAGGAGCCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGTCCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGAAGGATTTGGAAATTGATTAGTACCTCTTATATTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTATTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610556 Cryptochironomus sp. water mite diet isolate 3415-BHL032417-GBD10533_27108-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGATCAAAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTCGGTAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACACTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610557 Cryptochironomus sp. water mite diet isolate 4335-BHL032417-GBD27273_18841-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGAACAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTATAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTATTACCCCCATCCTTGACCCTACTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610558 Cryptochironomus sp. water mite diet isolate 4579-BHL032417-GBD8333_24722-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCGGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610559 Cryptochironomus sp. water mite diet isolate 5608-BHL032417-GBD23246_5328-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGGGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610560 Cryptochironomus sp. water mite diet isolate 5825-BHL032417-GBD23906_6409-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGTCGCCCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTACTACTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610561 Cryptochironomus sp. water mite diet isolate 6229-BHL032417-GBD25579_22287-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGTATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGTCCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATATTGGGAGCACCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTATTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610562 Cryptochironomus sp. water mite diet isolate 6401-BHL032417-GBD7685_16742-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGGCGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCATTTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTAGGAGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610563 Cryptochironomus sp. water mite diet isolate 7100-BHL032417-GBD26739_9424-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGTATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACAACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGTTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCTGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTATTACCCCCATCCTTGACTCTACTTCTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610564 Cryptochironomus sp. water mite diet isolate 7279-BHL032417-GBD14511_13947-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACATTATTTTTGGGGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAAAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCCTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATATTGGGAGCCCCAGATATACCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610565 Cryptochironomus sp. water mite diet isolate 7354-BHL032417-GBD7964_7835-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTCTGGAGCTTGATCAGGGATATTAGGAACTTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACTGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTAGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610566 Cryptochironomus sp. water mite diet isolate 8475-BHL101416-GBD23092_3817-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAGGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610567 Cryptochironomus sp. water mite diet isolate 9655-BHL032417-GBD22436_17557-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGAACAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610568 Cryptochironomus sp. water mite diet isolate 9848-BHL040517-GBD17535_24246-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCTTTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTATTGCCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610569 Cryptochironomus sp. water mite diet isolate 12114-BHL040517-GBD23092_3817-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAGGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610570 Cryptochironomus sp. water mite diet isolate 12597-BHL040517-GBD7760_17746-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACGGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATACAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610571 Cryptochironomus sp. water mite diet isolate 13940-BHL040517-GBD23068_8949-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATATCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGTCCCAGATATAACATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610572 Cryptochironomus sp. water mite diet isolate 13993-BHL040517-GBD11393_16274-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACATTATTTTTGGGGCTTGATCCGGGATATTAGGAAACTCATTAAGTATATTAATTCGAACAGAATTAGGACGACCAGGAACTTTTATTGGAGACAACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGAGTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610573 Cryptochironomus sp. water mite diet isolate 14022-BHL040517-GBD16444_2061-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACAACCAGGAACTTTTCTTGGAGACGACCAAATTTATAATGTAATTGTAACTGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTAATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGAGTTTGACTTTTACCCCCATCCTTGACTCTACTACTTTCAAGATCAAGTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610574 Cryptochironomus sp. water mite diet isolate 14045-BHL040517-GBD11154_11035-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACTTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGACAATCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTAATACTAGGAGCCCCAGATATAGCATTCCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610575 Cryptochironomus sp. water mite diet isolate 14064-BHL040517-GBD20183_4893-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAATCTCATTTAGTATATTAATTCGAGCAAAATTAGGACTACCAGGAACTTTTATTGGAGACAACCAAATTTATAACGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTAATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATGTAAGAGTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610576 Cryptochironomus sp. water mite diet isolate 14086-BHL040517-GBD25361_16818-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATCCGAGTAGAATTAGGACAACCAGGAACCTTTATTGGAGAAGATCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGAGTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610577 Cryptochironomus sp. water mite diet isolate 14296-BHL040517-GBD27871_12272-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGATCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTCTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATATCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGTCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTGGACTTTTACCCCCATCCTTGACTCTTCGTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610578 Cryptochironomus sp. water mite diet isolate 15202-BHL040517-GBD27856_12257-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGATCTTGATCAGGTATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTCTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATATCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTAGGAGTCCCAGACATAGCATTTCCCCGAATAAATAATATAAGATTTGGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610579 Culex pipiens water mite diet isolate 1181-BHL110116-GBD21087_28250-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCTGGTGTATTTATTGGAAATGGTCAAATTTATAATGTTATTGTCACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATTATAATTGGAGGTTTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.4% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610580 Culex pipiens water mite diet isolate 2966-BHL032417-GBD22724_4246-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGCAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610581 Culex pipiens water mite diet isolate 4247-BHL032417-GBD26791_8578-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTTAGTTTATTAATTCGAGCAGAATTAGGTCAACCTGGTGTATTTATTGGAAGTGTTCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATAGCCTTTCCTCGAATAAATAATATAAGATCTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610582 Culex pipiens water mite diet isolate 6662-BHL032417-GBD25415_6112-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATACAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGTCTTTCCTCGAGTAAATAATATAAGGTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610583 Culex pipiens water mite diet isolate 6701-BHL032417-GBD15679_17806-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTCAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAACATAAGTTCTGGAAAACTACCTCCTTCATTGACACAACCACATTCAAGTAGTTTAGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610584 Culex pipiens water mite diet isolate 6717-BHL032417-GBD21227_12597-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAGGTCAACCTGGTGTATTTATTGGAGATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATAGCCTTTCCCCGAATAAAAAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTATCAAGTAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.4% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610585 Culex pipiens water mite diet isolate 6734-BHL032417-GBD27918_13405-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTATTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATTATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATGGCTTTTCCTCGAATAAATAATATAAGATTTTGAATACTACCACCTTCATTGACACTACTACTTTCAAGTAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610586 Culex pipiens water mite diet isolate 6745-BHL032417-GBD17288_2646-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTAGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCATGTGTATTTATTGGAAATGATCAAATTTATAATGATATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACTCTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KU756485, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610587 Culex pipiens water mite diet isolate 6760-BHL032417-GBD26672_13849-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACTTTATATTTATTTTTGGGGCTTGAGCTGGTATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGACAACCTGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACCACTACTATCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610588 Culex pipiens water mite diet isolate 6798-BHL032417-GBD21141_8690-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGATCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGTAGAATTAAGTCAACCAGGTTTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAATTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGATTTTGAATACTACCACCTTCATTGACACTACTACTATCAAGAAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610589 Culex pipiens water mite diet isolate 6800-BHL032417-GBD12473_2968-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTGATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACACTGCTCCTTTCAAGTAGTTTAGTACAAAATGGCGCTGG	Using NCBI BLASTN in June 2018, this sequence was 98.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610590 Culex pipiens water mite diet isolate 6802-BHL032417-GBD3818_8307-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACTTTATATTTATTTTCGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTTATTCGAGCAGAATTAGGTCAACCAGGAATATTTATTGGAAATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610591 Culex pipiens water mite diet isolate 6804-BHL032417-GBD13801_7075-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAATCAACCTGGTGTATTTATTGGTAATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAATTAATATAAGTTTTTGAATACTACCCCCTTCTTTGACACTACTACTTTCAAGTAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610592 Culex pipiens water mite diet isolate 6810-BHL032417-GBD5656_13486-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGCTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAGGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTATTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATGTCAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACCCTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610593 Culex pipiens water mite diet isolate 6817-BHL032417-GBD24346_20844-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGAGCTTGAGCTGGAATATTTGGTACTTCTTTAAGTTTGCTAATTCTAGCAGAATTAGGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTCACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610594 Culex pipiens water mite diet isolate 6820-BHL032417-GBD24812_20099-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATATTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTGGGAGCTCCAGATATGGCCTTTCCTCAAATAAATAAAATAAGTTTTTGAATACTACCACCTGCATTGACACGACTACTGTCAAGTAGTTTAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610595 Culex pipiens water mite diet isolate 6830-BHL032417-GBD19747_15857-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGGACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGCTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTTTTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGAATACTACCCCCCTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610596 Culex pipiens water mite diet isolate 6855-BHL032417-GBD12461_2685-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGATCTGGAATAGTTGGAACTTCTTTAAGTTTCCTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGGAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGAATTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAATTTAGTAGAAACTGGAGCTGG	Using NCBI BLASTN in June 2018, this sequence was 98.0% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610597 Culex pipiens water mite diet isolate 6858-BHL032417-GBD15369_2506-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATATTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGAGTACTAATTCGAGCAGAATTAAGTCAACCAGGTTGATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACCTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610598 Culex pipiens water mite diet isolate 6873-BHL032417-GBD9315_27335-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGTGCTGGCATAGTTGGAACTTCTTTAAGTTTTCTAATTCGAGCAGAATTCAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATTATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTATCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610599 Culex pipiens water mite diet isolate 6878-BHL032417-GBD21330_3737-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGATCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTAATATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATCTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAACATAAGTTTTTGAATACTACCTCCTTCATTGTCCCTACGACTATCAAGTAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610600 Culex pipiens water mite diet isolate 6887-BHL032417-GBD13929_13998-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGTTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGAATATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTAGAATACTACCTCCTTCATTGACACTTCTACAATCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610601 Culex pipiens water mite diet isolate 6906-BHL032417-GBD9920_18847-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCATTTCTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAACAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACGACGGTCAAGTAGTTTAGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610602 Culex pipiens water mite diet isolate 6914-BHL032417-GBD11771_7096-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGTTATTGGCACATTATATTTATCTTTGGGTCTTGAGCTGGAATAGTTGGTACTTCTTTATGTTTACTGATTCGCGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610603 Culex pipiens water mite diet isolate 6926-BHL032417-GBD24785_9726-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTACATTATATTTATTTTTGGTGCTTGATCTGGAATAGTGGGAACTTCTTTAAGTTTATTAATTCGAGCAGAATTAGGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAAGGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610604 Culex pipiens water mite diet isolate 6933-BHL032417-GBD28068_19435-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACACTATATTTATTTAGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTTAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTCATTGGAAATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGACATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATAGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.7% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610605 Culex pipiens water mite diet isolate 7136-BHL032417-GBD24997_9418-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTCACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCCCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.0% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610606 Culex pipiens water mite diet isolate 8862-BHL101416-GBD11611_25194-Lq60 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAATCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGTCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.6% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610607 Culex pipiens water mite diet isolate 9587-BHL032417-GBD27490_16062-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACTAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTTCCTCCTACATTAACACTACTACGTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.7% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610608 Culex pipiens water mite diet isolate 10021-BHL040517-GBD26073_18497-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCGGAATTAAATCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTGACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGTCTTTCCTCGAATAAAAAATATAAGTGTTTGAATACTACCTCCTTCATTGACACTACTACAATCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610609 Culex pipiens water mite diet isolate 10132-BHL040517-GBD11606_11322-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTACTTTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAGGTCAACCAGGTGTATTTATTGGAGATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATAGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCCCCTTCATTGACACTACTTCTATCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.4% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610610 Culex pipiens water mite diet isolate 10155-BHL040517-GBD22786_11226-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTACATTATATTTATTTTTGGGGCTTGATCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAATCAACCTGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGTCTTTCCTCGAATAAATAAAATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTATCAAGTAGTTTAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.1% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610611 Culex pipiens water mite diet isolate 10164-BHL040517-GBD24612_20723-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGAGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTTATTCGAGCAGAATTAAATCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATAGTCTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.4% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610612 Culex pipiens water mite diet isolate 10275-BHL040517-GBD24671_6831-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTAGGTACTTCTTTAAGTTTATTAATTCGAGCAGAATTAGGTCAACCAGGTGCTTTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610613 Culex pipiens water mite diet isolate 10281-BHL040517-GBD26302_18886-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCCTGAGCTGGAATAGTTGGAACTTCTTTTAGTTTACTAATTCGAGCAGAATTATGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATAATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGGGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGATTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.4% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610614 Culex pipiens water mite diet isolate 10384-BHL040517-GBD20577_28228-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTCAACAAATCATAAAGATATTGGAACATTGTATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGTACTTATTTTTGTTTACTAATTCGAGCAGAATTAAATCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGTCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610615 Culex pipiens water mite diet isolate 10396-BHL040517-GBD10589_10404-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACCCTTTACTTTATTTTTGGAGCTTGATTTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCTGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610616 Culex pipiens water mite diet isolate 10422-BHL040517-GBD5459_24197-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACTTTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTATTAATTCGAGCAAAATTAAGTCAAACAGGTGTATTTATCGGAAATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTATCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610617 Culex pipiens water mite diet isolate 10447-BHL040517-GBD15586_6448-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAGTAGTTGGAACTTCTTTAAGTGTACTAATTCGAGCAGAATTAAATCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCGGATATGGTCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACCCTACTACTTTCAAATAGTTTAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.4% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610618 Culex pipiens water mite diet isolate 10454-BHL040517-GBD18097_24406-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGATTTGGAATAGTTGGAACTTCTTTTAGTTTACTAATTCGAGCAGAATTAGGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATAATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAACATAAGATTTTGAATACTACCTCCTTCATTGACACTACTACTATCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610619 Culex pipiens water mite diet isolate 10575-BHL040517-GBD10474_12697-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACATTATATTTATTTTTGGGGCTTGATCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCGGAATTATGTCGACCTGGTATATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610620 Culex pipiens water mite diet isolate 10615-BHL040517-GBD24623_22220-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTTTATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAATCAACCAGGTTTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTAATGCCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610621 Culex pipiens water mite diet isolate 10664-BHL040517-GBD26848_21161-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACACTATATTTATTTTCGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGAGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTGCCTCCTTCATTGACACTACTACTTTCAAGTAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.4% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610622 Culex pipiens water mite diet isolate 12660-BHL040517-GBD26720_20990-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACACTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGAAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610623 Culex pipiens water mite diet isolate 14144-BHL040517-GBD24403_25998-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAAAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATAGCCTTTCCTCGAATAAATATTATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.6% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610624 Culex sp. water mite diet isolate 4145-BHL032417-GBD16947_7588-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATTGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGATACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610625 Culex sp. water mite diet isolate 4206-BHL032417-GBD11281_25075-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTCAACAAATCATAAAGATATTGGCACATTATATTTATTTTTGGGGCTTGAGCTTGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGATCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAAATGATTAGTTCCTTTAATGTCAGGAGCTCCAGATATGGCCGTTCCTCGAATAAATAATATAAGGTCTTGAATACTACCTCCTTCAGTGACACTACTACTTGCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610626 Culex sp. water mite diet isolate 4250-BHL032417-GBD15257_16357-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTACTTCAAGCAGAACTTGGACGACCTGGTACTTTTATTGGAAATGGTCAAATTTATAATGTTATTGTAACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGAATAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGGCACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610627 Culex sp. water mite diet isolate 4289-BHL032417-GBD16340_16766-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTATTAATTCGAGTAGAATTAGGTCAACCAGGTGCATTTATTGGAAATGATCAAATTTATAATGTTATTGTTACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCCTTTCCTCGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACACTACTACTATCAGGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610628 Culex sp. water mite diet isolate 4322-BHL032417-GBD25233_11050-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATTTTATTGTAACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGCTTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATAAAAGTTCTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610629 Culex sp. water mite diet isolate 4329-BHL032417-GBD15750_3668-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGGCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGATTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTTCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTTTTACTTTCAAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610630 Culex sp. water mite diet isolate 4351-BHL032417-GBD18585_18062-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTTTATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCCCTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTCTTGAATACGACCTCCTACATTGACACAACATCAATCAAGTAGTTTAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610631 Culex sp. water mite diet isolate 4383-BHL032417-GBD27639_18394-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTAGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAATTGCCCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCGGATATGGCCTTTCCTCGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACATTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610632 Culex sp. water mite diet isolate 4392-BHL032417-GBD11519_21746-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACATTATATTTTATTTTTGGGGCTTGAGGTGGAATAGTTGGAACTTCTTTTAGTTTACTAATTCGAGTAGAATTATGTCAACCAGGAGTATTTATTGGAAATGGTCAAATTTATAATGTTCTTGTAACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTTGAATAAATAATATAAGATCTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610633 Culex sp. water mite diet isolate 4442-BHL032417-GBD17973_3288-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGGCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAACTTATAATGTTATTGTAACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGGTTTGGAAATTGATTAGTACATTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610634 Culex sp. water mite diet isolate 4453-BHL032417-GBD15766_7367-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAGGTCAACCAGGTGTATTTATTGGAGATGGTCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTCTTGAATACTACCCCCTTCATTGACACTACTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610635 Culex sp. water mite diet isolate 4463-BHL032417-GBD27099_19503-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAGTGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATGGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610636 Culex sp. water mite diet isolate 6703-BHL032417-GBD22598_22699-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTTCATTATACTTCATTTTTGGTGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610637 Culex sp. water mite diet isolate 6732-BHL032417-GBD20868_15776-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTTCATTATACTTCATTTTTGGTGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTTATTCGAGCAGAATTAGGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTGTCAAGTAGGGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610638 Culex sp. water mite diet isolate 6743-BHL032417-GBD26948_13903-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGCTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCCTCTTTCTAGTTTTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610639 Culex sp. water mite diet isolate 6859-BHL032417-GBD19340_7667-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTTGGAACTTCTTTAAATTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTAATACCAATCATAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610640 Culex sp. water mite diet isolate 6899-BHL032417-GBD25587_17419-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGCTGGAACTTCTTTAAGTTTACTAATTCGAGCAAAATTAAGTCAACCAGGTGTTTTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGGAACTGATTATTACCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610641 Culex sp. water mite diet isolate 9114-BHL032417-GBD2995_13082-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCGCCAGATATAGCTTTTCCTCGGATAAATAATATAAGTTTTTGATTACTCCCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610642 Culex sp. water mite diet isolate 9351-BHL032417-GBD15319_16486-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610643 Culex sp. water mite diet isolate 9729-BHL040517-GBD18034_12608-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAATAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610644 Culex sp. water mite diet isolate 9772-BHL040517-GBD14124_10563-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTTGAGCTTGCTCTGGTATAGTAGGTACTTCTTTATGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTGACTGCTCATGCTTTTATTACAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610645 Culex sp. water mite diet isolate 9911-BHL040517-GBD17496_7064-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGTCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTATTTCGAGCGGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAATTTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610646 Culex sp. water mite diet isolate 9956-BHL040517-GBD21551_15757-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATAGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGTCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610647 Culex sp. water mite diet isolate 9958-BHL040517-GBD27158_17478-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCGCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610648 Culex sp. water mite diet isolate 9984-BHL040517-GBD17028_20039-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCCTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610649 Culex sp. water mite diet isolate 10007-BHL040517-GBD22725_21603-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATACATTACTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTAATACCAATAATAATTAGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID FN395194, identified in GenBank as Culex torrentium. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610650 Culex sp. water mite diet isolate 10008-BHL040517-GBD18772_24781-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAATCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGTCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610651 Culex sp. water mite diet isolate 10016-BHL040517-GBD13541_16668-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGTCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610652 Culex sp. water mite diet isolate 10026-BHL040517-GBD4525_14696-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAGGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610653 Culex sp. water mite diet isolate 10029-BHL040517-GBD11740_18713-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCATCTCTAACATTATTACCTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610654 Culex sp. water mite diet isolate 10033-BHL040517-GBD24302_7656-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610655 Culex sp. water mite diet isolate 10060-BHL040517-GBD9611_15953-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGTTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCCTCTTCTTTCTAGCTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610656 Culex sp. water mite diet isolate 10064-BHL040517-GBD5847_12763-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTCAAGTTTACTGATTCGAGCAGAATTAAATCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.1% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610657 Culex sp. water mite diet isolate 10081-BHL040517-GBD22300_21988-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610658 Culex sp. water mite diet isolate 10142-BHL040517-GBD20582_27805-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCCCCTTCATTGACACTACTACTGTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610659 Culex sp. water mite diet isolate 10165-BHL040517-GBD19679_22137-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAATCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610660 Culex sp. water mite diet isolate 10171-BHL040517-GBD6150_25205-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCCTTAAGTATGCTAATACGAGCAGAACTTGGACGACCTGGTACTTTCATTGGAGATGACCAAATTTACAATGTAATTGTCACATCACACGCTTTTATTATAATTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCCTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610661 Culex sp. water mite diet isolate 10231-BHL040517-GBD23212_19132-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAATCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGACTTTCCTCGAATAAATAATATAAGGTTTTGAATACTACCTCCTACAGTGACACTGCTACTTGCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610662 Culex sp. water mite diet isolate 10232-BHL040517-GBD20492_28136-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTTTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTATACTAATTCGAGCAGAATTAAATCAACCAGGAGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCAGATATGGTCTTTCCTCGAATAAATAATATAAGATTCTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610663 Culex sp. water mite diet isolate 10246-BHL040517-GBD17274_13610-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAATCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGTCTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610664 Culex sp. water mite diet isolate 10290-BHL040517-GBD13341_5686-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610665 Culex sp. water mite diet isolate 10362-BHL040517-GBD10598_17903-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAATCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGTCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610666 Culex sp. water mite diet isolate 10385-BHL040517-GBD18113_11551-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610667 Culex sp. water mite diet isolate 10390-BHL040517-GBD15617_8337-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAATCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTGCCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610668 Culex sp. water mite diet isolate 10431-BHL040517-GBD16667_24588-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATACGAGCAAAACTTGGACGACCTGGTACTTTTATTGGAGATGATCAAATTTATAGTGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGGATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610669 Culex sp. water mite diet isolate 10442-BHL040517-GBD15529_4827-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACACTATATTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACTACCAGGAACTTTTATTGGAGACGACCATATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTTATTGACCCTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610670 Culex sp. water mite diet isolate 10445-BHL040517-GBD8690_19928-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTCATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610671 Culex sp. water mite diet isolate 10451-BHL040517-GBD16455_24389-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAATGGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCTCCAGATATGGTCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID FN395192, identified in GenBank as Culex torrentium. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610672 Culex sp. water mite diet isolate 10465-BHL040517-GBD8420_14375-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAATCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGACTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATGGTTTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCCCCTTCATTAACCCTACTTCTATCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610673 Culex sp. water mite diet isolate 10480-BHL040517-GBD14102_9780-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGATCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAATCAACCTGGTGTATTTATTGGTAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATGGTATTTCCTCGAATAAATAATATAAGATTCTGAATACTACCCCCTTCATTGACACTACTACTTTCCAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610674 Culex sp. water mite diet isolate 10497-BHL040517-GBD24407_18550-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGTAGAATTAAGTCAACCAGGTGTACTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610675 Culex sp. water mite diet isolate 10501-BHL040517-GBD25145_7166-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACCAATCATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGAATTGGAATAGTTGGAACTTCTTTAATTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTGTATAGTAATACCAATTATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACGTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610676 Culex sp. water mite diet isolate 10563-BHL040517-GBD26306_17896-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTTAGTTTACTAATTCGAGTAGAATTATATCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATAATAATTTTTTTTATAGTAATACCAATAATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGTCTTTCCACGAATAAATAATATAAGATTTTGAATACTACCACCTTCATTGACACTACTACTTTCAAGTAGTGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610677 Culex sp. water mite diet isolate 10572-BHL040517-GBD5913_22967-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGTTTACTAATTCGAGCAGAATTAAATCAACCAGGGGTATTTATTGGAGATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATAGTCTTTCCTCGAATAAATAATATAAGTTTTTGACTACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610678 Culex sp. water mite diet isolate 10651-BHL040517-GBD7807_25086-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGTCTTGAGCTTGGATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAGGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGTAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCATTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCTTCATTGACACTACTACTTTCAAGTAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610679 Culex sp. water mite diet isolate 12829-BHL040517-GBD15239_13691-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGACTTGAGCTGGAATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAATTAGGTCAACCTGGTGTTTTTATTGGAGATGATCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610680 Cyclopidae sp. water mite diet isolate 2174-BHL072216-GBD20234_18733-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTCTATTTGTTAGCGGGAGCTTGAGCTGGGTTTATTGGCACTGGCTTAAGGGTGTTGGTGCGGCTGGAGTTGGGAACACCAGGAAGTTTATTAGGTGATGATCACCTTTATAACGTTATTGTCACGGCCCATGCATTTATTATAATTTTTTTCATAGTCATACCCATCTTAATTGGGGGGTTTGGGAATTGGTTAGTACCTCTGATGCTTGGTTCTCCTGATATGGCTTTTCCTCGTATAAACAACATAAGGTTTTGATTCTTAATGCCTGCATTAATTATACTCTTGATAAGAGCTCTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID MG449514, identified in GenBank as Cyclopidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610681 Dero obtusa water mite diet isolate 1421-BHL110116-GBD10554_2414-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACATCATCCTTGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGACTACTAATTCGAATAGAACTAGCTCAACCAGGATCATTTCTAGGCAGAGATCAACTATATAATACACTAGTAACAGCACACGCATTCCTAATAATTTTCTTCTTAGTAATGCCTGTATTTATTGGTGGCTTCGGAAATTGATTAATTCCATTAATACTTGGAGCACCAGATATAGCATTTCCACGACTAAATAACCTAAGATTCTGACTTCTACCACCATCACTAATTCTATTAGTATCATCCGCAGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID MG423030, identified in GenBank as Dero obtusa. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW610682 Dero obtusa water mite diet isolate 1515-BHL110116-GBD23643_24454-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATATTTAATTTTAGGAGTTTGAGCAGGAATAATTGGTACAGGTACTAGAATATTAATTCGAATTGAATTATCTCAACCAGGATCATTTCTAGGCAGAGATCAACTATATAATACACTAGTAACAGCACACGCATTCCTAATAATTTTCTTCTTAGTAATGCCTGTATTTATTGGTGGCTTCGGAAATTGATTAATTCCATTAATACTTGGAGCACCAGATATAGCATTTCCACGACTAAATAACCTAAGATTCTGACTTCTACCACCATCACTAATTCTATTAGTATCATCCGCAGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID AF534838, identified in GenBank as Dero obtusa. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW610683 Dero obtusa water mite diet isolate 1755-BHL110116-GBD20739_8003-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACATCATCCTTGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGACTACTAATTCGAATAGAACTAGCTCAACCAGGATCATTTCTAGGCAGAGATCAACTATATAATACACTAGTAACAGCACACGCATTCCTAATAATTTTCTTCTTAGTAATGCCTGTATTTATTGGTGGCTTCGGAAATTGATTAATTCCATTAATACTTGGAGCACCAGATATAGCATTTCCACGACTAAATAACCTAAGATTCTGACTTCTACCACCATCACTAATTCTATTAGTATCATCCGCAGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID MG423030, identified in GenBank as Dero obtusa. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW610684 Dero sp. water mite diet isolate 1523-BHL110116-GBD4152_18885-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAGTTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCCTAATAATTTTCTTCTTAGTAATGCCTGTATTTATTGGTGGCTTCGGAAATTGATTAATTCCATTAATACTTGGAGCACCAGATATAGCATTTCCACGACTAAATAACCTAAGATTCTGACTTCTACCACCATCACTAATTCTATTAGTATCATCCGCAGCAGTTGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID MG423030, identified in GenBank as Dero obtusa. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW610685 Dero sp. water mite diet isolate 1528-BHL110116-GBD3596_13112-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACATCATCCTTGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGACTACTAATTCGAATAGAACTAGCTCAACCAGGATCATTTCTAGGCAGAGATCAACTATATAATACACTAGTAACAGCACACGCATTCCTAATAATTTTCTTCTTAGTAATGCCTGTATTTATTGGTGGCTTCGGAAATTGATTAATTCCATTAATACTTGGAGCACCAGATATAGCATTTCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG423030, identified in GenBank as Dero obtusa. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW610686 Dero sp. water mite diet isolate 9391-BHL032417-GBD18159_26545-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACATCATCCTTGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGACTACTAATTCGAATAGAACTAGCTCAACCAGGATCATTTCTAGGCAGAGATCAACTATATAATACACTAGTAACAGCACACGCATTCCTAATAATTTTCTTCTTAGTAATGCCTGTATTTATTGGTGGCTTCGGAAATTGATTAATTCCATTAATACTTGGAGCACCAGATATAGCATTTCCACGACTAAATAACCTAAGATTCTGACTTCTACCACCATCACTAATTCTATTAGTATCATCCGCAGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID MF544417, identified in GenBank as Dero digitata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW610687 Diaphanosoma sp. water mite diet isolate 1841-BHL072216-GBD10638_13962-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGGATTAGGGCAGTGTGGCAGTTTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGATTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACCCTTCTTTTGGCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610688 Diaphanosoma sp. water mite diet isolate 2123-BHL072216-GBD5254_8793-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610689 Diaphanosoma sp. water mite diet isolate 2183-BHL072216-GBD14149_11633-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGGTCAGGGATAGTTGGAACTGCCCTGAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGAAGACTTATTGGTGATGATCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTTTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610690 Diaphanosoma sp. water mite diet isolate 2193-BHL072216-GBD15508_15986-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGGTCCGGGATAGTTGGAACAGCCTTAAGTATACTTATTCGAGCTGAATTAGGGCAGCCTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTTTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATAGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACCCTTCTTTTGTCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610691 Diaphanosoma sp. water mite diet isolate 2200-BHL072216-GBD17648_24922-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATATTTTATTTTTGGAGTTTGATCCGGGATAGTTGGAACATCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTAATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTAGAAGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610692 Diaphanosoma sp. water mite diet isolate 2204-BHL072216-GBD18107_15563-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGTAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCTAGCTGCATTATGGCAGTGTGGCATTCTTATTGGTGATGACCACATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATATTTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCGTCTTTTGGTTGGAAGGGCAGTTGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610693 Diaphanosoma sp. water mite diet isolate 2207-BHL072216-GBD27194_19999-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCTTTAAGTATACTTATTCGAGCTGAACTAGGGCAGTGTGGCAGATTTATTGGTGATGATCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTTTCATTGGTGGCTTTGGTAATTGTCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTATAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTACTTTTGGCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610694 Diaphanosoma sp. water mite diet isolate 2213-BHL072216-GBD25909_12668-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTTGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGTTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTAATTGGTGGGTTTGGTAATTGGCTAGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGAATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTACTTTTGGCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610695 Diaphanosoma sp. water mite diet isolate 2226-BHL072216-GBD13576_4024-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGATTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATGCGAGCTGAATGAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGGTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTTGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGCTGAAAATGGTGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610696 Diaphanosoma sp. water mite diet isolate 2230-BHL072216-GBD11763_8012-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGGTCCGGGATAGTTGGAACATCCTTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGAGCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGATTAAACAATATAAGGTTTTGAATATTACCCCCTTCATTAACTCTTCTTTTGGCTGGAAGGACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610697 Diaphanosoma sp. water mite diet isolate 2245-BHL072216-GBD25795_7086-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACTTCCCTAAGTATACTTATTCGAGCTGAATTAGGGCATTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTAATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCTCCTGATATGGCTTTTCCGCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACCCTACTTTTGGCTGGAAGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610698 Diaphanosoma sp. water mite diet isolate 2247-BHL072216-GBD21908_12988-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTCTATCTCTTCTT	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610699 Diaphanosoma sp. water mite diet isolate 2252-BHL072216-GBD19984_28006-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGGTATGGCTTTTCCCCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610700 Diaphanosoma sp. water mite diet isolate 2253-BHL072216-GBD3852_15871-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTTGGAACTTCTTTAAGTATACTTATTCGAGCTGAATTTGGGCAGTGTGGTAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTCACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610701 Diaphanosoma sp. water mite diet isolate 2260-BHL072216-GBD27317_12830-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCTTAAGTATATTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTAATTGGTGATGACCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTACTATTAGCTAGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610702 Diaphanosoma sp. water mite diet isolate 2262-BHL072216-GBD24173_5616-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACTTCTTTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTTTCATTGGAGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGAATAAACAATATAAGATTTTGAATATTACCCCCTTCTTTAACTCTACTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610703 Diaphanosoma sp. water mite diet isolate 2263-BHL072216-GBD20424_5441-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCTTGAGATGGCGTTTCCTCGCTTAAACAAATTAAGGTTTTGAATATGAACCCCTTCTTTAACGCTTCTTTTGGTTGGAAGGGCAGTTCAAAATTGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610704 Diaphanosoma sp. water mite diet isolate 2278-BHL072216-GBD8722_23362-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGTGTTTGGTCAGGGATAGTTGGAACTGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGTTTTATTGGTGATGACCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTTATAATTTTTTCATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGACTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610705 Diaphanosoma sp. water mite diet isolate 2280-BHL072216-GBD20426_22089-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTCTCATTGGTGGCTTTGGTAATTGACTGGTGCCTTTAATACTAGGTGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACT	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610706 Diaphanosoma sp. water mite diet isolate 2282-BHL072216-GBD13260_18478-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGGTCCGGGATAGTTGGAACTTCCCTAAGTATATTTATTCGAGCTGAATTAGGGCAGTGTGGCAGTCTTATTGGTGATGACCAAATTTATAATGTTATTGTCACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTAATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGAATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTGCTTTTGGCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610707 Diaphanosoma sp. water mite diet isolate 2283-BHL072216-GBD6809_20354-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACTTCCTTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGAAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGACTGGTGCCTTTAATACTAGGTGCCCCTGATATAGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610708 Diaphanosoma sp. water mite diet isolate 2287-BHL072216-GBD25868_8585-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACATCTCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCAATTCTCATTGGTGGCTTTGGAAATTGACTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTCTAACTCTACTTTTGGCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610709 Diaphanosoma sp. water mite diet isolate 2296-BHL072216-GBD15913_2399-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAGTTAGGGCAGTTTGTCATACTTATTGGTGATGACCAAATTTATAATGTTATTGGAACCGCTCAAGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGTCTGGTGCCTTTAATATTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGTAGGGCAGTTGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610710 Diaphanosoma sp. water mite diet isolate 2314-BHL072216-GBD24892_13097-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GACTTTATATTTTATTTTCGGAGTATGGTCTGGTATAGTAGGGACCGCTCTTAGTATATTAATTCGAGCAGAGTTAGGCCAATGTGGTAGCCTTATTGGGGACGATCAAATCTACAATGTTATTGTAACTGCTCATGCTTTTGTTATAATTTTCTTTATGGTTATACCTATTCTTATTGGTGGGTTTGGAAACTGGTTGGTTCCTTTAATGTTAGGGGCTCCTGATATGGCCTTCCCTCGTTTAAATAATTTAAGATTTTGATTACTTCCTCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG449947, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610711 Diaphanosoma sp. water mite diet isolate 2319-BHL072216-GBD21089_14266-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACTGCCTTAAGTATACTTATTCGAGCTGAATTAGGGCAGCGTGGAAGTTTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCAATTCTCATTGGTGGATTTGGAAATTGGCTGGTCCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610712 Diaphanosoma sp. water mite diet isolate 2324-BHL072216-GBD9761_16723-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGCGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGACTGGTTCCTTTAATACTAGGTGCCCCTGATATGGCATTTCCTCGAATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTATTGGCTGGAAGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610713 Diaphanosoma sp. water mite diet isolate 2325-BHL072216-GBD5226_13116-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGAAGATTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCCCGTATAAACAACATAAGGTTTTGAATATTACCCCCTTCTTTAACCCTTCTTCTAGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610714 Diaphanosoma sp. water mite diet isolate 2330-BHL072216-GBD10374_2636-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTGTAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTAC-CT--TATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610715 Diaphanosoma sp. water mite diet isolate 2339-BHL072216-GBD27953_20897-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCTCTAAGTATACTTATTCGAGCTGAATTAGGGCAGCGTGGCAGTCTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTTTCATTGGTGGCTTTGGTAATTGATTGGTTCCTTTAATACTAGGTGCCCCTGATATAGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGCTGGAAGGACAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610716 Diaphanosoma sp. water mite diet isolate 2341-BHL072216-GBD10871_14481-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GACTTTATATTTTATTTTCGGAGTATGGTCTGGTATAGTAGGGACCGCTCTTAGTATATTAATTCGAGCAGAGTTAGGCCAATGTGGTAGCCTTATTGGGGACGATCAAATCTACAATGTTATTGTAACTGCTCATGCTTTTGTTATAATTTTCTTTATGGTTATACCTATTCTTATTGGTGGGTTTGGAAATTGGTTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID MG449947, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610717 Diaphanosoma sp. water mite diet isolate 2354-BHL072216-GBD25644_22629-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGAATAGTTGGAACAGCCTTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCTGACTTATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGGGCCCCTGATATGGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610718 Diaphanosoma sp. water mite diet isolate 2355-BHL072216-GBD25968_22596-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCAGGGATAGTTGGAACAGCCTTAAGTATACTTATTCGAGCTGAATTAGGGCAGCGTGGCAGATTTATTGGTGATGACCAAATTTATAATGTAATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCTCCTGATATGGCTTTTCCTCGTATAAACAATTTAAGTTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGCTGGAAGAGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610719 Diaphanosoma sp. water mite diet isolate 2360-BHL072216-GBD13326_24049-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACGTTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATGTTAGGGGCTCCTGATATGGCCTTCCCTCGTTTAAATAATTTAAGATTTTGATTACGTCCTCCTTCTTTAACTTTACTTTTAGTTGGTAGGGCTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610720 Diaphanosoma sp. water mite diet isolate 2368-BHL072216-GBD8472_8039-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACTGCCTTAGGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGTCTTATTGGTGATGACCAAATTTATAATGTAATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATACTACCCCCTTCTTTAACTCTTCTTTTGGCTGGAAGGACAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610721 Diaphanosoma sp. water mite diet isolate 2370-BHL072216-GBD20597_9651-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTCTTGTTCTAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAACATTACCCCCTTCTATAACCCCTCTTTCGGTTGGAAGCGCAGTTGAAAAAGGAGCCGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610722 Diaphanosoma sp. water mite diet isolate 2375-BHL072216-GBD7104_15137-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACATCCCTAAGAATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGATTTATTGGAGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTTTCATTGGTGGCTTTGGTAATTGACTGGTGCCTTTAATACTAGGAGCCCCTGATATGGCTTTTCCTCGTTTAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGCTGGAAGGGCAGTTGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610723 Diaphanosoma sp. water mite diet isolate 2376-BHL072216-GBD15560_14923-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCCTGGTCCGGGATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGGCATTCTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610724 Diaphanosoma sp. water mite diet isolate 2383-BHL072216-GBD28975_12244-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGTATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTCGGGCAGTGTGGCAGATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGTCTGGTTCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGATTAAACAATATAAGGTTTTGAATATTACCCCCGTCTTTAACTCTACTATTGGCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610725 Diaphanosoma sp. water mite diet isolate 2387-BHL072216-GBD15126_13492-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGATCCGGAATAGTTGGAACATCCCTTAGTATACTTATTCGAGCTGAATTAGGGCAGCGTGGAAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTACTCTAATTGGTGGCTTTGGAAATTGACTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610726 Diaphanosoma sp. water mite diet isolate 2390-BHL072216-GBD17689_17787-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGGTCCGGGATAGTTGGAACTGCCTTAAGTATACTTATTCGAGCTGAATTAGGGCAGCCTGGCAGATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGACTTTTCCTCGTTTAAACAATATAAGGTTTTGAATATTCCCCCCTTCTTTAACTCTTCCTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610727 Diaphanosoma sp. water mite diet isolate 2394-BHL072216-GBD20222_5424-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAACTTAAGGTTTTGAGTATGACCCCCTTCTTTAACTCGGCCTTTGGTTGGAAGGGCAGTTCACAATGGCGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610728 Diaphanosoma sp. water mite diet isolate 2395-BHL072216-GBD22675_20840-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGCTATAATTTTTTTATAGTTATGCCTATTTTAATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATAGCTTTTCCTCGTATAAACAATATAAGGTTTTGGATATTACCCCCTTCTTTAACTCTTCTTTTGGCTGGAAGGGCAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610729 Diaphanosoma sp. water mite diet isolate 2396-BHL072216-GBD12944_16138-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACTGCTTTAAGTATATTTATTCGAGCTGAATTAGGGCACTGTGGCTGATTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTAATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAATTCTACTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610730 Diaphanosoma sp. water mite diet isolate 2397-BHL072216-GBD26280_15605-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACTGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCATTGTGGAAGTCTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGATTTGGTAATTGACTGGTGCCTTTAATACTAGGTGCACCTGATATGGCATTTCCTCGTTTAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGCTGGAAGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610731 Diaphanosoma sp. water mite diet isolate 2401-BHL072216-GBD18537_24991-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACATCCTTAAGTATACTTATTCGAGCTGAATTAGGGCAGCGTGGCAGAATTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTAATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTATAAACAACATAAGGTTTTGAATATTACCCCCTTCTTTAACCCTTCTTTTGGTTGGAAGGGCAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610732 Diaphanosoma sp. water mite diet isolate 2407-BHL072216-GBD12229_19939-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGGGCTTGGTCCGGGATAGTTGGAACTGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGTCTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTAATGCTTTTGTTATAATTTTTTTATAGTTATGCCAATTCTCATTGGTGGCTTTGGTAATTGGCTGGTTCCTCTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610733 Diaphanosoma sp. water mite diet isolate 2409-BHL072216-GBD17000_13345-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACTGCCCTAAGTATACCTATTCGAGCTGAATTAGGGCATTGTGGCAGATTTATTGGTGATGATCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGACTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATATTGCCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGAGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610734 Diaphanosoma sp. water mite diet isolate 2410-BHL072216-GBD4643_17366-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGATCCGGGATAGTTGGAACTTCTTTAAGTATACTTATTCGAGCTGAATTAGGGCATCGTGGCACATTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTTTCATTGGTGGCTTTGGAAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTACTTTTGGTTGGAAGAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610735 Diaphanosoma sp. water mite diet isolate 2411-BHL072216-GBD19324_25469-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCTTAAGTATACTTATTCGAGCTGAATTAGGGCAATGTGGCAGTATTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTCTTTTATAGTTATGCCTATTCTAATTGGTGGCTTTGGTAATTGTCTAGTCCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610736 Diaphanosoma sp. water mite diet isolate 2422-BHL072216-GBD29188_16400-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGATCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGGGCCCCTGATATGGCTTTTCCTCGAATAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTACTTGTGGCTGGAAGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610737 Diaphanosoma sp. water mite diet isolate 2425-BHL072216-GBD29194_16733-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGGGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTGGAACGCTTCGGGGGGGGGGAAGGGCAGGTGAAAAGGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610738 Diaphanosoma sp. water mite diet isolate 2434-BHL072216-GBD11804_10987-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGGTCCGGGATAGTTGGAACTGCCTTAAGTATATTGATTCGAGCTGAATTAGGGCAGTGAGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATCGACTGGTGCCTTTAATACTAGGTGCCCCTGATATAGCTTTTCCTCGTTTAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610739 Diaphanosoma sp. water mite diet isolate 2442-BHL072216-GBD9765_23322-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGGTCCGGGATAGTTGGAACTGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGATTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTCATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAACTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCCCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGCTGGAAGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610740 Diaphanosoma sp. water mite diet isolate 2445-BHL072216-GBD27030_19678-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGGTCAGGGGTAGTTGGAACAGCCTTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGAGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGACTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTATAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTACTTTTGGCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610741 Diaphanosoma sp. water mite diet isolate 2449-BHL072216-GBD22189_24604-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGGCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGCGAGGCAGACTTATTGGTGATGACCAACTTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGACTGGTACCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTCTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACCCTTCTATTGGCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID LC060042, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610742 Diaphanosoma sp. water mite diet isolate 2450-BHL072216-GBD20007_26029-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTTCTT	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610743 Diaphanosoma sp. water mite diet isolate 2453-BHL072216-GBD25150_17943-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGATCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCATTGTGGCGGAGTTATTGGTGATGACCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGAGGCTTTGGTAATTGACTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGAATAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTATTGGCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610744 Diaphanosoma sp. water mite diet isolate 2456-BHL072216-GBD19325_25446-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCTTTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGTCTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCACGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGACTGGTGCCTTTAATACTAGGTGCCCCTGATATAGCTTTTCCTCGTATAAACAACATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGATAGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610745 Diaphanosoma sp. water mite diet isolate 2458-BHL072216-GBD29314_16548-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGTTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAATTTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTAGTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTCGGTGACCCTGATATGGCTTTTCCTCGTGTAAACAATTTAAGGGTTTGAATACGACCCCCTTCGGTAACGGGGCGGGGGGGGGGAAGGGCAGGGGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610746 Diaphanosoma sp. water mite diet isolate 2459-BHL072216-GBD26300_15801-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTATTTTTGAAGTTTGATCCGGGATAGTTGGAACTTCCTTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTAATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTACGCCTATTCTAATTGGTGGATTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610747 Diaphanosoma sp. water mite diet isolate 2469-BHL072216-GBD26708_18622-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCACATTTATTGGTGATGATCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGAAATTGACTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGGATAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTAGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610748 Diaphanosoma sp. water mite diet isolate 2470-BHL072216-GBD11571_28383-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTTTATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACATCTTTAAGTATACTTATTCGTGCAGAATTAGGTCATCCAGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610749 Diaphanosoma sp. water mite diet isolate 2473-BHL072216-GBD28408_18950-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCTTAAGTATATTTATTCGAGCTGAATTAGGGCAGTGTGGCAGAATTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTATTATAATTTTTTTATAGTTATGCCTATTTTAATTGGTGGGTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTATAAACAATTTAAGGTTTTGAATATTACCACCTTCTTTAACTCTACTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610750 Diaphanosoma sp. water mite diet isolate 2474-BHL072216-GBD28167_20290-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACTGCCTTAAGTATACTTATTCGAGCTGAATTAGGGCATTGTGGCAGATTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGAGGCTTTGGTAATTGGCTGGTGCCTCTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTATAAACAATTTAAGATTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGCTGGAAGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610751 Diaphanosoma sp. water mite diet isolate 2475-BHL072216-GBD25857_15159-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACATCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCATACTTATTGGTGATGACCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTCTAATTGGTGGGTTTGGAAATTGGTTGGTTCCTTTAATGTTAGGGGCTCCTGATATGGCCTTCCCTCGTTTAAATAATATAAGATTTTGATTACTTCCTCCTTCTTTAACTTTACTTTTAGTTGGTAGGGCTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610752 Diaphanosoma sp. water mite diet isolate 2483-BHL072216-GBD22372_13284-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTTAGTATACTTATTCGAGTTGAATTATGGCAGCGTGGCACATTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTCTAGTTATGCCTGTTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACCCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610753 Diaphanosoma sp. water mite diet isolate 2484-BHL072216-GBD21500_7220-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTT	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610754 Diaphanosoma sp. water mite diet isolate 2487-BHL072216-GBD26936_8032-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGAAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTAATTGGAGGCTTTGGGAATTGTCTTGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTATAAACAATTTAAGATTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGCTGGAAGAGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610755 Diaphanosoma sp. water mite diet isolate 2490-BHL072216-GBD5925_15271-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCAGGGATAGTTGGAACAGCCTTAAGTATACTTATTCGAGCTGAATTAGGGCAGCATGGCACATTTATTGGTGATGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTTTCATTGGTGGCTTTGGTAATTGACTGGTGCCTTTAATACTAGGTGCCCCTGATATAGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTAGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610756 Diaphanosoma sp. water mite diet isolate 2492-BHL072216-GBD14058_14245-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATAGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGAAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610757 Diaphanosoma sp. water mite diet isolate 2495-BHL072216-GBD19600_12825-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTCTGGAAGTCTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTTTAATTGGTGGATTTGGTAATTGACTAGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610758 Diaphanosoma sp. water mite diet isolate 2513-BHL072216-GBD7760_7577-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTATTTTTGGAGCTTGGTCCGGGATAGTTGGAACAGCCTTAAGTATACATATTCGAGCTGAATTAGGGCAGCGTGGCAGAATTATTGGCGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGAAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTAGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610759 Diaphanosoma sp. water mite diet isolate 2514-BHL072216-GBD13311_27310-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTATTTTTGGAGCTTGGTCTGGGATAGTTGGAACAGCTCTAAGTATACTTATTCGAGCTGAATTAGGGCAGCCTGGCAGTTTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTTTCATTGGTGGCTTTGGTAATTGGCTAGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACACTTCTTTTGGCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610760 Diaphanosoma sp. water mite diet isolate 2517-BHL072216-GBD17524_11280-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCT	Using NCBI BLASTN in June 2018, this sequence was 94.7% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610761 Diaphanosoma sp. water mite diet isolate 2526-BHL072216-GBD23367_19521-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATACTTTATTTTTGGAGCTTGGTCCGGGATAGTTGGAACTTCCTTAAGTATACTTATTCGAGCTGAATTAGGGCAGCGTGGCAGTTTTATTGGTGATGACCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTTTCATTGGTGGCTTTGGTAATTGACTGGTGCCTTTAATACTAGGTGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGCTAGAAGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610762 Diaphanosoma sp. water mite diet isolate 2529-BHL072216-GBD4373_21658-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTATTTTTGGAGTTTGGTCCGGAATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGGGTGGCAGAATTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCACATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTAATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATAGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACACTTCTTTTGGCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610763 Diaphanosoma sp. water mite diet isolate 2535-BHL072216-GBD4430_15208-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATTCTTATTCGAGCTGAATTAGGGCAGGGTGGCAGATTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGAGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610764 Diaphanosoma sp. water mite diet isolate 2538-BHL072216-GBD4267_15156-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTATTTTTGGAGCTTGGTCCGGGATAGTTGGAACATCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGCCTGGCACATTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGACTGGTGCATTTAATACTAGGTGCCCCTGATATGGCATTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTACTTTTAGCTGGAAGAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610765 Diaphanosoma sp. water mite diet isolate 2543-BHL072216-GBD21163_12122-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTATGGCACAGTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATAGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGAAGGAAGAGCAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610766 Diaphanosoma sp. water mite diet isolate 2545-BHL072216-GBD18629_25519-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGATCAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTGTTGAAGATGACCCCCTTCTTGAACACGGCGTTTGGATGGAAGGGCAGGTGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610767 Diaphanosoma sp. water mite diet isolate 2555-BHL072216-GBD20276_11935-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTTAGTATACTTATTCGAGCTGCATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTATGGAATATGACCCCCTGCTGTAACACGACATTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610768 Diaphanosoma sp. water mite diet isolate 2558-BHL072216-GBD18869_9173-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACTGCCTTAAGTATTCTTATTCGAGCTGAATTAGGTCAGTGTGGCAGTCTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTAATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCCGATATGGCATTTCCTCGTTTAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTACTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610769 Diaphanosoma sp. water mite diet isolate 2564-BHL072216-GBD9300_21000-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGTATTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTAGTTCCTTTAATACTAGGTGCCCCTGATATAGCTTTTCCTCGTTTAAACAATATAAGGTTCTGATTATTACCCCCTTCTTTAACTCTTCTTTTGGCTGGAAGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610770 Diaphanosoma sp. water mite diet isolate 2570-BHL072216-GBD23130_22361-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGATTTGGTAACTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATAGCTTTTCCTCGAATAAACAATCTAAGATTTTGAATATTACCCCCTTCTTTAACTCTTCTATTGGCTAGAAGAGCAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610771 Diaphanosoma sp. water mite diet isolate 2583-BHL072216-GBD24432_12033-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACTGCTCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGCCTTATTGGTGATGACCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGAGGCTTTGGTAATTGTCTGGTGCCTTTAATGCTAGGTGCCCCTGATATGGCCTTTCCTCGTATAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610772 Diaphanosoma sp. water mite diet isolate 2585-BHL072216-GBD26307_8302-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGTTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGAATTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTGATGCCTATTCTAATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCATTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTACTATTGGCTGGAACGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610773 Diaphanosoma sp. water mite diet isolate 2587-BHL072216-GBD25703_12238-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTTTATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCTCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCATTTTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTAATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATATAAGTTTTTGAATATTACCCCCTTCTTTAACACTTCTTTTGGCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610774 Diaphanosoma sp. water mite diet isolate 2589-BHL072216-GBD14775_23878-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGATCCGGGATAGTTGGAACTGCCTTAAGTATACTTATTCGAGCCGAATTAGGGCAGCGTGGGAATCTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGAGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610775 Diaphanosoma sp. water mite diet isolate 2592-BHL072216-GBD14679_23363-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTCAGTATATTAATTCGAGCAGAGTTAGGCCAATGTGGTAGCCTTATTGGGGACGATCAAGTCTACAATGTTATTGTAACTGCTCATGCTTTTGTTATAATTTTCTTTATGGTTATACCTATTCTTATTGGTGGGTTTGGAAATTGGTTGGTTCCTTTAATGTTAGGGGCTCCTGATATGGCCTTCCCTCGTTTAAATAATTTAAGATTTTGATTACTTCCTCCTTCTTTAACTTTACTTTTAGTTGGTAGGGCTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG449947, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610776 Diaphanosoma sp. water mite diet isolate 2595-BHL072216-GBD24095_19019-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCATATTTATAATGTTCTTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGTTGCCTTTAATACTAGGGGCCCCTGATATGGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACACTACTTTTGGCAGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610777 Diaphanosoma sp. water mite diet isolate 2596-BHL072216-GBD15386_23238-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGATCCGGGATAGTTGGAACTGCCTTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCATATTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTACTTTTGGTTGGAGGGGCAGTTGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610778 Diaphanosoma sp. water mite diet isolate 2598-BHL072216-GBD14998_24465-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACTGCCTTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGATTTATTGGAGATGACCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTTTCATTGGTGGCTTTGGAAATTGTCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTAGAAGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610779 Diaphanosoma sp. water mite diet isolate 2603-BHL072216-GBD29452_16821-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGATCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGAAATTGGCTGGTGCCTTTAATACTCGGTGCCCCTGATATGGCTTTTCCCCGAATAAACAATTTAAGGTTTTGAATATTACCCCCTTCGGTAACGCGGCGGGGGGGGGGAAGGGCAGGGGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610780 Diaphanosoma sp. water mite diet isolate 2604-BHL072216-GBD24120_24466-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATATTTTATTTTTGGAGCTTGGTCAGGGATAGTTGGAACAGCCTTAAGTATACTTATTCGAGCTGAATTAGGGCAGCCTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTTTCATTGGTGGTTTTGGTAATTGACTTGTTCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACCCTTCTTTTAGCTAGAAGAGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610781 Diaphanosoma sp. water mite diet isolate 2605-BHL072216-GBD18982_22916-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTGGGACAGTGTGGTACATTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTAATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCAGATATGGCTTTTCCACGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610782 Diaphanosoma sp. water mite diet isolate 2606-BHL072216-GBD17276_25849-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGCGTGGCAGATTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTACAGTTATGCCTATTCCAATTGGTGGCTTTGGTAATTGATTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCATTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610783 Diaphanosoma sp. water mite diet isolate 2612-BHL072216-GBD24017_15769-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGGTCCGGGATAGTTGGAACTTCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGTCTTATTGGTGATGAGCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTGTTCTCATTGGTGGCTTTGGAAATTGGCTGGTGCCTTTAATACTAGGTGCGCCTGATATGGCTTTTCCTCGTTTAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610784 Diaphanosoma sp. water mite diet isolate 2613-BHL072216-GBD22720_16099-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGGTCCGGGATATTTGGAACTTCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCACATTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGCTGGAAGAGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610785 Diaphanosoma sp. water mite diet isolate 2616-BHL072216-GBD7283_16626-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGTACTTCTTTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGATTTATTGGTGATGACCAAATTTATAATGTAATTGTAACCGCACATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTTTCATTGGTGGCTTTGGTAATTGACTTGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610786 Diaphanosoma sp. water mite diet isolate 2617-BHL072216-GBD22628_15349-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTATTTTCGGAGTTTGATCCGGGATAGTTGGAACATCCTTAAGTATATTTATTCGAGCTGAATTAGGGCAGCCTGGCAGATTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTAATTGGTGGCTTTGGTAATTGGCTGGTTCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACCCTTCTTTTGGCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610787 Diaphanosoma sp. water mite diet isolate 2618-BHL072216-GBD29075_16279-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTATTTTTGGAGTTTGATCCGGAATAGTTGGAACTGCCCTAAGTATACTTATTCGAGCTGAATTAGGACATTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTAATTGGTGGCTTTGGTAATTGACTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGCCTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610788 Diaphanosoma sp. water mite diet isolate 2627-BHL072216-GBD11074_13746-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTGTACTTATTCGAGCTGAATTAGGACAGTGTGGCAGTCTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCATATTCTCATTGGTGGATTTGGTAATTGACTGGTGCCTTTAATATTAGGTGCCCCTGATATGGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610789 Diaphanosoma sp. water mite diet isolate 2630-BHL072216-GBD20487_18040-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTCTTGGCTTCTTCCACCGTCTCTTACTCTTCTT	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610790 Diaphanosoma sp. water mite diet isolate 2632-BHL072216-GBD22797_27192-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCTCTAAGTATACTTATTCGAGCTGAATTAGGTCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGAAATTGGTTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCATTCCCTCGTATAAACAGTTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTACTTTTGGCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610791 Diaphanosoma sp. water mite diet isolate 2636-BHL072216-GBD17570_28653-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTATTTTTGGAGCTTGGTCCGGGATAGTTGGAACAGCCTTAAGTATACTTATTCGAGCGGAATTAGGGCAGGTTGGCAGATTTATTGGTGATGACCAAATTTATAATGTTATTGTGACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGACTGCTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAGTATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610792 Diaphanosoma sp. water mite diet isolate 2641-BHL072216-GBD9334_24182-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTATTTTTGGAGTTTGGTCCGGGATAGTTGGCACTGCTTTAAGTATATTTATTCGAGCTGAATTAGGGCAGTGTGGCAGATTTATTGGTGATGATCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGACTGGCGCCCTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACCCTTCTTTTGGTTGGAAGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610793 Diaphanosoma sp. water mite diet isolate 2647-BHL072216-GBD10288_3376-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATATTTATTTTTGGAGTTTGATCCGGGATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCTGAATTAGGTCAGCGTGGCAGTTTTATTGGTGATGATCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTTTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTCTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610794 Diaphanosoma sp. water mite diet isolate 2648-BHL072216-GBD18754_9862-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATATTTATTTTTGGAGTTTGATCCGGGATAGTTGGCACTTCTCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCACACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCACATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACGCTTCTTTTGGTTGGAAGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610795 Diaphanosoma sp. water mite diet isolate 2650-BHL072216-GBD25827_17859-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACTGCCCTAAGTATACTTATTCGAGCTGAATTCGGGCAGTGTGGCAGAATTATTGGTGATGACCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGACTGGTGCCTTTAATACTAGGTGCCCCTGATATAGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCGTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610796 Diaphanosoma sp. water mite diet isolate 2654-BHL072216-GBD28584_20238-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACATCCTTAAGTATACTTATTCGAGCTGAATTAGGGCAGTCTGGAATATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTAATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTACTTTTGGCTGGAAGAGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610797 Diaphanosoma sp. water mite diet isolate 2655-BHL072216-GBD22282_27360-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGATCCGGTATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAAGGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTAATTGGTGGCTTTGGTAATTGGCTGGTTCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTATAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTACTTTTGGTTGGAAGTGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610798 Diaphanosoma sp. water mite diet isolate 2669-BHL072216-GBD19538_14021-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACATCCTTAAGTATACTTATTCGAGCGGAATTAGGGCAGTGTGGCAGATTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGTTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCACGTATAAACAATATAAGGTTTTGAATATTACCCCCTTTTTTAACTTTACTTTTGGCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610799 Diaphanosoma sp. water mite diet isolate 2671-BHL072216-GBD21982_9270-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACTTCCCTAAGTATACTTATTCGAGCTGAATTAGGTCAGTGTGGCACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATATTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGTTTGGAACGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610800 Diaphanosoma sp. water mite diet isolate 2678-BHL072216-GBD10934_9137-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACATCCCTAAGTATACTTATTCGAGCTGAATTCGGGCAGTGTGGCTGTCTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTGATGCCTATTCTCATTGGTGGCTTTGGTAATTGTCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATATAAGGTTTTGAATATTACCCCCGTCATTAACTCTACTATTGGCTGGAACGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610801 Diaphanosoma sp. water mite diet isolate 2686-BHL072216-GBD14997_11252-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTACTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCGTGCTTTAAAACGGCGTTGGGGTGGAAGGGCAGTTGAAAATGGAGCGGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610802 Diaphanosoma sp. water mite diet isolate 14241-BHL040517-GBD4165_14164-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGATTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATCGGCTAGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACACTGCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610803 Diaphanosoma sp. water mite diet isolate 752-BHL040916-GBD13544_12306-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGAGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610804 Diaphanosoma sp. water mite diet isolate 813-BHL100916-GBD12814_11310-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCCGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACCCCACTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610805 Diaphanosoma sp. water mite diet isolate 1135-BHL110116-GBD28335_18903-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCTTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGTTTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGATTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610806 Diaphanosoma sp. water mite diet isolate 1762-BHL110116-GBD15294_13786-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTCTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610807 Diaphanosoma sp. water mite diet isolate 1851-BHL072216-GBD26392_11332-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACATCACTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCATTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610808 Diaphanosoma sp. water mite diet isolate 2061-BHL072216-GBD10680_6415-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATCGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610809 Diaphanosoma sp. water mite diet isolate 2190-BHL072216-GBD18065_3559-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGGGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGGTATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGATTACTACCCCCTTCTCTTACTCTTCTT	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610810 Diaphanosoma sp. water mite diet isolate 2258-BHL072216-GBD24400_10178-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCACCATCTCTTACT	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610811 Diaphanosoma sp. water mite diet isolate 2301-BHL072216-GBD13364_28768-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGTGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTATCTCTTCTT	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610812 Diaphanosoma sp. water mite diet isolate 2361-BHL072216-GBD6594_5844-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GACTTTATATTTTATTTTCGGAGTATGATCTGGTATAGTAGGGACCGCTCTTAGTATATTAATTCGAGCAGAGTTAGGCCAATGTGGTACCCTTATTGGGGACGATCAAATTTACAATGTTATTGTAACTGCTCATGCTTTTGTTATAATTTTCTTTATGGTTATACCTATTCTAATTGGTGGGTTTGGAAATTGGTTGGTTCCTTTAATGTTAGGTGCTCCTGATATGGCCTTCCCTCGTATAAATAATATAAGATTTTGATTACTTCCTCCTTCTTTAACCTTACTTTTAGTTGGTAGGGCTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG449947, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610813 Diaphanosoma sp. water mite diet isolate 2363-BHL072216-GBD4378_10305-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GACTTTACATTTTATTTTCGGAGTATGGTCTGGTATAGTAGGGACCGCTCTTAGTATATTAATTCGAGCAGAGTTAGGCCACTGTGGTAGCCTTATTGGGGAGGATCAAATCTACAATGTTATTGTAACTGCTCATGCTTTTGTTATAATTTTCTTTATGGTTATACCTATTCTTATTGGTGGGTTTGGAAATTGGTTGGTTCCTTTAATGTTAGGGGCTCCTGATATGGCCTTTCCTCGTATAAATAATTTAAGATTTTGATTACTTCCTCCTTCTTTAACTTTACTTTTAGTTGGTAGGGCTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG449947, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610814 Diaphanosoma sp. water mite diet isolate 2424-BHL072216-GBD7432_6853-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCGGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAATAATATAAGTTTTTGACTTTTACCACCCTCTTTAACTCTT	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610815 Diaphanosoma sp. water mite diet isolate 2463-BHL072216-GBD19627_22181-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGTTTGGTCTGGTATAGTAGGGACCGCTCTTAGTATATTAATTCGAGCAGAGTTAGGCCAATGTGGTAGCCTTATTGGGGACGATCAAATTTACAATGTTATTGTAACTGCTCATGCATTTGTTATAATTTTCTTTATGGTTATACCTATTCTTATTGGTGGGTTTGGAAATTGGTTGGTTCCTTTAATGTTAGGGGCTCCCGATATGGCCTTCCCTCGTTTAAATAATTTAAGATTTTGATTACTTCCTCCTTCTTTAACTTTACTTTTAGTTGGTAGGGCTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID MG449947, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610816 Diaphanosoma sp. water mite diet isolate 2491-BHL072216-GBD27588_21507-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGCCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGACTACTACCCCCTTCTTTAAC	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610817 Diaphanosoma sp. water mite diet isolate 12940-BHL040517-GBD22425_21790-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGTAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGATGGAAGGGCAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610818 Diaphanosoma sp. water mite diet isolate 13575-BHL040517-GBD7646_16419-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAGGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610819 Dicrotendipes modestus water mite diet isolate 5671-BHL032417-GBD6293_5056-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCTTTAAGTATACTTATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGTGGTTTCGGAAATTGATTAGTACCTTTAATATTAGGTGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR652336, identified in GenBank as Dicrotendipes modestus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610820 Dicrotendipes modestus water mite diet isolate 8566-BHL101416-GBD23194_23079-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGATCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTACTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID MG449574, identified in GenBank as Dicrotendipes modestus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610821 Dicrotendipes modestus water mite diet isolate 12205-BHL040517-GBD23194_23079-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGATCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTACTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID MG449574, identified in GenBank as Dicrotendipes modestus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610822 Dicrotendipes sp. water mite diet isolate 789-BHL040916-GBD16876_8623-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAATAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTGATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATGGTTATACCCATTCTAATTGGAGGTTTCGGAAATTGATTAGTCCCTATAATATTAGGAGCTCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCACCTTCTCTAACCCTTCTTCTTTCTAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610823 Dicrotendipes sp. water mite diet isolate 1184-BHL110116-GBD16471_10301-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610824 Dicrotendipes sp. water mite diet isolate 1224-BHL110116-GBD11962_20229-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAAAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTTACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR282179, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610825 Dicrotendipes sp. water mite diet isolate 1251-BHL110116-GBD12456_12641-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610826 Dicrotendipes sp. water mite diet isolate 1252-BHL110116-GBD11623_9105-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATATTTATTCGAGCAGAACTAGGTCGAGCTGGTACTTTTATTGGTGACGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTACTACTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610827 Dicrotendipes sp. water mite diet isolate 1291-BHL110116-GBD3723_8246-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTCTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR282179, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610828 Dicrotendipes sp. water mite diet isolate 1321-BHL110116-GBD20683_12518-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTC-TAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610829 Dicrotendipes sp. water mite diet isolate 1339-BHL110116-GBD8723_8503-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCAACCTGGAACTTTTATTGGTGATGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTGGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGGATAAATAACATAAGTTTTTGATTACTACCCCCATCTCTTACCCTTCTTCTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610830 Dicrotendipes sp. water mite diet isolate 1342-BHL110116-GBD12277_28390-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATTTTTATTCGAGCAGAACTAGGTCAACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTGATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCGCGGATAAATAATATAAGATTTTGATTACTACCCCCTTCACTTACTCTTCTTCTAACTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610831 Dicrotendipes sp. water mite diet isolate 1359-BHL110116-GBD21834_6209-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCTCTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGTCCTGGAACTTTTATTGGTGACGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGTGGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCTTCCCTTACTCTTCTACTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR282179, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610832 Dicrotendipes sp. water mite diet isolate 1361-BHL110116-GBD23410_18062-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTCTTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCTTCGGATAAATAATATAAGTTTTTGAATACGACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610833 Dicrotendipes sp. water mite diet isolate 1374-BHL110116-GBD24726_24142-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATATTTATTCGAGCTGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTATAACGTAATTGTTACAGCTTATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGTGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGATTTTGACTACTACCCCCCTCTCTAACTCTTCTACTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610834 Dicrotendipes sp. water mite diet isolate 1379-BHL110116-GBD23023_19622-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAATTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCAACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTTCTTCCTTTAATATTAGGAGCACCCGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACCCTTCTTCTATCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610835 Dicrotendipes sp. water mite diet isolate 1393-BHL110116-GBD22010_25694-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATATTAATTCGAGCAGAACTAGGTCGAGCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCATTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCACTAACTCTACTACTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610836 Dicrotendipes sp. water mite diet isolate 1399-BHL110116-GBD8032_23843-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATACTAATTCGAGCAGAACTAGGTCACCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTTGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTATCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610837 Dicrotendipes sp. water mite diet isolate 1414-BHL110116-GBD24916_7484-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATACTTATTCGAGCAGAACTAGGTCAACCTGGAACTTTTATTGGTGACGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATATGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCATCTCTAACTCTTCTTCTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610838 Dicrotendipes sp. water mite diet isolate 1669-BHL110116-GBD8105_17202-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAAATGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID JF412109, identified in GenBank as Dicrotendipes pelochloris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610839 Dicrotendipes sp. water mite diet isolate 2093-BHL072216-GBD18455_4341-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610840 Dicrotendipes sp. water mite diet isolate 2113-BHL072216-GBD6060_12303-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCCTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTAC-CTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610841 Dicrotendipes sp. water mite diet isolate 2133-BHL072216-GBD25322_6570-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610842 Dicrotendipes sp. water mite diet isolate 2143-BHL072216-GBD13356_14757-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAACAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGTGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR282179, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610843 Dicrotendipes sp. water mite diet isolate 2144-BHL072216-GBD11603_9585-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATGATATAAGTTTTTGGTTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610844 Dicrotendipes sp. water mite diet isolate 2153-BHL072216-GBD15959_3925-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTTGGAGCTTGAGCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGTAACTTTTATTGGTGACGTTCAAATTTCCAACGTAATTGTTACAGCGCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR746632, identified in GenBank as Dicrotendipes modestus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610845 Dicrotendipes sp. water mite diet isolate 2155-BHL072216-GBD5627_7269-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTTTACCACCCTCTTTAACTCTTTTACTGTCAAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610846 Dicrotendipes sp. water mite diet isolate 2160-BHL072216-GBD9974_2769-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACGCCCAGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.1% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610847 Dicrotendipes sp. water mite diet isolate 2172-BHL072216-GBD14534_5071-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTATACTTTATTTTCGGAGCTTGATCTGGAATAGTCGGAACTTCTTTAAGTATATTAATCCGTGCAGAATTAGGACACCCGGGAACTTTAATCGGAGATGATCTAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610848 Dicrotendipes sp. water mite diet isolate 2178-BHL072216-GBD26149_12302-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGGGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTGAACTCTCTTACTTTCTAGAACAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610849 Dicrotendipes sp. water mite diet isolate 2192-BHL072216-GBD15341_14467-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR294549, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610850 Dicrotendipes sp. water mite diet isolate 2231-BHL072216-GBD13763_26120-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTTGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATCGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610851 Dicrotendipes sp. water mite diet isolate 2274-BHL072216-GBD25398_21404-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTAGACCTGGTACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTAAAGCTCATGTTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGATGATTTGGAAATTGATTTGTTCCTTTAATATTAGGTGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCACCATCTCTTACTTTATTACATTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610852 Dicrotendipes sp. water mite diet isolate 2279-BHL072216-GBD6799_23732-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTCTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAGTGTAATTGTAACAGCTCACGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGACTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610853 Dicrotendipes sp. water mite diet isolate 2297-BHL072216-GBD11781_4289-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGCAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCATCCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCCTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCCTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610854 Dicrotendipes sp. water mite diet isolate 2316-BHL072216-GBD17401_14139-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR746632, identified in GenBank as Dicrotendipes modestus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610855 Dicrotendipes sp. water mite diet isolate 2327-BHL072216-GBD6529_12093-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTATAACGTAATTGTTACCGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTATCTAGTTCTACTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610856 Dicrotendipes sp. water mite diet isolate 2328-BHL072216-GBD6326_8872-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610857 Dicrotendipes sp. water mite diet isolate 2331-BHL072216-GBD22614_4633-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCTCTAAGTATACTTATTTGAGCAGAATTAGGTCGAACTGGAACATTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTTGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610858 Dicrotendipes sp. water mite diet isolate 2344-BHL072216-GBD25979_13414-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTCGGAGTATGGTCTGGTATAGTAGGGACCGCTCTTAGTATATTAATTCGAGCAGAGTTAGGCCAATGTGGTAGCCTTATTGGGGACGATCAAATTTACAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID KR290333, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610859 Dicrotendipes sp. water mite diet isolate 2372-BHL072216-GBD21359_19570-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATCTTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTTAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTTTTGGTTACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTACTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610860 Dicrotendipes sp. water mite diet isolate 2373-BHL072216-GBD6315_10854-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAAGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGGGGCTTTGGAAATTGACTATTGCCTCTTATACTCGGGGCTCCCGACATAGCCTTTCCTCGAATAAATAACATGAGATTCTGATTACTTCCCCCATCTATTTCTTTACTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR282179, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610861 Dicrotendipes sp. water mite diet isolate 2377-BHL072216-GBD13545_2665-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCTCTCGAATAAATAATATAAGTTTTTGATTATTGCCACCTTCTCTTAC-CTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610862 Dicrotendipes sp. water mite diet isolate 2379-BHL072216-GBD10815_25327-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTCTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCCTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGGTTTTGACCTTTACCACCCTCTTTAACTCTTTTACTTTCAAGATCAATTGCTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610863 Dicrotendipes sp. water mite diet isolate 2441-BHL072216-GBD24410_23056-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTCTAATATTAGGAGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTACCCCCCTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610864 Dicrotendipes sp. water mite diet isolate 2468-BHL072216-GBD10860_9497-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACATCTTTAAGTATACTTATTCGTGCAGAATTAGGTCATCCAGGCACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTTTTCTTTCTAAATCAATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 93.7% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610865 Dicrotendipes sp. water mite diet isolate 2472-BHL072216-GBD25707_21649-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAAAATTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACCACCCCCTTCACTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR670930, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610866 Dicrotendipes sp. water mite diet isolate 2552-BHL072216-GBD13167_25290-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCATCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR657857, identified in GenBank as Dicrotendipes modestus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610867 Dicrotendipes sp. water mite diet isolate 2566-BHL072216-GBD23443_17427-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGCACTTCTTTAAGTATATTTATTCGCCTAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGATTTTGATTACTACCCCCTTCACTAACCCTTCTTCTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610868 Dicrotendipes sp. water mite diet isolate 2588-BHL072216-GBD23315_18545-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGTAGAATTAGGACAACCTGGATCATTTATTGGAGACGATCAAATTTACAACGTAATTGTTACAGCACATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTAACCCTACTTCTTTCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR282179, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610869 Dicrotendipes sp. water mite diet isolate 2639-BHL072216-GBD10822_7052-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGCGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCTCCCGACATAGCCTTTCCTCGAATAAATAACATGAGATTCTGATTACTTCCCCCATCTATTTCTTTACTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR282179, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610870 Dicrotendipes sp. water mite diet isolate 2668-BHL072216-GBD22038_26934-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCAACCTGGAACTTTTATTGGTGATGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTAACTCTTCTACTTTCTAGGACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610871 Dicrotendipes sp. water mite diet isolate 2680-BHL072216-GBD18650_18518-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCAGGAAGTTTATTAGGTGATGATCACCTTTATAACGTTATTGTCACGGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.7% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610872 Dicrotendipes sp. water mite diet isolate 2689-BHL072216-GBD11726_7922-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCAACCTGGAACTTTTATTGGTGATGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCAACAGATATAGCTTTCCCTCGGATAAATAACATAAGTTTTTGATTACTACCCCCATCTCTAACTCTTCTTCTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610873 Dicrotendipes sp. water mite diet isolate 2694-BHL072216-GBD23896_13021-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACATCTTTAAGAATACTTATCCGAGCAGAATTAGGTCATCCAGGTACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTACTTCTTTCTAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610874 Dicrotendipes sp. water mite diet isolate 3757-BHL032417-GBD25141_20913-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTTTGACTCTTTTACTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR282179, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610875 Dicrotendipes sp. water mite diet isolate 6335-BHL032417-GBD26877_11602-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610876 Dicrotendipes sp. water mite diet isolate 7544-BHL040517-GBD8263_17228-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGA CCCGGGACATTTATTGGAGATGATCAAATCTACAATGCAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTTTATGG TTATACCTATTCTAATTGGAGGATTCGGAAACTGACTCGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAA TAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC AGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610877 Dicrotendipes sp. water mite diet isolate 7648-BHL040517-GBD4235_20469-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCGGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACG ACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTCATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATTGTT ATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCACGAAT AAATAATATAAGATTCTGACTATTACCTCCTTCTCTAACCCTACTGCTTTCTAGATCAATAGTAGAAAATGGAGCTGGAAC AGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610878 Dicrotendipes sp. water mite diet isolate 7657-BHL040517-GBD3719_9150-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTTGAGCCGAATTAGGACGA CCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGTTCATGCTTTTATTATAATTTTTTTTATGGTTA TACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGATCCCCCGATATAGCTTTCCCACGAATAA ATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAG G	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610879 Dicrotendipes sp. water mite diet isolate 7684-BHL040517-GBD6598_7009-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGA CCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATTGTTA TACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCAAATAA ATAACATAAGATTTTGATTATTACCACCTTCTTTAA- CATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610880 Dicrotendipes sp. water mite diet isolate 7687-BHL040517-GBD21665_4288-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGA CCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTA TACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAA ATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTATCAAGTACTATAGTAGAAAATGGAGCTGGAACAG G	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610881 Dicrotendipes sp. water mite diet isolate 7740-BHL040517-GBD3437_8675-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGA CCTGGGACATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTA TACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAA ATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610882 Dicrotendipes sp. water mite diet isolate 7749-BHL040517-GBD8118_9099-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGT CCCGGGACATTTATTGGAGATGATCAAGTTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTA TATCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAA ATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGAACAATTGTAGAAAATGGAGCTGGAACAG G	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610883 Dicrotendipes sp. water mite diet isolate 7773-BHL040517-GBD23336_16536-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCGGAATTAGGACG ACCCGGGACATTTATTGGAGATAATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATTGTT ATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAAT AAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTGCTTTCTAGCACAATTGTAGAAAATGGAGCTGGAAC AGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610884 Dicrotendipes sp. water mite diet isolate 7775-BHL040517-GBD24276_20227-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCCGT GACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCT ATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAA TATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610885 Dicrotendipes sp. water mite diet isolate 7789-BHL040517-GBD13419_7018-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCG GAACTTTCATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACC TATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATA ATATAAGTTTCTGGCTACTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.1% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610886 Dicrotendipes sp. water mite diet isolate 7798-BHL040517-GBD22050_16872-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGTATGCTAATTCGAGCAAAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAGATTTATAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCGCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCCTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610887 Dicrotendipes sp. water mite diet isolate 7808-BHL040517-GBD17326_10456-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTTTATTTTATTTTTGGAGCTTGATCTGGAATAGTCGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACACCCTGGGACATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTGTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610888 Dicrotendipes sp. water mite diet isolate 7817-BHL040517-GBD6777_9226-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATTTTTGGGGCTTGATCCGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCAAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGTTCATGCTTTTATTATAATTTTTTTATGGTTATACCTATTCTAATTGGAGGTTTCGGAAATTGATTAGTCCCTTTAATATCAGGAGCACCTGATATAGCTTTCCCATGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610889 Dicrotendipes sp. water mite diet isolate 7823-BHL040517-GBD11601_12654-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGAACATTCATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATTGTTATACCTATTTTAATTGGAGGATTCGGAAACTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTGCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610890 Dicrotendipes sp. water mite diet isolate 7838-BHL040517-GBD7617_25276-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATGGTTATACCTATTCTAATTGGAGTATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCCGATATAGCTTTCCCACGAATAAATAATATAAGATCCTGACTATTACCTCCTTCTCTAACCCGACTTCTTTCTAGAACAATAGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610891 Dicrotendipes sp. water mite diet isolate 7885-BHL040517-GBD28368_17807-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGACGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGACCCCGATATAGCTGTCCCACGAATAAATAAAATAAGTATCTGACTATTACCTCCTTCTCTAACTCTACTACTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610892 Dicrotendipes sp. water mite diet isolate 7900-BHL040517-GBD27351_22497-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAATTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAGTCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATGGTTATACCTATTCTAAATGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCCCCTTCTCTAACCCTTCTTCTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610893 Dicrotendipes sp. water mite diet isolate 7914-BHL040517-GBD24299_14798-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATATGGAATAGTAGGAACTTCCTTAAGTATGCTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATTTACAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTCATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCCACTTTCTAGATCAATGGTAAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610894 Dicrotendipes sp. water mite diet isolate 7919-BHL040517-GBD29221_16766-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCTTTAAGTATACTTATTCGAGCAGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATGGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTACTGCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610895 Dicrotendipes sp. water mite diet isolate 7941-BHL040517-GBD17227_19778-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTACTCGAGCCAAATTAGGACGACACGGGACATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACAGCTCAAGCTTTTATTATAATTTTTTTATTGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCATGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTGCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610896 Dicrotendipes sp. water mite diet isolate 7973-BHL040517-GBD13686_10978-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAGTAATAGGAACTTCCTTAAGTATACTTATTCGAGCTGAATTAGGACCACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATTGTTATACCTATTTTAATTGGAGTATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTGCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610897 Dicrotendipes sp. water mite diet isolate 7988-BHL040517-GBD11031_17820-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGAATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGGTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTTGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAATTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610898 Dicrotendipes sp. water mite diet isolate 7990-BHL040517-GBD24213_5332-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAATTTACTTAAGTATACTTATTCGAGCCGAATTAGGACGAACCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGTTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGTTTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCACCCGATATAGCTTTCCCGCGAATAAATAATATAAGGTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610899 Dicrotendipes sp. water mite diet isolate 7992-BHL040517-GBD28312_19787-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCCTTAAGTATACTAATTCGAGCCGAATTAGGTCGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGATGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCTCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610900 Dicrotendipes sp. water mite diet isolate 7996-BHL040517-GBD11514_17361-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGTTATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTATCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610901 Dicrotendipes sp. water mite diet isolate 7998-BHL040517-GBD21676_23868-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCCTTAAGTATATTTATTCGAGCCGAATTAGGACGTCCCGGGACATTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610902 Dicrotendipes sp. water mite diet isolate 8008-BHL040517-GBD23213_15387-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTTTACTTTATTTTTGGAGCTTGATCCGGAATAGTAGGAACTTCCTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTCGGAAATTGACTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610903 Dicrotendipes sp. water mite diet isolate 8045-BHL040517-GBD16054_2904-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTACTCGAGCCGAATTAGGACGACCCTTTACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGTGCATGCTTTTATTATAATTTTTTTTATTGTTATACCTATTCTAATTGGAGGTTTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCACCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610904 Dicrotendipes sp. water mite diet isolate 8076-BHL040517-GBD14850_16848-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATATTTATTCGAGCAGAATTAGGACGACCCGTTTCTTTTATTGGAGATGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATTGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTGCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610905 Dicrotendipes sp. water mite diet isolate 8087-BHL040517-GBD15583_2800-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAGTAGTGGGAGCTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGTGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTAGAGTTCATGCTTTTATTATAATTTTTTTTATTGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTCCTCTAACCCTTCTGCTTTCTAGATCAATTGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610906 Dicrotendipes sp. water mite diet isolate 8090-BHL040517-GBD16232_3354-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTGTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCTTTACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTTGAGGATTAGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACTCTTCTTCTTTCTAAATCAATTGTAGAAAATGGAGCTGGACCAG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610907 Dicrotendipes sp. water mite diet isolate 8113-BHL040517-GBD25891_19269-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCAGAACTAGGACGACCCGGGACATTTATTGGAGATGATCAAGTTTACAATGTAATTGTTACAGCTCATGCTTTTAGTATAATTTTTTTCATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATAATAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610908 Dicrotendipes sp. water mite diet isolate 8124-BHL040517-GBD18064_21735-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGATACTTCCTTATGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAACAATATAAGGTTCTGACTATTACCTCCTTCTCTAACCCTGCCTCTTTCGAGATCAAGTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610909 Dicrotendipes sp. water mite diet isolate 8127-BHL040517-GBD25582_12401-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACTACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAACATAAGTTTCTGACTATTACCTCCTTATCTAACTCTTCTTCTATCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610910 Dicrotendipes sp. water mite diet isolate 8133-BHL040517-GBD20785_10714-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTCATTTTCGGTGCCTGATCAGGGATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCTTGCTTTTATTATAATTTTTTTTATTGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTGCTTTCTAGATCAAACGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610911 Dicrotendipes sp. water mite diet isolate 8152-BHL040517-GBD12347_10688-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTACTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610912 Dicrotendipes sp. water mite diet isolate 8166-BHL040517-GBD4528_16400-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACCTTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGTTCATGCTTTTTTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCACCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCCCCTTCTCTAACCCTTCTTCTTTCTAGATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610913 Dicrotendipes sp. water mite diet isolate 8167-BHL040517-GBD9487_25717-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCTCCAGATATAGCGTCCCCACGAATAAATAATATAAGATTCTGACTATTACCTCCTTCTCTAACCCTACTTCTATCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610914 Dicrotendipes sp. water mite diet isolate 8208-BHL040517-GBD24912_13803-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTATAATGTAATTATTACAGCCCATGCTTTTATTATAATTTTTTTTATTGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCCAACCCTTCTGCTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610915 Dicrotendipes sp. water mite diet isolate 8211-BHL040517-GBD24569_11064-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATATTTATTCGAGCCGAATTAGGACGCGCCGGTTCATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAACATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTACTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610916 Dicrotendipes sp. water mite diet isolate 8214-BHL040517-GBD23183_26900-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGTCCCGGAACATTTATTGGAGATGTTCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTATTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTATTACCTCCTTCTCTAACTCTACTTCTTTCAAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610917 Dicrotendipes sp. water mite diet isolate 8216-BHL040517-GBD8926_19207-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAACTATACTTATTCGATCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAGTCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTAACTCTTCTTCTTTCTAAATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610918 Dicrotendipes sp. water mite diet isolate 8228-BHL040517-GBD14345_27453-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGCCCCGGGACATTTATTGGAGATGATCAAATCTATAATGTAATTGTTGCAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTATTCCCTTTAATATTAGGAGCCCCTGATATAGCTTTCCCACGAATAAATAATATAAGTTCCTGACTATTACCTCCTTCTCTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610919 Dicrotendipes sp. water mite diet isolate 8233-BHL040517-GBD6657_22774-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTTAGAGCTTGATCAGAGATATTAGGGACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGGTATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610920 Dicrotendipes sp. water mite diet isolate 8244-BHL040517-GBD16264_2814-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTATACTTTATTTTTGGAGCTTGATCGGGAATAGTAGGAACTTCCTTAAGTATATTGATTCGAGCCGAATTAGGACTACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATAATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGCGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610921 Dicrotendipes sp. water mite diet isolate 8253-BHL040517-GBD19163_7452-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTTTACTTTATTTTTGGTGCCTGATCTGGAATAGTAGGAACTTCCTTAAGTATATTTATTCGAGCCGAATTAGGACGTCCCGGGACATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTATTACCTCCTTCTCTAACCCTTCTACTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610922 Dicrotendipes sp. water mite diet isolate 8284-BHL040517-GBD19580_11186-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATTTACAATGTAATTGTTATAGCTCATGCTTTTATTATAATTTTTTTTATTGTTATGCCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTGCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610923 Dicrotendipes sp. water mite diet isolate 8307-BHL040517-GBD11534_14905-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGTGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTGCCATTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTATTACCACCTTCTCTAACTCTACTTCTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610924 Dicrotendipes sp. water mite diet isolate 8313-BHL040517-GBD26505_16110-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGCCCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTAATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCTCCGATATAGCATTCCCACGAATAAATAATATAAGTTTCTGATTATTACCTCCTTCTCTAACCCTACTACTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610925 Dicrotendipes sp. water mite diet isolate 8315-BHL040517-GBD28966_19408-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACAACCTGGGACATTTATTGGAGATGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTACTGCTATCTAGATCAATTGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610926 Dicrotendipes sp. water mite diet isolate 8324-BHL040517-GBD24443_24138-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTATGTATACTTATTCGAGCCGACTTAGGACGACCCGGGACATTTATTGGAGATGATCATATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTTGAGGATTCGGAAATTGATTAGTTCCTTTAATATTAGGAGACCCCGATATAGCATTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610927 Dicrotendipes sp. water mite diet isolate 8341-BHL040517-GBD6682_22473-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATATTAGGTACTTCCTTAAGTATACTTATTCGAGCCGCATTAGGATGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGTTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGTTTCAGAAATTGATTAGTCCCTTTAATATTAGGAGCACCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGATTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610928 Dicrotendipes sp. water mite diet isolate 8346-BHL040517-GBD3565_11648-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATTTACAATGTAATTGTTACAGTTCATGCTTTTATTATAATTTTTTTTATTGTTATACCCATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACTAATAAATAATATAAGTTTCTGACTATTACCCCCTTCTCTAACCCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610929 Dicrotendipes sp. water mite diet isolate 8355-BHL040517-GBD8905_14109-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAGTATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTTACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610930 Dicrotendipes sp. water mite diet isolate 8356-BHL040517-GBD5524_23436-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGCATTAGGACGACCCGAGACATTTATTGGAGATTATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGTAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGTCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTTCTTCTCTAACTCTTCTTCTTTCTAAATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610931 Dicrotendipes sp. water mite diet isolate 8360-BHL040517-GBD22604_11545-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAGTCTACAATGTAATTGTTACAGCTCATGCTTTTATTGTAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610932 Dicrotendipes sp. water mite diet isolate 8363-BHL040517-GBD5161_17783-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCCTTCAGTATACTTATTCGAGCCGCATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGGCTATGACCTCCTTCTCTAACCCATCATCAATCTAGAGCAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610933 Dicrotendipes sp. water mite diet isolate 8886-BHL032417-GBD11327_2198-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACGGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR273898, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610934 Dicrotendipes sp. water mite diet isolate 8902-BHL032417-GBD20375_15543-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610935 Dicrotendipes sp. water mite diet isolate 8907-BHL032417-GBD8142_5040-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACGCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR284424, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610936 Dicrotendipes sp. water mite diet isolate 8908-BHL032417-GBD23009_3772-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610937 Dicrotendipes sp. water mite diet isolate 8923-BHL032417-GBD14311_1847-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGATTTTGATTACTACCCCCATCACTTACTCTACTACTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610938 Dicrotendipes sp. water mite diet isolate 8959-BHL032417-GBD24335_24253-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCGCCAGATATAGCTTTTCCTCGGATAAATAATATAAGTTTTTGATTACGCCCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.7% identical to accession ID KR180045, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610939 Dicrotendipes sp. water mite diet isolate 8963-BHL032417-GBD23243_21287-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCGTCTCTAACTCTACGACGATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610940 Dicrotendipes sp. water mite diet isolate 8975-BHL032417-GBD6601_6077-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAGCTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATCATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCGTCCCCCTTCATTAACGCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610941 Dicrotendipes sp. water mite diet isolate 8979-BHL032417-GBD3825_10066-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGAGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTGCTTCTTTCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610942 Dicrotendipes sp. water mite diet isolate 8983-BHL032417-GBD18275_17131-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTTTATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCAACCAGGAACTTTTATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTACTTCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610943 Dicrotendipes sp. water mite diet isolate 8995-BHL032417-GBD13437_7103-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATCGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID KR670930, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610944 Dicrotendipes sp. water mite diet isolate 9020-BHL032417-GBD23330_22028-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTCCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTCTAACAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGGTTTTGACTTTTACCCCCCGTTCTTACTCTTCTCCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610945 Dicrotendipes sp. water mite diet isolate 9033-BHL032417-GBD18537_25430-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATACTTATTCGAGCAGAATTAGGTCAACCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGTACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTAACTCTACTTCTTTCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610946 Dicrotendipes sp. water mite diet isolate 9039-BHL032417-GBD4900_21008-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTCCTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATCAGTTCCTTTAATATTAGGGGCGCCAGATATAGCTTTTCCTCGGATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277564, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610947 Dicrotendipes sp. water mite diet isolate 9053-BHL032417-GBD24316_22187-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAGCTAGGTCAACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGATTTTGACTACTACCCCCTTCTCTTACTCTTCTACTTTCTAGAACAATAGTAGAAAATGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR285427, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610948 Dicrotendipes sp. water mite diet isolate 9054-BHL032417-GBD10262_11911-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610949 Dicrotendipes sp. water mite diet isolate 9057-BHL032417-GBD11534_21413-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACTTTATATTTCATTTTTGGAGCCTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCAACCTGGAACTTTTATTGGTGACGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCGCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTAACTCTTCTACTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR155720, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610950 Dicrotendipes sp. water mite diet isolate 9083-BHL032417-GBD9463_23234-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATAGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610951 Dicrotendipes sp. water mite diet isolate 9090-BHL032417-GBD21996_21283-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATCTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATATTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCGCCTGATATAGCATTTCCTCGGATAAATAATATAAGTTTTTGATTACTCCCCCCTTCACTAACTCTACTACTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR277564, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610952 Dicrotendipes sp. water mite diet isolate 9091-BHL032417-GBD6838_16750-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGTACTTCTCTAAGTATACTAATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGGTTTGGGAATTGATTGGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCACTAACTCTACTACTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610953 Dicrotendipes sp. water mite diet isolate 9106-BHL032417-GBD11006_27496-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATACTTATTCGAGCAGAACTAGGCCAACCTGGAACTTTTATTGGTGACGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTGGGGGCACCAGATATAGCATTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCGTCACTTACTCTACTACTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610954 Dicrotendipes sp. water mite diet isolate 9136-BHL032417-GBD21270_26678-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTCCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGACATTGATTAGTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610955 Dicrotendipes sp. water mite diet isolate 9153-BHL032417-GBD4967_9468-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGATTGGTTCCTTTAATACTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGGTTTTGAATACTACCCCCTTCTCTTACTCTTCTTCTGGCTAGAACAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610956 Dicrotendipes sp. water mite diet isolate 9157-BHL032417-GBD9173_27009-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGTACTTTTATTGGAGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCTTTAATATTAGGAGCACCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTACTTCTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610957 Dicrotendipes sp. water mite diet isolate 9158-BHL032417-GBD16675_28593-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATACTTATTCGAGCAGAACTAGGTCAACCTGGAACTTTTATTGGTGACGATCAAATTTATAACGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCGTTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACCCTACTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610958 Dicrotendipes sp. water mite diet isolate 9159-BHL032417-GBD7443_5073-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTCTTTATAGCTATACCAATTTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTGGGGGCCCCTGATATAGCTTTCCCTCGAATAAATAATACAAGTTTTTGACTTTTACCTCCTTCTTTAACTCTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KJ088118, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610959 Dicrotendipes sp. water mite diet isolate 9160-BHL032417-GBD24144_6015-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCAACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGGAATTGTTACTGCTCATGCTTTTATAATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTACCTTTAATATTAGGTGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTAACTCTACTACTTTCTAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610960 Dicrotendipes sp. water mite diet isolate 9173-BHL032417-GBD24569_19755-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATATTTATTCGAGCAGAACTAGGACGACCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTGGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCTTCTCTAACTCTTCTTCTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610961 Dicrotendipes sp. water mite diet isolate 9177-BHL032417-GBD25363_16185-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTAATTCGAGCAGAGTTGGGTCAACCTGGAACATTTATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCATCTCTAACCCTACTTCTTTCTAGAACAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610962 Dicrotendipes sp. water mite diet isolate 9178-BHL032417-GBD21829_7473-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGCATAGTTGGAACTTCTCTAAGTATATTTATTCGAGCAGAACTCGGTCAACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACCGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGTGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCGTCACTTACTCTTCTTCTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610963 Dicrotendipes sp. water mite diet isolate 9184-BHL032417-GBD13525_24774-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCCGGAATAGTTGGAACTTCTTTAAGTATACTTATTCGAGCAGAACTAGGACGACCAGGAACTTTTATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTCCCTTTAATATTTGGAGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610964 Dicrotendipes sp. water mite diet isolate 9194-BHL032417-GBD23365_26021-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCCACCAGGAACTTTTATTGGTGACGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCGCGGATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTAACTCTACTTCTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610965 Dicrotendipes sp. water mite diet isolate 9211-BHL032417-GBD23384_26027-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATATTTATTCGAGTAGAATTAGGACGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCGCGAATAAATAATATAAGATTTTGATTACTACCCCCTTCACTTACCCTACTTCTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR282179, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610966 Dicrotendipes sp. water mite diet isolate 9215-BHL032417-GBD23326_20211-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGCGCAGAACTAGGTCATCCTGGAACTTTTATTGGTGACGATCAATTTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGAGCACCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTAACACTACTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610967 Dicrotendipes sp. water mite diet isolate 9217-BHL032417-GBD8940_16066-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATACTTATTCGAGCAGAACTCGGTCAACCTGGAACTTTTATTGGTGACGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGGATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTTACTCTACTTCTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610968 Dicrotendipes sp. water mite diet isolate 9221-BHL032417-GBD6803_21765-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTTTAAGTATACTTATTCGAGCAGAACTAGGTCAACCTGGATCTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCGCCAGATATAGCATTCCCTCGGATAAATAATATAAGTTTTTGATTACTTCCCCCTTCACTTACTCTACTACTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610969 Dicrotendipes sp. water mite diet isolate 9224-BHL032417-GBD20768_14337-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGTAGAATTAGGACAACCTGGAACATTTATTGGTGACGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTTTAATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTAACCCTACTTCTTTCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610970 Dicrotendipes sp. water mite diet isolate 9225-BHL032417-GBD24077_15402-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATCGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCGTTTCCTCGGATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTAACCCTACTACCAACTAGAACAATTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610971 Dicrotendipes sp. water mite diet isolate 9229-BHL032417-GBD20986_20060-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATGCTTATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGTGATGACCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTTGTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTTCCCCCTTCACTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610972 Dicrotendipes sp. water mite diet isolate 9235-BHL032417-GBD20631_14275-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGTATACTTATTCGAGCAGAATTAGGACAACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACCGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610973 Dicrotendipes sp. water mite diet isolate 9241-BHL032417-GBD17427_16736-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCAACCTGGAACATTTATTGGTGACGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCACGGATAAATAATATAAGATTTTGATTACTACCACCTTCTCTTACTCTACTTCTTTCTAGAACAATGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610974 Dicrotendipes sp. water mite diet isolate 9256-BHL032417-GBD14230_4244-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610975 Dicrotendipes sp. water mite diet isolate 9259-BHL032417-GBD24571_17853-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATACTTATTCGAGCAGAACTAGGTCGACATGGAACTTTTATTGGAGATGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGATTGGTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGACTACTACCCCCTTCACTAACTCTTCTACTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610976 Dicrotendipes sp. water mite diet isolate 9270-BHL032417-GBD19567_17712-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATTCTTATTCGAGCAGAACTCGGTCGAACTGGAACTTTTATTGGAGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTGATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGAGCACCAGATATAGCATTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCACTTACTCTACTACTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610977 Dicrotendipes sp. water mite diet isolate 9290-BHL032417-GBD24065_20999-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTGAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAGATTTACAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGGGCACCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KP047722, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610978 Dicrotendipes sp. water mite diet isolate 9292-BHL032417-GBD18344_26442-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGACGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGTTTCCTTTAATATTAGGTGCCCCAGATATAGCTTTCCCTCGGATAAATAATATAAGATTTTGATTACTACCCCCCTCTCTAACTCTTCTACTTTCTAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610979 Dicrotendipes sp. water mite diet isolate 9295-BHL032417-GBD23518_9066-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCTGGTATAGTTGGTACTTCTTTAAGTTTACTTATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTACCCCCTTCACTAACTCTTCTACTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610980 Dicrotendipes sp. water mite diet isolate 9298-BHL032417-GBD27440_10101-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTAATTCGAGCAGAGCTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCCGATAAATAATATAAGTATTTGATTACTACCCCCTTCTCTTACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610981 Dicrotendipes sp. water mite diet isolate 9312-BHL032417-GBD29108_15833-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAGATTTACAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGAGGCGCCAGATATAGCTTTTCCTCGGATAAATAATATAAGATTTTGATTACTCCCCCCTTCGCTAACTCAGCTACTTGCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277564, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610982 Dicrotendipes sp. water mite diet isolate 9316-BHL032417-GBD20025_7950-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACGTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTGGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACGCGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCGCCAGATATAGCTTTTCCTCGGATAAATAATATAAGTTTTTGATTACTCCCCCCTCCTCTTACTCTTCTTCTTTCTAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR180045, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610983 Dicrotendipes sp. water mite diet isolate 9325-BHL032417-GBD9984_4296-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTTGGTACTTCTTTAAGTATACTTATTCGAGCAGAACTTGGTCGACCTGGTACTTTTATTGGTGATGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCACTTACTCTTCTACTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610984 Dicrotendipes sp. water mite diet isolate 9336-BHL032417-GBD27505_17855-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATACTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCACTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGAGATGATCAAATTTATAACGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTTGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR282179, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610985 Dicrotendipes sp. water mite diet isolate 9362-BHL032417-GBD5376_14084-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTCTAAGTATATTAATTCGAGCAGAACTAGGTCAACCTGGAACTTTTATTGGTGACGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTAACTCTTCTTCTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610986 Dicrotendipes sp. water mite diet isolate 9372-BHL032417-GBD22644_3958-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGACTACCTGGAACTTTTATTGGTGATGATCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCGCCAGATATAGCTTTTCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCATCTCTAACCCTTCTTCTATCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KP040317, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610987 Dicrotendipes sp. water mite diet isolate 9388-BHL032417-GBD24842_24626-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTTTAAGTATACTTATTCGAGCAAAGCTGGGTCAACCTGGATCTTTTATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATAATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTACCTCCTTCTCTAACTCTACTACTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610988 Dicrotendipes sp. water mite diet isolate 9396-BHL032417-GBD8558_5907-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGATCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAACTGATTGGTTCCATTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACGACCCCCTTCTCTTACTCTTCTTCTTTCTAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR285427, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610989 Dicrotendipes sp. water mite diet isolate 9399-BHL032417-GBD29235_12967-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCAACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCTCTAATATTAGGGGCACCAGATATAGCGTTCCCTCGAATAAATAATATAAGTTTTTGACTACTACCCCCTTCTCTAACTCTTCTACTTTCAAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR282179, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610990 Dicrotendipes sp. water mite diet isolate 9402-BHL032417-GBD26991_12403-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGACAAGCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAACTGATTAGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGGATAAATAATACAAGTTTTTGATTACTACCCCCTTCACTAACTCTACTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610991 Dicrotendipes sp. water mite diet isolate 9409-BHL032417-GBD25831_7372-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACCTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGGATAAATAATATAAGATTTTGATTACTACCACCATCTCTTACTCTATTACTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610992 Dicrotendipes sp. water mite diet isolate 9411-BHL032417-GBD28303_15493-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTCCTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCGCCAGATATAGCTTTTCCTCGGATAAATAATATAAGTTTTTGATTACTCCCCCCTTCTCTTACTCTTCTTCTTTCTAAATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR166245, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610993 Dicrotendipes sp. water mite diet isolate 9417-BHL032417-GBD6239_6040-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGCACTTCTCTAAGTATACTTATTCGACTAGAATTAGGTCGACCTGGATCTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCGCCAGATATAGCTTTTCCTCGGATAAATAATATAAGATTTTGATTACTACCCCCTTCACTTACTCTACTTCTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR277564, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610994 Dicrotendipes sp. water mite diet isolate 9418-BHL032417-GBD4978_19813-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAAAACTAGGTCGCCCTGGAACTTTTATTGGTGACGATCAAATTTATAACGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCGCCCGATATAGCTTTTCCCCGGATAAATAATATAAGTTTTTGATTACTCCCCCCTTCTCTTACCCTTCTTCTATCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR287225, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610995 Dicrotendipes sp. water mite diet isolate 9434-BHL032417-GBD12128_3236-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTTTAAGTATATTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCCCATGCTTTTATAATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCGCCAGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGATTACTCCCCCCGTCTCTTACTCTTCTACTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR277564, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW610996 Dicrotendipes sp. water mite diet isolate 9437-BHL032417-GBD15379_10472-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTACTCGAGCAGAATTAGGTCAACCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGAGCACCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCTTCCCTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610997 Dicrotendipes sp. water mite diet isolate 9442-BHL032417-GBD25268_22039-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTTTAAGTATACTTATTCGAGCAGAACTAGGTCGTCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCGCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACTCCCCCCTTCTCTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR155720, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610998 Dicrotendipes sp. water mite diet isolate 9443-BHL032417-GBD25309_8993-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGGACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCAAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR169284, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW610999 Dicrotendipes sp. water mite diet isolate 9449-BHL032417-GBD15089_19025-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGTAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGAGCACCAGATATAGCATTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTAACTTTGCTATTATCTAGATCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611000 Dicrotendipes sp. water mite diet isolate 9450-BHL032417-GBD25194_5481-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCATCCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTATTTCCTTTAATATTAGGGGCGCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTCCCCCCTCTTTTACTCTTCTACTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR277499, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611001 Dicrotendipes sp. water mite diet isolate 9451-BHL032417-GBD24209_21850-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTCGGTCAAACTGGTACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTAACTCTACTACTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611002 Dicrotendipes sp. water mite diet isolate 9466-BHL032417-GBD19839_19689-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATACTTATTCGAGCAGAACTAGGACGACCCGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611003 Dicrotendipes sp. water mite diet isolate 9472-BHL032417-GBD18985_12187-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATATTTATTCGAGCAGAACTAGGACGACCAGGAACTTTTATTGGTGACGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGGGCACCAGATATAGCATTCCCTCGGATAAATAATATAAGATTTTGATTACTACCCCCATCTCTGACTCTTCTTCTGTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611004 Dicrotendipes sp. water mite diet isolate 9475-BHL032417-GBD22193_25280-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGTACTTCTTTAAGTATTCTTATTCGAGCAGAACTGGGTCAACCTGGTACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTAACTCTACTACTATCTAGATCACTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR155429, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611005 Dicrotendipes sp. water mite diet isolate 9477-BHL032417-GBD7880_20031-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACGACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATACAAGTTTTTGATCACGACCCCCTACTCCTACAATTCATAAATCTAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611006 Dicrotendipes sp. water mite diet isolate 9478-BHL032417-GBD23183_14736-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGCATAGTTGGCACTTCTCTAAGTATACTTATTCGAGCAGAACTCGGTCGACCTGGTACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGGGCCCCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCACTAACTCTACTATTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR291220, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611007 Dicrotendipes sp. water mite diet isolate 9483-BHL032417-GBD22864_22333-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCATGATCAGGAATAGTTGGAACTTCTTTAAGTATTTTTATTCGAGCAGAACTAGGTCGCCCTGGTTCTTTTATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTTGGGAATTGATTGGTTCCTTTAATATTAGGAGCACCAGATATAGCATTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCGTCACTAACTCTACTACTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611008 Dicrotendipes sp. water mite diet isolate 9485-BHL032417-GBD18057_23597-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATATTTGGAACTTCTCTGAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTCTTTGATCACGACCCCCTTCTCCAACACTTCATAAATCTAGATCAAGTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611009 Dicrotendipes sp. water mite diet isolate 9488-BHL032417-GBD21790_3967-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTTGGAACTTCTCTAAGTATTTTTATTCGAGCAGAATTAGGTCATCCTGGATCTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTAACACTACTTCTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611010 Dicrotendipes sp. water mite diet isolate 9501-BHL032417-GBD22966_7897-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGTCCTGGAACTTTTATTGGTGACGATCAAATTTATAACGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGGCACCTGATATAGCTTTCCCACGAATAAATAATATAAGATTTTGATTACTACCCCCATCTCTTACTCTACTTCTTTCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611011 Dicrotendipes sp. water mite diet isolate 9506-BHL032417-GBD21066_18149-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCAAACTGGCTCTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCACCTGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTGCTACCCCCTTCACTTACTCTACTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611012 Dicrotendipes sp. water mite diet isolate 9508-BHL032417-GBD16656_24290-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGTACTTCTCTAAGTATTTTTATTCGAGCAGAACTCGGTCACCCTGGATCTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACCGCTCATGCTTTTATTATAATTTTTTTTATAGTGATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCGTCACTAACCCTACTACTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KP041813, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611013 Dicrotendipes sp. water mite diet isolate 9510-BHL032417-GBD7459_20094-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACTTTATATTTCATTTTTGGAGCCTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGACGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGATTAGTTCCTTTAATATTAGGAGCGCCAGATATAGCTTTTCCTCGGATAAATAATATAAGATTTTGACTACTCCCCCCTTCTCTTACTCTTCTTCTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR155720, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611014 Dicrotendipes sp. water mite diet isolate 9511-BHL032417-GBD24913_21975-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGACTAGAACTAGGACAACCTGGATCATTTATTGGTGACGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCTTCACTAACCTTACTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR282179, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611015 Dicrotendipes sp. water mite diet isolate 9512-BHL032417-GBD27945_19834-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGAGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCATTAACTCTTCTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611016 Dicrotendipes sp. water mite diet isolate 9515-BHL032417-GBD18714_11050-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGCACTTCTTTAAGTATGCTAATTCGAGCAAAACTAGGTCAACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCCCACGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCGCCAGATATAGCTTTTCCTCGGATAAATAATATAAGTTTTTGATTACTCCCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR769982, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611017 Dicrotendipes sp. water mite diet isolate 9535-BHL032417-GBD10235_22910-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACTTTATATTTCATTTTTGGAGCTTGATCCGGAATAGTTGGGACTTCTCTTAGTATACTTATTCGAGCAGATCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCACCAGATATAGCTTTCCCACGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR155720, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611018 Dicrotendipes sp. water mite diet isolate 9801-BHL040517-GBD15005_12114-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGGACTTCCTTAAGTATACTTGTTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAATCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGACGATTACCTCCTTCACTAACCCTTCTTCTGTCTAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611019 Dicrotendipes sp. water mite diet isolate 9927-BHL040517-GBD7552_8090-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGGACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACCTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611020 Dicrotendipes sp. water mite diet isolate 9965-BHL040517-GBD9287_25246-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAATCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611021 Dicrotendipes sp. water mite diet isolate 9969-BHL040517-GBD23970_8861-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATACGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.4% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611022 Dicrotendipes sp. water mite diet isolate 9975-BHL040517-GBD20886_5898-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCAGGAACATTTATTGGAGATGATCAAATTTTTAATGTAATTGCTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAGTTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTATTACCTCCTTCTCTAACCCTACTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611023 Dicrotendipes sp. water mite diet isolate 9977-BHL040517-GBD19990_4732-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTTCAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTATTACTTCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611024 Dicrotendipes sp. water mite diet isolate 10009-BHL040517-GBD17941_9816-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAATAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGAACCGGGACATTCATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCGCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611025 Dicrotendipes sp. water mite diet isolate 10010-BHL040517-GBD20080_15307-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611026 Dicrotendipes sp. water mite diet isolate 10019-BHL040517-GBD25930_14524-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACTTTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGATTATACCTATTCTAATTGGAGGAATCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCCTTCCCACGAATAAATAAAATAAATATCTGACCATCACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611027 Dicrotendipes sp. water mite diet isolate 10028-BHL040517-GBD4700_20497-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTGCTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611028 Dicrotendipes sp. water mite diet isolate 10043-BHL040517-GBD10725_9927-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTTCAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAA---TTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611029 Dicrotendipes sp. water mite diet isolate 10047-BHL040517-GBD20209_13156-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGGACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTACTCCCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611030 Dicrotendipes sp. water mite diet isolate 10053-BHL040517-GBD25948_9275-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGATACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611031 Dicrotendipes sp. water mite diet isolate 10057-BHL040517-GBD13462_26618-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGATTTTGACTTTTGCCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611032 Dicrotendipes sp. water mite diet isolate 10071-BHL040517-GBD8715_18364-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAATAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATGCCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCGCGAATAAATAATATAAGTTTCTGACTATTACCCCCTTCTCTAACCCTACCTCTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611033 Dicrotendipes sp. water mite diet isolate 10109-BHL040517-GBD19440_12572-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTTTATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGGACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCCCCTTCTCTAACCCTTCTTCTTTCTAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611034 Dicrotendipes sp. water mite diet isolate 10114-BHL040517-GBD23038_17749-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAATCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611035 Dicrotendipes sp. water mite diet isolate 10123-BHL040517-GBD14861_15565-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGGACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCCTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611036 Dicrotendipes sp. water mite diet isolate 10152-BHL040517-GBD7956_15974-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTTCAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATAAAGCTTTCCCACGAAAAAAAAAAAAAAGGTTCTGACCAATACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611037 Dicrotendipes sp. water mite diet isolate 10192-BHL040517-GBD11535_18643-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGGGCTTGATCCAGAATAGTGGGAACTTCATTAAGAATGCTTATTTGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCGCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611038 Dicrotendipes sp. water mite diet isolate 10225-BHL040517-GBD12830_15200-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTATTACCTTCTTCTCTAACCCTTCATAAATCTAGAGCAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611039 Dicrotendipes sp. water mite diet isolate 10256-BHL040517-GBD5260_12796-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAATAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTACTTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTCCCCGCGAATAAATAATATAAGATTCTGACTATTACCTCCTTCTCTAACCCTTCTTCCTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611040 Dicrotendipes sp. water mite diet isolate 10274-BHL040517-GBD28766_12215-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAACCGAATTAGGACGACCCAGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTACCTATAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTATTACCTCCATCTCTAATCCTACTACTTTCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611041 Dicrotendipes sp. water mite diet isolate 10284-BHL040517-GBD14022_22949-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATACTTGGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACGGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611042 Dicrotendipes sp. water mite diet isolate 10287-BHL040517-GBD16475_8559-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATCTTAGGAGTTTGAGCTGGAGTAGTAGGGACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611043 Dicrotendipes sp. water mite diet isolate 10308-BHL040517-GBD10078_13957-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGGACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCAGGGACATTTATTGGTGATGATCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTACTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611044 Dicrotendipes sp. water mite diet isolate 10324-BHL040517-GBD4438_11364-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGCTCTGGAATAGTAGGTACTTCCTTATGTATACTTATTCGCGCCGAATTCGGACGACCCGGGACATTTATTGGACATGCTCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATCATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611045 Dicrotendipes sp. water mite diet isolate 10344-BHL040517-GBD24099_20157-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCTTTAAGTATTCTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATTTTCAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAACAAATAATATAAGTTTCTGACTATTACCTCCTTCACTAACCCTACTACTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611046 Dicrotendipes sp. water mite diet isolate 10356-BHL040517-GBD29535_16895-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGGACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACTTTTATTGGAGATGATCAAATTTACAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTCTTCCCCCCTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611047 Dicrotendipes sp. water mite diet isolate 10358-BHL040517-GBD2662_12041-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGCATACTTATTCGAGCCGAATTATGACGACCCGAGACATTTACTGGAGATGGTCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGTAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611048 Dicrotendipes sp. water mite diet isolate 10364-BHL040517-GBD9847_22500-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTAAACTAGGACATCCCGGAACTTTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAGTAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTACATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.4% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611049 Dicrotendipes sp. water mite diet isolate 10418-BHL040517-GBD25537_10841-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAATAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTTGGAAACTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCTCGAATAAATAATATAAGATTCTGACTATTACCTCCCTCTCTAACCCTTCTACTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611050 Dicrotendipes sp. water mite diet isolate 10428-BHL040517-GBD23583_26063-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGGACTTCCTTAAGTATATTTATTCGAGCCGAATTAGGACATCCCGGGACATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTATTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTATTACCTCCTTCTCTAACCCTTCTACTTTCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611051 Dicrotendipes sp. water mite diet isolate 10459-BHL040517-GBD7354_16268-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGCATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCAGAAATCGATTAGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCCTCCTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611052 Dicrotendipes sp. water mite diet isolate 10542-BHL040517-GBD14691_2193-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTGTACTTTATTTTTGGAGCTTGATCTGGAATAATAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGTGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATGGTTATGCCTATTCTAATTGGAGGATTAGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCGCGAATAAATAATATAAGTTTCTGACTATTCCCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611053 Dicrotendipes sp. water mite diet isolate 10576-BHL040517-GBD23629_24072-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACCTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCATTCCCACGAATAAATAATATAAGATTCTGACTATTACCTCCTTCTCTAACCCTTCTACAATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611054 Dicrotendipes sp. water mite diet isolate 10581-BHL040517-GBD16941_11493-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCGCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611055 Dicrotendipes sp. water mite diet isolate 10593-BHL040517-GBD6656_16835-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGGACTTCCTTATGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGCTGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCGCTAACCCGGCTTCTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611056 Dicrotendipes sp. water mite diet isolate 10606-BHL040517-GBD26114_19995-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGCACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTTCAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACGATTACCACCTTCTCTAACCCTACTACTTTCTAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611057 Dicrotendipes sp. water mite diet isolate 10679-BHL040517-GBD17821_12589-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTCTTTTTGGAGCTTGATCTGGAATAGTAGGGACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCATCTCTAACCCTTCTTCTTGCTAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611058 Dicrotendipes sp. water mite diet isolate 10692-BHL040517-GBD26665_8142-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTTTACTTTATTTTCGGAGCCTGATCTGGAATAATAGGAACTTCCTTAAGTATACTTATTCGAGCTGAATTAGGACGACCCGGTACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTCTTTTATGGTTATGCCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCGCGAATAAATAATATAAGTTTCTGACTGTTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611059 Dicrotendipes sp. water mite diet isolate 10739-BHL101516-GBD11193_6547-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGAAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611060 Dicrotendipes sp. water mite diet isolate 10743-BHL101516-GBD8710_19476-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCCTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTCCCACCGTCTCTTTCTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611061 Dicrotendipes sp. water mite diet isolate 10765-BHL101516-GBD7580_20389-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTTTAAGTATACTTATTCGAGCAGAGTTGGGTCAACCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCATCTCTTACTCTACTTCTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611062 Dicrotendipes sp. water mite diet isolate 10773-BHL101516-GBD21711_7872-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTTATTTTTGGAGCTTGATCCGGAATAGTTTGAACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTACTACCCCCTTCTCTTACTCTACTTCTTTCTAGATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611063 Dicrotendipes sp. water mite diet isolate 10775-BHL101516-GBD17743_21405-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611064 Dicrotendipes sp. water mite diet isolate 10792-BHL101516-GBD6328_5143-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGTACTTCTCTAAGTATATTTATTCGAGCAGAGCTGGGTCGAGCTGGTTCTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATAATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCAATTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCACTTACTCTACTACTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR155429, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611065 Dicrotendipes sp. water mite diet isolate 10806-BHL101516-GBD4779_7016-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTTTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTCTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGGGCTCCAGATATGGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTACCACCATCTCTTACTCTACTTCTTTCAAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611066 Dicrotendipes sp. water mite diet isolate 10807-BHL101516-GBD18027_19551-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCTCTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGCCGACCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTATTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTCTAACTCTATTTCTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611067 Dicrotendipes sp. water mite diet isolate 10817-BHL101516-GBD17333_22533-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGTTTGATCAGGAATAGTTGGGACTTCTCTATGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATGGCTGCCCCACGACTAAATAATTTAAGATTCAGACTACTACCACCATCTCTAATCTTACCAATTGCTTCTGCAGCA---GTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611068 Dicrotendipes sp. water mite diet isolate 10820-BHL101516-GBD21639_15767-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTCTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCTGAGTTAGGACGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTCTGACTCTACTACTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611069 Dicrotendipes sp. water mite diet isolate 10825-BHL101516-GBD15173_13944-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATATTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTATGATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTACCACCATCTCTTACTCTACTTCTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611070 Dicrotendipes sp. water mite diet isolate 10835-BHL101516-GBD22992_16038-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTAATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCTCCATCTCTAACTCTGCTACTTGCGAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611071 Dicrotendipes sp. water mite diet isolate 10844-BHL101516-GBD16854_18426-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGACAACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCCTTTATAATAATTTTCTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCTCCTTCACTTACCCTACTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611072 Dicrotendipes sp. water mite diet isolate 10846-BHL101516-GBD18050_17373-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGTAGAGCTAGGACAACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTGATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTACTACCCCCTTCACTTACCCTACTTCTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611073 Dicrotendipes sp. water mite diet isolate 10849-BHL101516-GBD17735_24468-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGACCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGGTATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTCTTACCCTACTACCAACTAGAACAATTGCAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611074 Dicrotendipes sp. water mite diet isolate 10851-BHL101516-GBD7588_9914-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTCCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAGTGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCTCCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTACTTCCCCCCTCTCTTACTCTACTTCTTTCTAGATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611075 Dicrotendipes sp. water mite diet isolate 10862-BHL101516-GBD23822_6219-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTCATTTTTGGTGCTTGATTAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGGCCTGGAACTTTTATTGGTGAGGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCTCCTTCTCTAACTCTACTACTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611076 Dicrotendipes sp. water mite diet isolate 10880-BHL101516-GBD21302_11504-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTCTTGGAGCTTGATCGGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCGCTTACACAACATCAATCTAGAGCAATTGTAGAAAATGGAGCTGAAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611077 Dicrotendipes sp. water mite diet isolate 10885-BHL101516-GBD11065_16504-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATACTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTACCCCCTTCTCTTACTCTACTTCTTTCTAGATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611078 Dicrotendipes sp. water mite diet isolate 10886-BHL101516-GBD17749_12669-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGTATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACCCTACTACCTTCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611079 Dicrotendipes sp. water mite diet isolate 10887-BHL101516-GBD22693_19308-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCAACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTGCTGCCCCCTTCACTAACTCTACTTCTATCTAGATCAATTGTAGAAAATGGAGCTGGAAGAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611080 Dicrotendipes sp. water mite diet isolate 10896-BHL101516-GBD9367_17242-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCAGCATGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCTCTAACTCTACTTCTGTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611081 Dicrotendipes sp. water mite diet isolate 10904-BHL101516-GBD19321_28390-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGTTGGGTCAAGCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATAATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACTACCACCTTCTCTAACACTACTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611082 Dicrotendipes sp. water mite diet isolate 14484-BHL040517-GBD13211_25303-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACATTATATTTTGTTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATATTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCAGATATAGCATTCCCTCGGATAAATAATATAAGTTCTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611083 Dicrotendipes sp. water mite diet isolate 14675-BHL040517-GBD6592_16115-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTATTTTATTTTTGGAGCTTGATCTGGAATAGTATGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGTCATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTATCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611084 Dicrotendipes sp. water mite diet isolate 14725-BHL040517-GBD19477_19832-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATATTTATTCGAGCCGAATTAGGACAACCTGGCACATTTATTGGAGATGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTACTTCTTTCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611085 Dicrotendipes sp. water mite diet isolate 14727-BHL040517-GBD26088_11936-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGGTATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.4% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611086 Dicrotendipes sp. water mite diet isolate 14740-BHL040517-GBD23368_17787-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGACTAGTATGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGATCATGGTTTTATTATAATTTTTTTTATGGTTATACCTGTTCTAATTGGAGGATTTGGAAAATGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTAACTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611087 Dicrotendipes sp. water mite diet isolate 14755-BHL040517-GBD2528_16789-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGCGCTTGATCTGGAATAGTAGGAACTTCTTTCAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGAGATTTATTGGAGATGATCAAAACTACAATGTAATTGTTACAGCTCCTGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGGTATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACTCGTCTTCTTTCTAGATCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611088 Dicrotendipes sp. water mite diet isolate 14779-BHL040517-GBD26811_9211-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCAAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGGGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGGTATAGCTTTCCCACGAATAAATAATATAAGTTTCTGTCTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611089 Dicrotendipes sp. water mite diet isolate 14796-BHL040517-GBD15040_10821-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACGTTATTTTTGGAGCTTGATCTAGAATAGTAGGAACTTCCTTAAGTATACTGATTCGAGCCGAATTAGGACGACCCGGGACATTGATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCCATTCTAATTGGAGGTTTCGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611090 Dicrotendipes sp. water mite diet isolate 14869-BHL040517-GBD20460_9417-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGTGACATTTATTGGAGATGATCTAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGATTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGATCCCCCGGTATAGCTTTCCCACGAATAAATAAAATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611091 Dicrotendipes sp. water mite diet isolate 14887-BHL040517-GBD2296_14681-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTCATTTTCGGTGCCTGATCAGGAATAGAGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATCGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611092 Dicrotendipes sp. water mite diet isolate 14931-BHL040517-GBD8984_26780-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTTGGAGCTTGATCTGGAATAGTATGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCAGGGACATTTATTGGAGATGATCAAATATACAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611093 Dicrotendipes sp. water mite diet isolate 14961-BHL040517-GBD18269_18302-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATATTTATTCGAGCCGAATTAGGACGACCCGGGAAATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGTTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTATCTCCTTCTCTAACTCTTCTTCTTTCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611094 Dicrotendipes sp. water mite diet isolate 14973-BHL040517-GBD11488_5996-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCCCCTTCTCTAACCCTTCTTCTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611095 Dicrotendipes sp. water mite diet isolate 15000-BHL040517-GBD27386_22059-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTACTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCATGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGGTATAGCTTTCCCATGAATAAATAATATAAGTTTCTGACTATGACCTCCTTCTCTAGCCCTTCTTCTCTCTAGATCATTTGTAGAAAATGGCGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611096 Dicrotendipes sp. water mite diet isolate 15016-BHL040517-GBD4774_14757-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGTCCCGGGACATTGATTGGTGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCCATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTATAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTATTACCTCCTTCTCTAACCCTACTTCTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611097 Dicrotendipes sp. water mite diet isolate 15034-BHL040517-GBD18660_6999-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTGGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGTACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACATATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAAGGAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611098 Dicrotendipes sp. water mite diet isolate 15065-BHL040517-GBD24166_18477-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCTGGGACATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGAGGATTTGGAAATTGACTACTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611099 Dicrotendipes sp. water mite diet isolate 15067-BHL040517-GBD19975_7183-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGATGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTGATTGTTACAGCTCATGCCTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGGTATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTCTCTAGATCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611100 Dicrotendipes sp. water mite diet isolate 15120-BHL040517-GBD17534_12343-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGCACTTCCTTAAGTATATTTATTCGAGCCGAATTAGGACAACCCGGGACATTTTTTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGTTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGACACCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTATCTCCTTCTCTAACCCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611101 Dicrotendipes sp. water mite diet isolate 15142-BHL040517-GBD21357_10722-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTACTTTATTTTTGGAGCTTGATCTGGAATAGTGTGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACTTTTATTGGAGATGATCAAATCTATAATGTAATAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCTATTTTAATTGGAGGATTCGGAAACTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611102 Dicrotendipes sp. water mite diet isolate 15146-BHL040517-GBD24295_21986-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACATCCCGGAACATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCTTACTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611103 Dicrotendipes sp. water mite diet isolate 15226-BHL040517-GBD7982_8610-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTATGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATCATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGACATGGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611104 Dicrotendipes sp. water mite diet isolate 15255-BHL040517-GBD26308_17116-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTATGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGTTCAAATCTACAGTGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCTCGAATAAATAATATAAGATTCTGACTATTACCTCCTTCTCTAACCCTTCTACTTTCTAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611105 Dicrotendipes sp. water mite diet isolate 15272-BHL040517-GBD22400_9703-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGAACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAACTGATTAGTCCCTTTAATATTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611106 Dicrotendipes sp. water mite diet isolate 15285-BHL040517-GBD4776_14902-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGGTTGATCTGGAATAGTATGAACTTCCTTAAGTATTCTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAAAAATATAAGTTTCTGACCATCACCTCCTTCTCCAACCCTTCTTCTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611107 Dicrotendipes sp. water mite diet isolate 758-BHL040916-GBD19882_3878-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTTCTTAAGTATACTTATTCGAGCCGAATTAGGACGACACGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGTATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACACTTCTTCTTTCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611108 Dicrotendipes sp. water mite diet isolate 773-BHL040916-GBD28031_8934-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACAACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATTGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTATTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTGCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611109 Dicrotendipes sp. water mite diet isolate 965-BHL100916-GBD2813_12133-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTAATGGAGATGATCAAATCTACAATGTAATTGTTACAGTTCATGCTTTTATTATAATTTTTTTCATGGTTATACCTATTCTAATTGGAGGTTTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCACCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCATTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611110 Dicrotendipes sp. water mite diet isolate 2502-BHL072216-GBD6524_14295-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACAACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGGTATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTACTTCTATCTAGATCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611111 Dicrotendipes sp. water mite diet isolate 7638-BHL040517-GBD8930_7334-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATTTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATTGTTATACCTACTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGATCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTGCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611112 Dicrotendipes sp. water mite diet isolate 7725-BHL040517-GBD8378_6187-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGAACATTTATTGGAGATGATCAAATCTACAATGTTGTTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATTGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACTCTTCTTCTTTCTAGATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611113 Dicrotendipes sp. water mite diet isolate 7738-BHL040517-GBD23863_22352-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGTCGACCCGGTACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACCCCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCATTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTACTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611114 Dicrotendipes sp. water mite diet isolate 7928-BHL040517-GBD20391_10672-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACAACCCGGGACATTTATTGGAAATTATCAAGTCTACAATGTAATTGTTACAGCTCATGCTTTTATTATTATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCTCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611115 Dicrotendipes sp. water mite diet isolate 7960-BHL040517-GBD20551_19246-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACGGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCACGAATAAATAATATAAGATTCTGACTATTACCCCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611116 Dicrotendipes sp. water mite diet isolate 8074-BHL040517-GBD17497_3871-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCCTTAAGTATACTTATGCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGAAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCACGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTCCCTCCTTCTCTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611117 Dicrotendipes sp. water mite diet isolate 8091-BHL040517-GBD6653_22148-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATCCTTATTCGAGCCGAATTAGGACGACCCGGAACATTTATTGGTGATGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGATTTTGACTATTACCTCCTTCTCTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611118 Dicrotendipes sp. water mite diet isolate 8098-BHL040517-GBD10552_3467-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACATCCTTAAGTATCCTTATTCGAGCCGAATTAGGACGACCCGGTACATTTATTGGAGATGATCAAATCTATAACGTAATTGTTACAGCTCATGCTTTTATAATAATTTTTTTTATGGTTATACCTATTCTAATTGGATGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCTCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611119 Dicrotendipes sp. water mite diet isolate 8106-BHL040517-GBD29629_16537-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAACTAGGACGACCCGGAACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATAACTATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGACCCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611120 Dicrotendipes sp. water mite diet isolate 8134-BHL040517-GBD12398_22008-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCCTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGTCCCGGGACATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGTTTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCACCCGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611121 Dicrotendipes sp. water mite diet isolate 8194-BHL040517-GBD28533_11091-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGTCGACACGGAACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATCATTTTTTTTATTGTTATACCTATTCTAATTGGTGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCAGCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611122 Dicrotendipes sp. water mite diet isolate 8198-BHL040517-GBD25022_11968-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTCATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAGTCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATAGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCGCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCACTAACCCTTCTTCTTTCTGGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611123 Dicrotendipes sp. water mite diet isolate 8263-BHL040517-GBD20523_24162-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGATATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTACAATTTTTTTTATTGTTATACCTATTCTAATTGGAGGATACGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTGCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611124 Dicrotendipes sp. water mite diet isolate 8316-BHL040517-GBD18520_4064-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGTAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGAACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACATCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATCTTAGGAGCTCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTATAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611125 Dicrotendipes sp. water mite diet isolate 8317-BHL040517-GBD7062_5550-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATTTTTGGGGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCAAAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAGTCTACAATGTCATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAGATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611126 Dicrotendipes sp. water mite diet isolate 8856-BHL101416-GBD23501_7494-Lq60 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTATTTATTTTTGGAGCTTGATCTGGAATAGTAGGGACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGTGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611127 Dicrotendipes sp. water mite diet isolate 9562-BHL032417-GBD19240_11403-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGAGACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAGATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611128 Dicrotendipes sp. water mite diet isolate 9944-BHL040517-GBD6378_13058-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATGCCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCGCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611129 Dicrotendipes sp. water mite diet isolate 10184-BHL040517-GBD8422_11352-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611130 Dicrotendipes sp. water mite diet isolate 10549-BHL040517-GBD15748_13579-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATTTTTGGAGCTTGATCTGGAATAGTAGGGGCTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGGTTCGGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGAGCAATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611131 Dicrotendipes sp. water mite diet isolate 13796-BHL040517-GBD26289_22949-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGTACATTTATTGGAGATGATCAAATCTACAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAAATGGAGGTTTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCACCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611132 Dicrotendipes sp. water mite diet isolate 14687-BHL040517-GBD20983_5634-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGAACATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCAAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611133 Dicrotendipes sp. water mite diet isolate 14910-BHL040517-GBD24038_22811-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCTGAATTAGGACGACCCGGATCATTTTTTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTATTACCTCCTTCTCTAACCCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611134 Dicrotendipes sp. water mite diet isolate 14922-BHL040517-GBD28436_10032-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGTACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCTCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTACTACCCCCTTCTCTAACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611135 Dicrotendipes sp. water mite diet isolate 14944-BHL040517-GBD10732_27866-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATATTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAACAATATAAGTTTCTGACTATTATCTCCTACTCTAACCCAGCTTCTTGCTAGATTAATTGTAGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611136 Dicrotendipes sp. water mite diet isolate 15019-BHL040517-GBD24269_15759-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTACTTTATTTTTGGAGCTTGATCTGGAATGGTAGGAACTTCCTTAAGTATACTTATTCGCGCCGAATTAGGACGACCCGGAACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAGGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611137 Dicrotendipes sp. water mite diet isolate 15093-BHL040517-GBD14712_3252-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTGTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCTTTACATTTATTGGATATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATCCCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCCAGATCACTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611138 Dicrotendipes sp. water mite diet isolate 15121-BHL040517-GBD12780_26922-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATAGTAGGAGCCTCCGATATAGCTTTCCCACGAATAAATAAGATAAGTGTCTGACTATTACCTCCTTCTCTAACCCTGCTTCTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611139 Dicrotendipes sp. water mite diet isolate 15126-BHL040517-GBD22530_23362-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTACTTTATTTAGGAGCTTGATCTGGAATAGTATGAACTTCCTTAAGAATACTTATTCGAGTTGAATTAGGACGACCCGGAACATTTATTGGAGATGATCAAATCTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611140 Dicrotendipes sp. water mite diet isolate 15129-BHL040517-GBD22786_11352-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTACTTTATTTTTGGTGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGTCCCGGGACATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611141 Dicrotendipes sp. water mite diet isolate 15240-BHL040517-GBD11250_20544-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATACGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTAGAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGACCCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCGTCGTCTTTCTAGGTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611142 Dicrotendipes sp. water mite diet isolate 15258-BHL040517-GBD16570_6295-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTGTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGTGACATTTATTGGAGATGATCAAATCTACAATGGAATTGTTACAGCGCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTAGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611143 Dicrotendipes tritomus water mite diet isolate 770-BHL040916-GBD26484_10651-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCTGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACTTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTACTACTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611144 Dicrotendipes tritomus water mite diet isolate 906-BHL100916-GBD7504_7524-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCGGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTGTAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611145 Dicrotendipes tritomus water mite diet isolate 1124-BHL110116-GBD11121_18082-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611146 Dicrotendipes tritomus water mite diet isolate 1258-BHL110116-GBD27504_11524-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTCGTTCCTTTAATATTAGGGGCACCAGATATAGCATTCCCTCGGATAAATAATATAAGTTTTTGATTACTTCCCCCTTCTCTAACTCTACTACTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR280239, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611147 Dicrotendipes tritomus water mite diet isolate 1288-BHL110116-GBD14062_12005-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAGCTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATCGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACACTTCATCAATCTAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611148 Dicrotendipes tritomus water mite diet isolate 1306-BHL110116-GBD15716_4788-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCTACCTGGAACTGTTATTGGTGACGATCAAATTTACAACGGAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGTGTCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTCCCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGCGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611149 Dicrotendipes tritomus water mite diet isolate 1309-BHL110116-GBD12411_18853-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACATACACCTTCTCTTACACTACTTCGTTCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611150 Dicrotendipes tritomus water mite diet isolate 1313-BHL110116-GBD1915_14918-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGAGATGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGTTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCATCTCTTACTCTTCTTCTATCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611151 Dicrotendipes tritomus water mite diet isolate 1318-BHL110116-GBD20371_12563-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCAACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCATCTCTTACGCTACTACTTTCTAGAGCAATAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611152 Dicrotendipes tritomus water mite diet isolate 1326-BHL110116-GBD29056_12326-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGACGACCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTGCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGATTTTGACTACTACCCCCTTCTCTTACTCTTCTTCTTCCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611153 Dicrotendipes tritomus water mite diet isolate 1327-BHL110116-GBD2058_17048-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATACTTATTCGAGCTGAACTAGGTCGACCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611154 Dicrotendipes tritomus water mite diet isolate 1328-BHL110116-GBD14610_28530-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATCCTAATTCGAGCAGAACTAGGTCTACCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611155 Dicrotendipes tritomus water mite diet isolate 1340-BHL110116-GBD2684_15679-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGAGGCTCCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCATACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611156 Dicrotendipes tritomus water mite diet isolate 1344-BHL110116-GBD25638_20763-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGTCCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTAACTCTTCTACTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611157 Dicrotendipes tritomus water mite diet isolate 1349-BHL110116-GBD26255_15388-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGCACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATGGGGGAATTGATTGGTTCCTTTAATATTAGGGGCACCAAATATAGCTTTCCCTCGGATAAAAAATATAAGTTTTTGATTACTACCCCCTTCTCTTACGCTGCGTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611158 Dicrotendipes tritomus water mite diet isolate 1364-BHL110116-GBD13246_28489-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGGACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCCCCGATAAATAAAATAAGTTTTTGATTTCTTCCCCCTTCTCTTACTCTTCTTCTTTCCAGATCAATTGTAGGAAATGGAACTGGAACAGGA	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611159 Dicrotendipes tritomus water mite diet isolate 1371-BHL110116-GBD5116_12155-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTACTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGAGGCACCAGATATAGCTTTCCCTCTGATAAATAATATAAGTTTTTGATTACAAACCCCTTCTCTTAATCTGCTTCGTTCTAGATCAATTGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611160 Dicrotendipes tritomus water mite diet isolate 1381-BHL110116-GBD26537_10140-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAAAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAGATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCGTCACTAACTCTACTTCTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611161 Dicrotendipes tritomus water mite diet isolate 1389-BHL110116-GBD9104_4483-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTATAACGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611162 Dicrotendipes tritomus water mite diet isolate 1427-BHL110116-GBD10275_15033-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611163 Dicrotendipes tritomus water mite diet isolate 1459-BHL110116-GBD12234_22149-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTCCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGTGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACGTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611164 Dicrotendipes tritomus water mite diet isolate 1469-BHL110116-GBD18332_6822-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTTAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGTACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCTCCTTCTCTTACACTACTACTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR155429, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611165 Dicrotendipes tritomus water mite diet isolate 1503-BHL110116-GBD26803_7542-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATGGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTTATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCGCCAGATATAGCTTTTCCTCGGATAAATAATATAAGTTTTTGATTACTCCCCCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR277564, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611166 Dicrotendipes tritomus water mite diet isolate 1557-BHL110116-GBD2304_18085-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTTACTCTACTTCTTTCTAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KT110535, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611167 Dicrotendipes tritomus water mite diet isolate 1655-BHL110116-GBD21795_5934-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGCCGACCTGGAACTTTTATTGGTGACGGTCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611168 Dicrotendipes tritomus water mite diet isolate 1666-BHL110116-GBD4847_12451-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCAAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611169 Dicrotendipes tritomus water mite diet isolate 1731-BHL110116-GBD27492_17768-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCGCCAGATATAGCTTTTCCTCGGATAAACAATATAAGTTTTTGATTACTCCCCCCTTCTCTAACTCTACTACTTTCTAGATCAATCGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR277564, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611170 Dicrotendipes tritomus water mite diet isolate 1779-BHL110116-GBD27502_20437-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGAACTGGAACTTTTATTGGTGACGTTCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGTATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTCCCTCGCATAAATAATATAAGTTTTTGATTACTTCCCCCTTCTCTTACTCGACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR282179, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611171 Dicrotendipes tritomus water mite diet isolate 1817-BHL011116-GBD16920_8446-Ldc73 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTCTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAAAGCTGGGTCGACCTGGAACTATTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611172 Dicrotendipes tritomus water mite diet isolate 1853-BHL072216-GBD23496_22020-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGTGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTACTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611173 Dicrotendipes tritomus water mite diet isolate 2064-BHL072216-GBD6413_15270-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611174 Dicrotendipes tritomus water mite diet isolate 7785-BHL040517-GBD12303_25621-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTCCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACACTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611175 Dicrotendipes tritomus water mite diet isolate 8865-BHL101416-GBD3632_9128-Lq60 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTCCTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611176 Dicrotendipes tritomus water mite diet isolate 8873-BHL032417-GBD24416_14473-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611177 Dicrotendipes tritomus water mite diet isolate 8875-BHL032417-GBD17717_7543-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGCACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611178 Dicrotendipes tritomus water mite diet isolate 8876-BHL032417-GBD9200_19313-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCGCCAGATATAGCTTTTCCTCGGATAAATAATATAAGTTTTTGATTACTCCCCCCTTCTCTTACTCTTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR277564, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611179 Dicrotendipes tritomus water mite diet isolate 8878-BHL032417-GBD5747_10705-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTCCATTTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTTTTCGAGCGGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611180 Dicrotendipes tritomus water mite diet isolate 8904-BHL032417-GBD17258_6732-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCAACCTGGAACATTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCATCTCTTACTCTTCTTCTATCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611181 Dicrotendipes tritomus water mite diet isolate 8928-BHL032417-GBD14600_23422-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCAGCCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCCATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR273898, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611182 Dicrotendipes tritomus water mite diet isolate 8940-BHL032417-GBD6825_16343-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGTGTCGACCTGGAACTTTCATTGGTGACGATCAAATTTACAATGTACTTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTTCCACCTTCTCTTACTCTACTTCTTTCTAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611183 Dicrotendipes tritomus water mite diet isolate 8943-BHL032417-GBD12903_14725-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTCGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCTCTTACTCTACTTCTTTCTAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR282179, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611184 Dicrotendipes tritomus water mite diet isolate 8947-BHL032417-GBD17086_11330-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGACTCCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCTCTTACTTTACTACTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611185 Dicrotendipes tritomus water mite diet isolate 8950-BHL032417-GBD12749_2209-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGACCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATACTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTACCTCCTTCACTTACTCTACTTCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611186 Dicrotendipes tritomus water mite diet isolate 8952-BHL032417-GBD23935_13835-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCCAAGTATACTTATTCGAGCAGAGCTGGGTCGAACTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCGCCTTCTCATACTCGACTTCTTTCTAGATCAAGTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611187 Dicrotendipes tritomus water mite diet isolate 8962-BHL032417-GBD4272_13337-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCGGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGATTTTGATTACTACCCCCATCTCTTACCCTACTTATTTCTAGATCAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611188 Dicrotendipes tritomus water mite diet isolate 8967-BHL032417-GBD26501_18743-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTACGTATACTTATTCGAGCAGAGCGGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCGAACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611189 Dicrotendipes tritomus water mite diet isolate 8970-BHL032417-GBD22310_20148-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTTTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCTCCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCGTCTCTTACTCTACTTCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611190 Dicrotendipes tritomus water mite diet isolate 8994-BHL032417-GBD4944_23899-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGTATAGTTTGAACTTCTCTAAGTGTACTTATTCGAGCAGAACTAGGTCGACCTGGTACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCGACTTCTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611191 Dicrotendipes tritomus water mite diet isolate 9002-BHL032417-GBD26394_15859-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACGACCCCCTGCGCTTACACTACTGCTGTCTAGGGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611192 Dicrotendipes tritomus water mite diet isolate 9010-BHL032417-GBD11445_4084-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATACTTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGACACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACCCTTCTTCTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611193 Dicrotendipes tritomus water mite diet isolate 9018-BHL032417-GBD17045_5863-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTGTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAGGTATACTTATTCGAGCAGAACTAGTTCTACCTGTAACTTTTATTGGCGACGATCTAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611194 Dicrotendipes tritomus water mite diet isolate 9027-BHL032417-GBD8522_21140-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTTTAAGTATACTTATTCGAGCAGAGCTGGGTCGAGCTGGTACTTTTATTGGAGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR155429, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611195 Dicrotendipes tritomus water mite diet isolate 9028-BHL032417-GBD15876_15213-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTGGTTCCTTTAATATTATGGGCACCAGATATAGCTTTCCCACGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACACTTCATCTGTCTAGAGCAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611196 Dicrotendipes tritomus water mite diet isolate 9029-BHL032417-GBD28561_13367-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAGTTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAACTTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTCTTACTCTACTTCTTTCTAGATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611197 Dicrotendipes tritomus water mite diet isolate 9030-BHL032417-GBD13417_4275-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGAATACTTATTCGAGCAGAGCTGGGTCTACCTGGAACTTTTATTGGTGGCGATCAAATTTACATTGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTCCTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611198 Dicrotendipes tritomus water mite diet isolate 9032-BHL032417-GBD19511_21938-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTTTTGGTGACGATCAAATTTACAACGTCATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACAAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTAACGCTACTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611199 Dicrotendipes tritomus water mite diet isolate 9037-BHL032417-GBD14603_23609-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGACAACCTGGAACTTTTATTGGTGACGATCAAATTTATAACGTAGTTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTTACTCTTCTTATTTCTAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611200 Dicrotendipes tritomus water mite diet isolate 9048-BHL032417-GBD15113_26962-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGCATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTCTTTGATTACTTCCCCCTGCTCTTACTCTTCTTCTAGCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR273898, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611201 Dicrotendipes tritomus water mite diet isolate 9051-BHL032417-GBD7076_5823-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACGTTTATTGGTGACGATCAAATTTACAATGTAATTGTTGCAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGAGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTACTTTCTAAATCAATTGTAGAAAATGGAGCTGAAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611202 Dicrotendipes tritomus water mite diet isolate 9060-BHL032417-GBD11995_18791-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAACAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCAACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTACTTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAAATGATTAGTTCCTTTAATATTAGGTGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCACCTTCTCTAACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611203 Dicrotendipes tritomus water mite diet isolate 9065-BHL032417-GBD27244_14235-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGACACCAGATATAACTTTCCCTCGGAAAAAAAAAAAAGTTTTTGATTACTACCCCCTTCTCTAACTCTTCTTCTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611204 Dicrotendipes tritomus water mite diet isolate 9067-BHL032417-GBD8947_23583-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTTGGAACTTCTCTTAGTATACTTATTCGAGCAGAACTAGGTCGTCCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611205 Dicrotendipes tritomus water mite diet isolate 9068-BHL032417-GBD13962_14136-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTAGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTATGCCGACCTGGAACATTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACCCTACTTCTTTCTAGAGCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611206 Dicrotendipes tritomus water mite diet isolate 9071-BHL032417-GBD16727_22390-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGTATAGTTGGGACTTCTTTAAGTATACTTATTCGAGCAGAGCTCGGTCAACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCTCCTTCTCTAACTCTACTTCCATCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611207 Dicrotendipes tritomus water mite diet isolate 9076-BHL032417-GBD25074_25021-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTATCTAGGTATACTTATTCGAGCAGATCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTCATAGTTATACCAATTTTAATTGTAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTGTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611208 Dicrotendipes tritomus water mite diet isolate 9080-BHL032417-GBD18217_17013-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGGCGACCTGGTACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGAAAAATAATATAAGGTTTTGATTACTACCCCCTTCCATTACTCCTCTTCCTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611209 Dicrotendipes tritomus water mite diet isolate 9088-BHL032417-GBD22968_19062-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611210 Dicrotendipes tritomus water mite diet isolate 9089-BHL032417-GBD12623_16224-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTCGGTCGACCTGGATCTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTATTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAGTATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCATTTACTCTACTTCTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611211 Dicrotendipes tritomus water mite diet isolate 9094-BHL032417-GBD26161_23232-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGACGACCTGGAACTTTTATTGGAGATGATCAAATTTACAACGTAATTGTTACAGCACATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGATTTTGACTACTACCCCCTTCTCTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR282179, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611212 Dicrotendipes tritomus water mite diet isolate 9095-BHL032417-GBD20880_12008-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTTATTCGAGCAGAACTCGGTCGCCCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611213 Dicrotendipes tritomus water mite diet isolate 9096-BHL032417-GBD7864_14579-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACATTATTTTTGGAGCTTGATCAGGAATAGTTGGGACATCTCTAAGTATACTCATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACCCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611214 Dicrotendipes tritomus water mite diet isolate 9097-BHL032417-GBD18811_28366-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATTTTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCTACCTGGAACTTTTATTGGTGACGATCAATTTTGCAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATGGCTTTTCCCCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611215 Dicrotendipes tritomus water mite diet isolate 9100-BHL032417-GBD19205_4126-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGATCTGGAACTTTTATTGGAGACGATCAAATTTATAATGTAATTGCTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGGTTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCTCCATCTCTTACTCTACTTCTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611216 Dicrotendipes tritomus water mite diet isolate 9102-BHL032417-GBD8071_15717-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGCACTTCTCTAAGTATACTTATTCGAGCAGAACCAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTCCCCGCGGATAAATAATATAAGATTTTGATTACTACCCCCTTCACTTACCCTTCTTCTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611217 Dicrotendipes tritomus water mite diet isolate 9104-BHL032417-GBD2611_12965-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCACTCGGATAAATAATATAAGTTTTTGATTACAACCCCCTTCTCGTACTCTTCGTCGGTCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611218 Dicrotendipes tritomus water mite diet isolate 9131-BHL032417-GBD26447_14644-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACTTCCTTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTACAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACGTCCTCCTTCTCTTACTCTACTTCATTCTAGAGCAATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611219 Dicrotendipes tritomus water mite diet isolate 9134-BHL032417-GBD20937_18511-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGTAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCGTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGTGGCTCCAGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGATTACATCCTCCTTCTCTTACTCTACTTCGTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611220 Dicrotendipes tritomus water mite diet isolate 9138-BHL032417-GBD26139_17755-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTCATTTTTGGAGCCTGATCAGGAATAGTTGGAACCTCTCTAAGTATACTTATTCGAGCTGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTAACTCTTCTACTTTCTAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611221 Dicrotendipes tritomus water mite diet isolate 9141-BHL032417-GBD9115_3154-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTCATTCTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATATTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTGCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTTACTCTTTTTCTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611222 Dicrotendipes tritomus water mite diet isolate 9147-BHL032417-GBD15881_4829-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGGTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGTTCAACCTGGAACTATTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAGTTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTCCTCTTACTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611223 Dicrotendipes tritomus water mite diet isolate 9149-BHL032417-GBD10988_8506-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTTAGTATACTTATTCGAGCAGAACTAGGTCTACCTGGAACTTTTATTGGTGACGATCAAATTTACAACTTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCACGGATAAATAATATAAGTTTTTGATTACTACCACCTTCTCTTACCCTTCTTCTTTCTAGAGCAACTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611224 Dicrotendipes tritomus water mite diet isolate 9154-BHL032417-GBD19191_3476-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTTATTTTTGGAGCTTGATCCGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGTTGGGTCGACCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611225 Dicrotendipes tritomus water mite diet isolate 9162-BHL032417-GBD25409_12419-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCAACCTGGAACTTTTATTGGTAACGATCAAATTTACAATTTAATTGTTACAGCACATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTAACTCTACTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611226 Dicrotendipes tritomus water mite diet isolate 9164-BHL032417-GBD3793_16340-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTCGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGATCTTTGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTATTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGTGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611227 Dicrotendipes tritomus water mite diet isolate 9168-BHL032417-GBD29127_15740-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACCTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGCACTAGGTCGACCTGGAACTTTTATTGGTGTCGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTCGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTACTACTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611228 Dicrotendipes tritomus water mite diet isolate 9175-BHL032417-GBD20388_8064-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGTACTTCTCTATGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTGTTCCTCGAATAAATAATATAGGTGTTTGATTACTTCCTCCTTCTCTTACTCTACCTCTTTCTAGAACAAGTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611229 Dicrotendipes tritomus water mite diet isolate 9176-BHL032417-GBD27380_16654-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGTATAGTTGGTGCTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTATTGATTACTACCCCCTTCTCCTACTCTACATCTTTCTAGATCAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611230 Dicrotendipes tritomus water mite diet isolate 9180-BHL032417-GBD23644_20582-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAACTTACAACGTAATTGTTGCAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGTGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCATACTCGACTTCATTCTAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611231 Dicrotendipes tritomus water mite diet isolate 9182-BHL032417-GBD24778_24495-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAACTTTAATTGGAGGATTTGGAGATTGATTAGTTCCTTTAATATTAGGGTCTCCAGATATAGCTTTTCCTCGAATAAGTAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCCAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611232 Dicrotendipes tritomus water mite diet isolate 9198-BHL032417-GBD20959_11607-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTATTTATAGTTATACCAACTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCTCCTTCTCTTACACTACTATTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611233 Dicrotendipes tritomus water mite diet isolate 9203-BHL032417-GBD24615_11694-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTCCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGAGGCACCAGATATAGATGTCCCTCGGATAAATAATATAAGGTTTTGATTACTACCCCCTTCTCTTACTCTGCTACTTTCTAGATCAAGTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611234 Dicrotendipes tritomus water mite diet isolate 9205-BHL032417-GBD23376_26017-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGTGTCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTACACTTACTCTTCTGCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611235 Dicrotendipes tritomus water mite diet isolate 9207-BHL032417-GBD6148_7259-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCAACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTCCTCCCCCCTTCTCATACCCTCCTTCTTTCTAGACCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611236 Dicrotendipes tritomus water mite diet isolate 9208-BHL032417-GBD14776_27368-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATATTAATTCGAGCAGAACTAGGTCGCCCTGGAACTTTTATTGGTGACGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCGATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCTGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611237 Dicrotendipes tritomus water mite diet isolate 9212-BHL032417-GBD27676_16022-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTCTATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGCCGACCTGGAACTTTTATTGGAGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATACTTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGTCTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTACCTAGATCAATTGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611238 Dicrotendipes tritomus water mite diet isolate 9223-BHL032417-GBD21139_13682-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCCCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACCTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAAGAAGATAAGTTTTTGATTACTACCCCCTTCTCTTACGCTGCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGGACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611239 Dicrotendipes tritomus water mite diet isolate 9233-BHL032417-GBD29201_18572-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAGCTTTTATTGGAGATGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCAACAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTAACTCTACTACTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611240 Dicrotendipes tritomus water mite diet isolate 9238-BHL032417-GBD21293_8624-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTCTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTGTACTTATTCGAGCAGAACTAGGCCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCGTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR282179, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611241 Dicrotendipes tritomus water mite diet isolate 9244-BHL032417-GBD27513_19088-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAATATACTTATTCGAGCAGCTCTGGGGCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCCTACTCTACTACTTTCTAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611242 Dicrotendipes tritomus water mite diet isolate 9245-BHL032417-GBD13430_3760-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGATGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCTAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTCGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAACTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611243 Dicrotendipes tritomus water mite diet isolate 9247-BHL032417-GBD20301_25652-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTCCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATACGAGTAGAGCTGGCTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCATTTATAATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCTCCTTCTCTTACTCTACTACTTTCTAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611244 Dicrotendipes tritomus water mite diet isolate 9251-BHL032417-GBD9779_21622-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTGCCACGAATAAATAATATAAGTTTTTGAATACGTCCTCCTTCTCTTACACTACTTCTGTCTAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611245 Dicrotendipes tritomus water mite diet isolate 9255-BHL032417-GBD8939_20259-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGCGCTTGATCAGGAATAGTTGGAACTTCTCTATGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCGTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTGTTTGATTACTACCCCCTTCGCTTACTCTGCTTCTTTCTAGATCAAGAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611246 Dicrotendipes tritomus water mite diet isolate 9257-BHL032417-GBD27055_19173-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTACCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611247 Dicrotendipes tritomus water mite diet isolate 9260-BHL032417-GBD26889_10049-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCAAACTGGAACTTTTATTGGAGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGTGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTAACTCTACTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611248 Dicrotendipes tritomus water mite diet isolate 9263-BHL032417-GBD12374_7863-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGAATACTTATTCGAGCAGAGCTGGGTCGGCCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCTCTAACTCTACTACTTTCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611249 Dicrotendipes tritomus water mite diet isolate 9266-BHL032417-GBD16060_28288-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCCCCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTCTAACTCTTCTACTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611250 Dicrotendipes tritomus water mite diet isolate 9271-BHL032417-GBD22057_26483-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGGAGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTTCCCCCTTCTCTGACTCTTCTACTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611251 Dicrotendipes tritomus water mite diet isolate 9272-BHL032417-GBD20771_27441-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATCTCGTTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTCACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGTGTCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTCCCTCCTTCGCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611252 Dicrotendipes tritomus water mite diet isolate 9274-BHL032417-GBD27834_16635-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTGGGAAATTGATTAGTTCCTTTAATATTAGAGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGGTTTTGATGACTTCCTCCTTCTCTTACTCAACATCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611253 Dicrotendipes tritomus water mite diet isolate 9275-BHL032417-GBD14024_3649-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCTACCTGGAACTTTTATAGGTGACGATCAAATTTACAACGTAATTGTTACAGATCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGTATAAATAATATAAGTTTTTGATTACTCCCCCCTTCTCTTTCTCTTCTTCTTTCTCGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611254 Dicrotendipes tritomus water mite diet isolate 9276-BHL032417-GBD15758_4165-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTAATTCGAGCAGAACTAGGTCTACCTGGAACGTTTATTGGAGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCTCAAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCCTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611255 Dicrotendipes tritomus water mite diet isolate 9282-BHL032417-GBD22498_14074-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCCGGAATAGTTGGAACTTCTTTAAGTATACTTATTCGAGCAGAACTAGGACGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGTGCACCAGATATAGCATTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCCTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611256 Dicrotendipes tritomus water mite diet isolate 9306-BHL032417-GBD15713_28979-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGCCAACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCGATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR282179, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611257 Dicrotendipes tritomus water mite diet isolate 9314-BHL032417-GBD4058_22802-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCGTCTCTTACTCTACTACTATCTAGATCAATAGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611258 Dicrotendipes tritomus water mite diet isolate 9320-BHL032417-GBD4251_14461-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGTCCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCTCTTACTCTACTGCTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611259 Dicrotendipes tritomus water mite diet isolate 9331-BHL032417-GBD18571_28435-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTTAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTCTTGGTGACGATCAAATTTACAACGTTATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGCTAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTAACACTACTTCTTTCTAGATCAACTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611260 Dicrotendipes tritomus water mite diet isolate 9338-BHL032417-GBD8155_14413-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCTGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATATATAACGTACTTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTTGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGATTTTGATTACTACCACCTTCTCTTACTCTACTTCTTTCTAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611261 Dicrotendipes tritomus water mite diet isolate 9339-BHL032417-GBD9119_19726-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGTCCTGGAACTTTTATTGGTGACGATCAAATTTATAACGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTTCCTCGGATAAATAATATAAGTTTTTGATTTCTACCCCCTTCTCTAACTCTTCTTCTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR273898, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611262 Dicrotendipes tritomus water mite diet isolate 9356-BHL032417-GBD13004_18691-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGCTCAACCAGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTTTTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAAATCAGTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611263 Dicrotendipes tritomus water mite diet isolate 9357-BHL032417-GBD8202_12431-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTCACAACGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAACTGACTGGTCCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTCTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611264 Dicrotendipes tritomus water mite diet isolate 9360-BHL032417-GBD20621_25891-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATTCTTATTCGAGCAGAGCTGGGTCGAACAGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATACTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTGCCTCCTTCTCTAACTCTACTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611265 Dicrotendipes tritomus water mite diet isolate 9370-BHL032417-GBD24893_10475-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATACTTATTCGAGCAGAACTAGGCCGACCTGTAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAACTTTAATTGGAGGATTTGGGAATTGATTGTTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTTACTCTACTACTTTCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611266 Dicrotendipes tritomus water mite diet isolate 9383-BHL032417-GBD9796_22563-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGACAACCTGGATCTTTTATTGGTGACGATCAAATTTATAACGTAATTGTTGCAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCACTTACCCTACTTCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611267 Dicrotendipes tritomus water mite diet isolate 9389-BHL032417-GBD15602_3452-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACGTTATATTCCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTGATGCGAGCAGAGCTGGGTCGACCTGTAACTTTTATTGGGGACGATCTAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGTATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACCGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611268 Dicrotendipes tritomus water mite diet isolate 9390-BHL032417-GBD24257_21207-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTGCCCCCTACGCTTACTCATCTTCATTCTAGAGCAAGTGTAGAAGATGGAGCTGAAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611269 Dicrotendipes tritomus water mite diet isolate 9392-BHL032417-GBD21024_21350-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTGGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTAGGACCACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCTTTTAATATTAGGGGATCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611270 Dicrotendipes tritomus water mite diet isolate 9398-BHL032417-GBD16943_1930-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGTACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCACTTACACTACAACTATCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR155429, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611271 Dicrotendipes tritomus water mite diet isolate 9400-BHL032417-GBD23933_23380-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCCAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTTACAGCTCATGCTTTTCTTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTTGGGGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611272 Dicrotendipes tritomus water mite diet isolate 9410-BHL032417-GBD12799_8531-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGGCAACAGATATAGCTGTCCCTCTGATAAATAATATAAGTTTTTGATTACTACCCACTTCTCATACGCTTCTTCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611273 Dicrotendipes tritomus water mite diet isolate 9416-BHL032417-GBD28004_8925-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTCTATTTTTGGAGCTTGATCAGGAATGGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCAACCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATAATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTAACACTACTACTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611274 Dicrotendipes tritomus water mite diet isolate 9424-BHL032417-GBD27003_21786-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTTTAAGTATACTTATTCGAGCAGAGCTGGGTCGTGCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATAATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATCTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTAACTCTACTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611275 Dicrotendipes tritomus water mite diet isolate 9430-BHL032417-GBD28097_18885-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTAGCGATCAACTTTACAATGTACTTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATATTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCTCCTTCTCTTACTCTACTACTTTCTAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611276 Dicrotendipes tritomus water mite diet isolate 9433-BHL032417-GBD27236_21357-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAGGTATACTTATTCGAGCAGGACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTACTTCAATCTAGAACAATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611277 Dicrotendipes tritomus water mite diet isolate 9435-BHL032417-GBD23746_24727-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTCCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGGCCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAACATTAGGGGCTCCAGATATAGCTTTGCCTCGAATAAATAATATAAGTTTTTGATTACGTCCTCCTTCACTTACTCTACTTCTTGCTAGAGCAAGTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611278 Dicrotendipes tritomus water mite diet isolate 9436-BHL032417-GBD13666_8190-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTCGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTACACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAGTATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTATTGATTACGACCCCCTTCTCTTACACGTCATCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611279 Dicrotendipes tritomus water mite diet isolate 9438-BHL032417-GBD27496_20735-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATATTTATTCGAGCAGAACTAGGTCGACCTGGAGCTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTGCTCTAACCCTTCTTCCATCTAGGTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611280 Dicrotendipes tritomus water mite diet isolate 9440-BHL032417-GBD11748_15024-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTATGCTGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCACTTACCCTACTTCTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611281 Dicrotendipes tritomus water mite diet isolate 9441-BHL032417-GBD28339_21392-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATAATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCATTTACTCTATTACTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611282 Dicrotendipes tritomus water mite diet isolate 9444-BHL032417-GBD23525_25949-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGCATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCAGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCTCCAGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCGTCACTAACTCTACTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611283 Dicrotendipes tritomus water mite diet isolate 9447-BHL032417-GBD23224_10171-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATATTTATTCGAGCAGAGCTGGGTCACCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCACTTACTCTACTACTAGCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611284 Dicrotendipes tritomus water mite diet isolate 9453-BHL032417-GBD18363_11630-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTGCAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTCGATTACTACCTCCTTCTCTTACTCTACTTCTTTCTAAATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611285 Dicrotendipes tritomus water mite diet isolate 9459-BHL032417-GBD11239_19558-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTCCATTTTTGGAGCCTGATCAGGAATAGTTGGGACTTCTCTAAGTATATTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCTCCTTCTCTAACTCTACTTCTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611286 Dicrotendipes tritomus water mite diet isolate 9469-BHL032417-GBD28028_13575-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATTCTTATTCGAGCAGAACTATGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCATTTAATATTAGGGGCACCAGATATAGCATTCCCTCGGATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611287 Dicrotendipes tritomus water mite diet isolate 9470-BHL032417-GBD20140_24149-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATCCTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACCCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611288 Dicrotendipes tritomus water mite diet isolate 9471-BHL032417-GBD23873_16727-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCGGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTGTTTATAGTTATACCAATTTTAATCGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTAACTCGTCTTCTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611289 Dicrotendipes tritomus water mite diet isolate 9479-BHL032417-GBD13584_16248-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTTTAAGTATACTTATTCGGGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAGTTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCACTTACTCTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611290 Dicrotendipes tritomus water mite diet isolate 9491-BHL032417-GBD5257_7635-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCTGAACTAGGACGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATCTGGAAATTGATTAGTTCCTCTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTACTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611291 Dicrotendipes tritomus water mite diet isolate 9492-BHL032417-GBD9866_5600-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGATCAGAGCTGGGTCGACCTGTAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAACTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGATCCAGATATAGCTTCTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCGTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611292 Dicrotendipes tritomus water mite diet isolate 9493-BHL032417-GBD6140_20525-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGTATAGTTGGTGCTTCTCTAAGTATGCTTGTTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTTCTTCCTCCTTTTCTTACTCTACTTCTTTCTAGAGCAATTGTAGAAAATGGCGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611293 Dicrotendipes tritomus water mite diet isolate 9494-BHL032417-GBD19735_23211-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTCCATTTTTGGAGCTTGATCAGGAATAGTTGGTACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGTACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCACATGCTTTTAGTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTGTTGATTACTTCCTCCTTCTCTTACTCTACTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611294 Dicrotendipes tritomus water mite diet isolate 9499-BHL032417-GBD24422_22837-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATACTTATTCGAGCAGAATTAGGTCGATCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTTATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATAAAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCCTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611295 Dicrotendipes tritomus water mite diet isolate 9518-BHL032417-GBD17747_19085-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGCACTTCTCTAAGTATACTTATTCAAGTAGAACTAGGTCGACCTGGAACATTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCACATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTTACCCTACTTCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611296 Dicrotendipes tritomus water mite diet isolate 9519-BHL032417-GBD9083_26648-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGTAGAGCTGGGTCGACCTGGAGCTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGATGATTTGGGAATTGATTGGTTCCTTTAATATTAGAGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTCATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611297 Dicrotendipes tritomus water mite diet isolate 9521-BHL032417-GBD26051_13028-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTTAGTATACTTATTCGAGTTGAACTAGGACAACCTGGAACTTTTATTGGTGACGATCAAATTTATAACATAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTCTAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611298 Dicrotendipes tritomus water mite diet isolate 9522-BHL032417-GBD28144_12528-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCGGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCAACCTGGAACTTTTATTGTTGACGATCAAATTTACAACATAATTGTTACAGCTCATGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGACACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGACTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAGTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611299 Dicrotendipes tritomus water mite diet isolate 9526-BHL032417-GBD15620_7742-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTTATTTTTGGAGCTTGATCCGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGATCTGGGTCGACCTGGAACTTTTATTGGTGACGATAAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611300 Dicrotendipes tritomus water mite diet isolate 9531-BHL032417-GBD23151_8580-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCAACCTGGAACTTTTATTGGAGACGATCAAATTTACAACATAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGGATAAATAATATAGGTTTTTGATTACTACCCCCTTCTCTTACTCTACTACTTTCTAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611301 Dicrotendipes tritomus water mite diet isolate 9618-BHL032417-GBD4708_23930-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACCAGGTCGACCTGGAACTTTTACTGGTGACGATCAAATTTACAACGTAATCGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCCTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611302 Dicrotendipes tritomus water mite diet isolate 10710-BHL101516-GBD6267_23534-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGCCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTGTGATTACTTCCTCCTTCTCATACTCTACTTCTATCTAGAGCAATGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611303 Dicrotendipes tritomus water mite diet isolate 10712-BHL101516-GBD16360_1926-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTCTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCTCCTTCACTTACACTACGACTATCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611304 Dicrotendipes tritomus water mite diet isolate 10713-BHL101516-GBD3542_19547-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGATCTGGGTCGACCTGGAACTTTTATTGGGGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGCTTTTGATTTCTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGGGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611305 Dicrotendipes tritomus water mite diet isolate 10720-BHL101516-GBD10126_25053-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATATTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACGTCCGCCTTCTCTTACACTACATCTTTCTAGAGCAAGTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611306 Dicrotendipes tritomus water mite diet isolate 10721-BHL101516-GBD27200_12155-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTTTAAGTATACTTATTCGAGCAGAGCTGGGACGACCTGGAACTTTTATTGGAGACGATCAGATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCTCTTACTCTACTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611307 Dicrotendipes tritomus water mite diet isolate 10723-BHL101516-GBD23283_19166-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTCTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTATTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCGTCTCTAACTCTACTACTATCTAGATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611308 Dicrotendipes tritomus water mite diet isolate 10728-BHL101516-GBD16013_12856-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAATTGGAACTTCTCTAAGTATACTTATTCGAGCAGAGCTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCTCTTACCCTACTTCTATCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611309 Dicrotendipes tritomus water mite diet isolate 10730-BHL101516-GBD12000_21355-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGACAACCTGGAACTTTTATTGGAGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611310 Dicrotendipes tritomus water mite diet isolate 10734-BHL101516-GBD26853_13911-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGCAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATATTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCTCCTTCTCTTACCCTACTACTTTCTAGATCAACTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611311 Dicrotendipes tritomus water mite diet isolate 10735-BHL101516-GBD2997_19079-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTTGGGACTTCTTTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGATGACCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATGGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611312 Dicrotendipes tritomus water mite diet isolate 10737-BHL101516-GBD24898_22930-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTCGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTACCTCCTTCTCTAACTCTACTTCTTTCTAGAACAACTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611313 Dicrotendipes tritomus water mite diet isolate 10740-BHL101516-GBD12256_2455-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGAGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATAATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTACCTCCTTCTCTTACCCTACTACTTTCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611314 Dicrotendipes tritomus water mite diet isolate 10745-BHL101516-GBD8200_9757-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGCACTTCCTTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611315 Dicrotendipes tritomus water mite diet isolate 10746-BHL101516-GBD20565_7255-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGTGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGATACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGTGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACCTCTTGCGAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611316 Dicrotendipes tritomus water mite diet isolate 10747-BHL101516-GBD23776_6121-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGATCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTCTTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCATCTCTTACGCGACTTCTTGCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611317 Dicrotendipes tritomus water mite diet isolate 10752-BHL101516-GBD20994_2385-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTATTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTATTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAACATAAGTTTTTGATTACTTCCCCCATCTCTAACCCTACTTCTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611318 Dicrotendipes tritomus water mite diet isolate 10756-BHL101516-GBD20916_11277-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAACTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGAGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCTAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACCTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611319 Dicrotendipes tritomus water mite diet isolate 10760-BHL101516-GBD4400_19941-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATACTAGGGGCTCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCTCCTCTTACTCTACTTCTTTCTAGATCAACTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611320 Dicrotendipes tritomus water mite diet isolate 10762-BHL101516-GBD26635_11531-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTCTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGCACTGGAACTTTTATTGGTGACGTTCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAGATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTACTATCTAGACCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611321 Dicrotendipes tritomus water mite diet isolate 10766-BHL101516-GBD11245_17363-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACCTTATATTTCATTCTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTATTGATTACTTCCTCCTTCTCTTACTCTGCTTCTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611322 Dicrotendipes tritomus water mite diet isolate 10767-BHL101516-GBD18543_22757-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGTACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTACTCCTTCTCTTACTCTACCGCTGTCTAGATCAATTGTAGAAAAGGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611323 Dicrotendipes tritomus water mite diet isolate 10769-BHL101516-GBD7127_19393-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGAACTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCTCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTATCTAGATCACCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611324 Dicrotendipes tritomus water mite diet isolate 10774-BHL101516-GBD19001_10961-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGGTCCGGGATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGGTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTGGCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611325 Dicrotendipes tritomus water mite diet isolate 10778-BHL101516-GBD4514_23357-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATATTTCATTTTTGGAGCTTGATCAGGACTAGTTGGGATTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAACTTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTGTCTTACTCTACGTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611326 Dicrotendipes tritomus water mite diet isolate 10779-BHL101516-GBD25716_18730-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTTTAAGTATTCTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAATTTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAGTTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCACCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611327 Dicrotendipes tritomus water mite diet isolate 10780-BHL101516-GBD12406_21015-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTACCTCCTTCACTTACCCTACTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611328 Dicrotendipes tritomus water mite diet isolate 10783-BHL101516-GBD10654_8595-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGAGGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCGGGTATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTACCACCTTCTCTTACTCTACTACTTTCTAGAGCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611329 Dicrotendipes tritomus water mite diet isolate 10784-BHL101516-GBD26252_16364-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGTGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACGTCCTCCTTCTCTAACTCTACTTCGTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611330 Dicrotendipes tritomus water mite diet isolate 10785-BHL101516-GBD24975_19428-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTTTAATTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTCTTGACTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAAGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611331 Dicrotendipes tritomus water mite diet isolate 10794-BHL101516-GBD14349_3432-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGTCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611332 Dicrotendipes tritomus water mite diet isolate 10796-BHL101516-GBD17043_15107-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATATTTATTCGAGCAGAGCTGTCTCGACCTGGAACTTTTCTTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATTGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCTCCTTCTCTTACCCTACTTCTTTCTAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611333 Dicrotendipes tritomus water mite diet isolate 10799-BHL101516-GBD27807_13643-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGTCCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGCTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTTCCTCCTTCTCTAACTCTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611334 Dicrotendipes tritomus water mite diet isolate 10802-BHL101516-GBD5195_22370-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCCCTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAACTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTGTTCCTCGAATAAATAATATAAGGGTTTGATTACTTCCTCCTTCTCTTACTCTACTACTTTCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611335 Dicrotendipes tritomus water mite diet isolate 10804-BHL101516-GBD19031_25764-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGTACTTCTTTAAGTATACTTATTCGAGCAGAACTGGGTCAAACTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCACCTTCTCTTACTCTACTACTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611336 Dicrotendipes tritomus water mite diet isolate 10808-BHL101516-GBD24433_7450-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTCTAAGAATATTTATTCGAGCAGAGCTGGGTCTACCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTATTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611337 Dicrotendipes tritomus water mite diet isolate 10811-BHL101516-GBD20301_2488-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTAGGTCACCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTACTTCCTCCTTCTCTTACTTTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611338 Dicrotendipes tritomus water mite diet isolate 10812-BHL101516-GBD25942_7134-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGTACTTCTCTAAGTATACTTATTCGAGCAGAGCTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGGTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611339 Dicrotendipes tritomus water mite diet isolate 10814-BHL101516-GBD27232_21268-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAGTAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTTGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTTCTTCCTCCTTCTCTTACTCTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611340 Dicrotendipes tritomus water mite diet isolate 10819-BHL101516-GBD22901_18466-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACCTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAACTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGAGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTACTCTTACTCAACGTCAATCTAGATCAATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611341 Dicrotendipes tritomus water mite diet isolate 10823-BHL101516-GBD28043_15021-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGTATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGATCTGGGTCGAACTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCGTCTCTAACACTACTTCTTTCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611342 Dicrotendipes tritomus water mite diet isolate 10824-BHL101516-GBD26934_15619-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGTATAGTTGGGACTTCTTTAAGTATACTTATTCGAGCAGCGCTGGGTCGTCCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCACTTACTCTACTACTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611343 Dicrotendipes tritomus water mite diet isolate 10826-BHL101516-GBD27146_8196-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTGACTCTACTCCGTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611344 Dicrotendipes tritomus water mite diet isolate 10827-BHL101516-GBD4502_22781-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCTACCGGGAACTTTTATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTACTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611345 Dicrotendipes tritomus water mite diet isolate 10830-BHL101516-GBD11002_18597-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTTTAAGTATACTTATTCGAGCAGAGTTGGGACGACCAGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTTATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611346 Dicrotendipes tritomus water mite diet isolate 10832-BHL101516-GBD28577_13200-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATATTTATTCGAGCAGAGCTAGGACGATCTGGAACTTTTATTGGTGACGATCACATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611347 Dicrotendipes tritomus water mite diet isolate 10838-BHL101516-GBD14591_24716-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACATTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGAATACTTATTCGAGCAGAGTTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCTTTGACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611348 Dicrotendipes tritomus water mite diet isolate 10842-BHL101516-GBD28177_18855-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGAACTGGAGCTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTATTTCCTCCTTCTCTTACCCTACTTCTTGCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611349 Dicrotendipes tritomus water mite diet isolate 10845-BHL101516-GBD13517_4885-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTCTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCTAATTTACAATGTTATTGTTACAGCTCCTGCTTTTATTATCATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGCTCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611350 Dicrotendipes tritomus water mite diet isolate 10850-BHL101516-GBD15694_26603-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCCTTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTCTTCGAGCGGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTAAAGCTCATGCTTATATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCTCTTACTCTACTTCTTTCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611351 Dicrotendipes tritomus water mite diet isolate 10854-BHL101516-GBD5385_16259-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATTCTTATTCGAGCAGAGCTGGGTCGAACTGGATCTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTCGATTACTTCCTCCTTCTCTAACTCTACTACTTTCTAGATCAATAGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611352 Dicrotendipes tritomus water mite diet isolate 10855-BHL101516-GBD17318_5190-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGATCTGTAACTTTTATTGGGGACGATCTAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCACTTTTAATTGGAGGATTTGGAAATTTATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611353 Dicrotendipes tritomus water mite diet isolate 10860-BHL101516-GBD26695_18099-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTCGGAACTTCTCTAAGTATACTTATTCGAGCTGAACTAGGACAACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCTCCTTCTCTAACTCTACTACTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611354 Dicrotendipes tritomus water mite diet isolate 10864-BHL101516-GBD12898_20263-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTCTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGACGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCTCTTACTCTACCTCTTTCTAGATCAATGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611355 Dicrotendipes tritomus water mite diet isolate 10867-BHL101516-GBD7007_15186-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTAGGTCGACCAGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCGCTAACTCTACTACTTTCTAGAACAATTGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611356 Dicrotendipes tritomus water mite diet isolate 10868-BHL101516-GBD18493_6039-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCTGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCAACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTATTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCTCCAGATATAGCTTTACCTCGAATAAATAATATAAGATTTTGATTACTTCCTCCTTCTCTAACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611357 Dicrotendipes tritomus water mite diet isolate 10869-BHL101516-GBD23076_23175-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGATCTGGGTCGAACTGTCACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGACTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACGTCCTCCTTCTCGTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611358 Dicrotendipes tritomus water mite diet isolate 10870-BHL101516-GBD6355_20481-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGGGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCTCCAGATATAGCTTTTCCTCAAATAAATAATAAAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611359 Dicrotendipes tritomus water mite diet isolate 10873-BHL101516-GBD27874_10148-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGATCTGGAACTTTTATTGGTGACAATCATATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGTGGCTCCAGATATAGCTTTTCCTCGTATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTAACTCTACTACTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611360 Dicrotendipes tritomus water mite diet isolate 10875-BHL101516-GBD10074_15446-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATCTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGTGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCTCCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCTCTTACTCTACTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611361 Dicrotendipes tritomus water mite diet isolate 10877-BHL101516-GBD7615_11266-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTTTAAGTATATTTATTCGAGCAGAGTTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTATTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTATTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCACGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCGTACTCTACGTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611362 Dicrotendipes tritomus water mite diet isolate 10881-BHL101516-GBD8217_23937-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTAATTCGAGCAGAGTTAGGTCAACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611363 Dicrotendipes tritomus water mite diet isolate 10883-BHL101516-GBD21456_7888-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGTACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTGGGAAATTGATTAGTTCCTTTAATATTAGGTGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCACCTTCCCTTACGCGACTTCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611364 Dicrotendipes tritomus water mite diet isolate 10889-BHL101516-GBD5307_13261-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTCTTGGAGCTTGATCAGGAATAGTTGGGACTTCTTTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACATCTCATGCTTTTATTATAATTTTCTTTATAGTTATACAAATTTTAATTAGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCGCCTGCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611365 Dicrotendipes tritomus water mite diet isolate 10892-BHL101516-GBD6076_6153-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCTGAACTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTCATTGTTACAGCTCATGCTTTTATTATAATTTACTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCATTAATATTAGGTGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACCCTACTACTTTCTAGAGCAACTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611366 Dicrotendipes tritomus water mite diet isolate 10895-BHL101516-GBD13898_11551-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGCCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTCTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCGTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCACTAACTCTACTTCTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611367 Dicrotendipes tritomus water mite diet isolate 10897-BHL101516-GBD5945_22937-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGTTCATGATTTTATTATAATTTTATTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTTATTAGTTCCTTTAATATTAGAGGCTCCAGCTATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611368 Dicrotendipes tritomus water mite diet isolate 10898-BHL101516-GBD22734_10189-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTTTACTTATTCGAGCAGAGCTGGGTCAACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTACCTCCTTCTCTTACTCTACTTCATTCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611369 Dicrotendipes tritomus water mite diet isolate 10899-BHL101516-GBD26334_24407-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGACTCGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGATCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATATAATTGTTACAGCTCATGCTTTTATTATAATTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGTGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCACCTTCTCTTACTCAACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611370 Dicrotendipes tritomus water mite diet isolate 10902-BHL101516-GBD15303_6621-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGCACTTTTATCGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTACCACCTTCTCTTACTATACATCATTCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611371 Dicrotendipes tritomus water mite diet isolate 10909-BHL101516-GBD23606_17933-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGTGTCGAACTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGATTTTATTATAATTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACGTCCTCCTTCTCTTACGCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611372 Dicrotendipes tritomus water mite diet isolate 10910-BHL101516-GBD16521_4719-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCTACCTGTAACTTTTATTGTTGACGATCATATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTCTTTATAGTTATACCAATTTTAATTGTAGGATTTGGAAATTTATTAGTTCCTTTAATATTAGGGTCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGTAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611373 Dicrotendipes tritomus water mite diet isolate 10945-BHL101516-GBD8310_20878-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTACTTGTTACAGCTCATGCTTTTATTATAATTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTTGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTATTTCTAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611374 Dicrotendipes tritomus water mite diet isolate 11004-BHL110116-GBD17735_27572-Lq74 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGGGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGTACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTCTTTATAGTTATACCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTCGATTACTTCCTCCTTCTCTTACTCTACTACTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611375 Dicrotendipes tritomus water mite diet isolate 11020-BHL110116-GBD17827_12134-Lq75 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGTGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAGATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611376 Dicrotendipes tritomus water mite diet isolate 11027-BHL110116-GBD14199_12166-Lq76 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCCCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611377 Dicrotendipes tritomus water mite diet isolate 11158-BHL110116-GBD8580_26074-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTATTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTACTTCTTTCTAGATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611378 Dicrotendipes tritomus water mite diet isolate 11423-BHL101516-GBD10959_25430-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTTAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTACTTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCACCTTCTCTTACCCTACTACTTTCTAGAGCAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611379 Dicrotendipes tritomus water mite diet isolate 11457-BHL101516-GBD18543_6555-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTCTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCCTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGTTTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611380 Dicrotendipes tritomus water mite diet isolate 11497-BHL101516-GBD6135_13649-Lq80 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGTCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACCTTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611381 Dicrotendipes tritomus water mite diet isolate 11618-BHL101516-GBD17224_9752-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTACATTCTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCATACACTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611382 Dicrotendipes tritomus water mite diet isolate 11774-BHL101516-GBD8892_15862-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTGGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611383 Dicrotendipes tritomus water mite diet isolate 12679-BHL040517-GBD20379_15840-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTGCTCTTACTCTTCTTCTTTCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611384 Dicrotendipes tritomus water mite diet isolate 12752-BHL040517-GBD22439_14526-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTATTTCCTTTAATATTAGGTGCGCCAGATATAGCTTTTCCTCGGATAAATAATATAAGATTTTGATTACTCCCCCCTTCTCTTACTCTACTTCTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR277564, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611385 Dicrotendipes tritomus water mite diet isolate 12869-BHL040517-GBD27411_11490-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611386 Dicrotendipes tritomus water mite diet isolate 14551-BHL040517-GBD16305_27121-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAAAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611387 Diptera sp. water mite diet isolate 1781-BHL110116-GBD10770_20808-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACAACCTGGAGCATTCATTGGAGATGACCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTATGATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCACTTACACTATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID KJ496572, identified in GenBank as Diptera environmental sample. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611388 Diptera sp. water mite diet isolate 1929-BHL022317-GBD14211_22403-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGTCGCCCCGGGACTTTTATTGGAGATGATCAAATTTATAATGTGATTGTAACAGCTCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTCTAATACTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTAACCCTACTTCTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.6% identical to accession ID KT895423, identified in GenBank as Anopheles minimus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611389 Diptera sp. water mite diet isolate 1984-BHL022317-GBD27537_16717-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGCGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGGCCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGCAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.7% identical to accession ID KT594079, identified in GenBank as Anastrepha canalis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611390 Diptera sp. water mite diet isolate 1988-BHL022317-GBD24526_6609-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGACTTGATCTGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGA-CTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTAATACTAGGGGCTCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTAACCCTTCTACTTTCAAGAACAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.6% identical to accession ID MF381737, identified in GenBank as Anopheles pseudotibiamaculatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611391 Diptera sp. water mite diet isolate 1997-BHL022317-GBD25928_11502-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTCGGGGCCTGATCTGGAATAGTGGGAACTTCTTTAAGAATGTTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAAAGTGATTGTTACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTATTTCCTCTAATACTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCATCCCTAACCCTTCTACTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.4% identical to accession ID KY646204, identified in GenBank as Ochlerotatus refiki. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611392 Diptera sp. water mite diet isolate 2024-BHL022317-GBD7516_20331-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCTTTAAGAATGTTTATTCGGGTAGAATTAGGACGCCCCGGGACAGTTATTGGAGAAGACCAAATTTATAATGTGATTGTTACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGGTTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCATCCCTAACCCTTCTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.6% identical to accession ID KR014851, identified in GenBank as Anopheles maculipalpis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611393 Diptera sp. water mite diet isolate 2040-BHL022317-GBD21292_20022-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAGCATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGA-CTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCGTAGTAATACCTATTTTAATTGGAGGCTTCAGAAATTGATTAGTTCCTCTTATACTAGGAGCTCCTGATACAGCATTCCCTCGAATAAATAATATAAGATTTTGAATACTTCCCCCATCCCTTACCCTACTTCTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID JF966741, identified in GenBank as Anopheles fluviatilis T. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611394 Diptera sp. water mite diet isolate 2097-BHL072216-GBD13229_5938-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCTTATACTTTATTTTCGGAGCTTGATCTGGAATAGTCGGAACTTCTTTAAGTATATTAATCCGTGCAGAATTAGGACACCCGGGAACTTTAATCGGAGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.0% identical to accession ID KM389470, identified in GenBank as Anopheles dthali. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611395 Diptera sp. water mite diet isolate 2384-BHL072216-GBD24650_16272-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACCTTATACTTTATTTTCGGAGCTTGATCTGGAATAGTCGGAACTTCTTTAAGTATATTAATCCGTGCAGAATTAGGACACCCGGGAACTTTAATCGGAGATGATCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATGATTTTCTTCATAGTTATGCCTATTTTAATTGGGGGCTTTGGGAATTGATTAGTTCCCCTAATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.5% identical to accession ID KM389466, identified in GenBank as Anopheles sacharovi. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611396 Diptera sp. water mite diet isolate 2433-BHL072216-GBD25798_24321-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACTTTATATTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGGCATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGGGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTGCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.4% identical to accession ID KM389466, identified in GenBank as Anopheles sacharovi. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611397 Diptera sp. water mite diet isolate 2446-BHL072216-GBD11614_20911-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAAAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGGGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KM389466, identified in GenBank as Anopheles sacharovi. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611398 Diptera sp. water mite diet isolate 2508-BHL072216-GBD25610_23543-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGATCATTATATTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCCTTAAGCATGTTTATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCATTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGAGGCTTTGGGAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTC-TCTTACTTTCTAGAACAATAGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.3% identical to accession ID HQ877374, identified in GenBank as Anopheles minimus C. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611399 Diptera sp. water mite diet isolate 2544-BHL072216-GBD14510_25929-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTCTTTATGGTTATACCTATTCTTATTGGTGGGTTTGGAAATTGGTTGGTTCCTTTAATGTTAGGGGCTCCTGATATGGCCTTCCCTCGTTTAAATAATTTAAGATTTAGGTTACTTCCTCCTTCTTTAACTTTACTTTTAGTTGGTAGGGCTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.4% identical to accession ID KU932145, identified in GenBank as Potamia littoralis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611400 Diptera sp. water mite diet isolate 2565-BHL072216-GBD27647_11566-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTATACTTTATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGCCCAGGAACTTTTATTGGAGATGACCAAATCTATAATGTAATTGTCACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAATTCCTTTAATATTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTTCTACTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID MF381737, identified in GenBank as Anopheles pseudotibiamaculatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611401 Diptera sp. water mite diet isolate 4995-BHL032417-GBD9077_8247-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID MF511748, identified in GenBank as Ophyra spinigera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611402 Diptera sp. water mite diet isolate 5061-BHL032417-GBD9907_9969-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATTTTCGGAGCTTGATCGGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATATCTATTTTAATTGAAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID EU493571, identified in GenBank as Chymomyza procnemis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611403 Diptera sp. water mite diet isolate 5794-BHL032417-GBD7709_15557-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCCTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCTATCTTTAACTCTTCTTCTTTCTAATTCAT-TTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.6% identical to accession ID KR262681, identified in GenBank as Toxonevra carterosoma. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611404 Diptera sp. water mite diet isolate 5816-BHL032417-GBD12422_24943-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGCACTTCCTTAAGTATACTTATTCGAGCAGAGTTAGGACGGCCAGGAACTTTTATTGGTGACGACCAATTTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAATTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.4% identical to accession ID KR262649, identified in GenBank as Neosilba zadolicha. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611405 Diptera sp. water mite diet isolate 5889-BHL032417-GBD5495_17735-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTTTATATTTATTTTTGGTGCATGATCAGGAATAATTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATCGGAGATGACCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTATAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.5% identical to accession ID KX161627, identified in GenBank as Lucilia sericata. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611406 Diptera sp. water mite diet isolate 6280-BHL032417-GBD10331_6696-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGTCATCCTGGAACTTTTATTGGTGACAACCAAATTTATAATGTTATTGTAATAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.6% identical to accession ID HM022405, identified in GenBank as Anopheles peryassui. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611407 Diptera sp. water mite diet isolate 9992-BHL040517-GBD9384_10874-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611408 Diptera sp. water mite diet isolate 10160-BHL040517-GBD8003_14290-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTTCATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTA	Using NCBI BLASTN in June 2018, this sequence was 89.5% identical to accession ID KY288015, identified in GenBank as Simulium dycei. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611409 Diptera sp. water mite diet isolate 10340-BHL040517-GBD2027_13802-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACCCTATATTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGGGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGTATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.5% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611410 Diptera sp. water mite diet isolate 10410-BHL040517-GBD16211_5868-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGGTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCCCCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTCCCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.5% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611411 Diptera sp. water mite diet isolate 10481-BHL040517-GBD16650_9955-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTCGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID FN395192, identified in GenBank as Culex torrentium. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611412 Diptera sp. water mite diet isolate 10491-BHL040517-GBD16580_18417-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTCTTAGTGATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.8% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611413 Diptera sp. water mite diet isolate 10517-BHL040517-GBD23045_6283-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTCAACAAATCATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTATGAATGCTTATTCGCGCAGAATTAGGACGACCCGGAACTTTCATTGGATATGACCATATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGTCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACGACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611414 Diptera sp. water mite diet isolate 10534-BHL040517-GBD11392_6680-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATACACTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTACTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.9% identical to accession ID AF425847, identified in GenBank as Culex tarsalis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611415 Diptera sp. water mite diet isolate 11281-BHL110116-GBD6839_10644-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTTCATTATACTTCATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTACTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTCGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAG--CAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID JF966742, identified in GenBank as Anopheles claviger. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611416 Diptera sp. water mite diet isolate 11865-BHL101516-GBD22341_25385-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAG--CAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.9% identical to accession ID MF381726, identified in GenBank as Anopheles darlingi. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611417 Diptera sp. water mite diet isolate 12528-BHL040517-GBD21401_18411-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGGACACTTTACTTTATTTTTGGAGCTTGATCCGGAATAGTAGGAACATCTTTAAGAATATTAATTCGAGCAGAATTAGGGCACCCAGGAACATTGATTGGGGATGATCAAATTTACAATGTAATTGTAACAGCCCATGCTTTTATTATATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.6% identical to accession ID KR262649, identified in GenBank as Neosilba zadolicha. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611418 Diptera sp. water mite diet isolate 13267-BHL040517-GBD21032_9796-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGACTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCAATAACCTTGCTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.6% identical to accession ID KR262681, identified in GenBank as Toxonevra carterosoma. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611419 Diptera sp. water mite diet isolate 13335-BHL040517-GBD16503_2746-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTATTTTTGGAGCCCGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACTCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 89.1% identical to accession ID KM455055, identified in GenBank as Philophylla caesio. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611420 Diptera sp. water mite diet isolate 14254-BHL040517-GBD3275_13435-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACATTATATTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATGGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATGGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID MF381706, identified in GenBank as Anopheles eiseni geometricus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611421 Diptera sp. water mite diet isolate 14667-BHL040517-GBD26712_23886-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTATCGCTCATGCATTTGTAATAATTTTTTTTATAATTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACACTATTATTAGCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.8% identical to accession ID KX161505, identified in GenBank as Pollenia rudis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611422 Diptera sp. water mite diet isolate 14682-BHL040517-GBD21252_5404-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGA-CATTGATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGACTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACACTATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID KU932128, identified in GenBank as Azelia zetterstedtii. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611423 Diptera sp. water mite diet isolate 14684-BHL040517-GBD15535_2623-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATAGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACACTATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 88.5% identical to accession ID KU728953, identified in GenBank as Rhinoleucophenga punctulata. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611424 Diptera sp. water mite diet isolate 14706-BHL040517-GBD17504_25747-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAAAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATAGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGATTCTGACCACTACCACCTTCACTTACACTATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.8% identical to accession ID KJ496572, identified in GenBank as Diptera environmental sample. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611425 Diptera sp. water mite diet isolate 14747-BHL040517-GBD26521_21325-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCGTCACTAACACTAGTATTAGGAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID EU493679, identified in GenBank as Scaptomyza frustulifera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611426 Diptera sp. water mite diet isolate 14787-BHL040517-GBD13753_27128-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTAGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTGTAATTGGTGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGCATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTAACACGATGATTAGTAAGAAGTACAGTAGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID KR262659, identified in GenBank as Prochyliza xanthostoma. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611427 Diptera sp. water mite diet isolate 14829-BHL040517-GBD21167_20122-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTCGGACACCCTGAAACATTAATTGGAGACGAACAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGTATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTGCTTCCTCCTTCACGTACACTATTATTAGTAAGAAGTATAGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.1% identical to accession ID AY788423, identified in GenBank as Ceratitis curvata. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611428 Diptera sp. water mite diet isolate 14870-BHL040517-GBD22710_23434-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACACTTTATTTTATTTTTGGAGCATGATCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGATCAAATTTATAATATAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTCCCACGAATAAATAATATAAGTTTTTGACTACTTCCTCCTTCACTTACACTATTATTAGCAAGAAGTCTAGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.1% identical to accession ID KJ496572, identified in GenBank as Diptera environmental sample. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611429 Diptera sp. water mite diet isolate 14970-BHL040517-GBD24080_4822-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATTAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTAGTGCTGAATTAGGACACCCTGAAGCACTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGATCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATAATAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTACCTCCTTCACATACACTATTATTAGTAAGAAGTATAGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID AY788423, identified in GenBank as Ceratitis curvata. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611430 Diptera sp. water mite diet isolate 15002-BHL040517-GBD20969_22250-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACACTTTATTTTATATTTGGAGCATGAGCAGGAATATTCGGAACTTCTCTTAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATAATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGATTTTGACTACTACCTCCTTCACTAACACTATTATGAGCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID AY788423, identified in GenBank as Ceratitis curvata. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611431 Diptera sp. water mite diet isolate 15025-BHL040517-GBD23274_12361-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATAGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.3% identical to accession ID MF381608, identified in GenBank as Anopheles darlingi. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611432 Diptera sp. water mite diet isolate 15104-BHL040517-GBD26996_14255-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATTTTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTAAATTAGGACACCCTGGAGCATTAATTGTAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCAGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTACTTCCTCCTTCACTTACCCTATTATTATCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID MF381608, identified in GenBank as Anopheles darlingi. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611433 Diptera sp. water mite diet isolate 15155-BHL040517-GBD11930_21319-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACAAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACAATATTAT---CTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.6% identical to accession ID KJ496572, identified in GenBank as Diptera environmental sample. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611434 Diptera sp. water mite diet isolate 15193-BHL040517-GBD6698_21556-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAGTAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAACAATATAAGTTTCTGACTATTACATCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.7% identical to accession ID HQ011959, identified in GenBank as Apsiphortica longiciliata. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611435 Diptera sp. water mite diet isolate 15224-BHL040517-GBD27195_22610-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACACTTTATTTTATCTTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACATCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTTATAATTTTTTTTATAGTTATACCAATTTTAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCGCTCTTACACTACTTCTT--TCAAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.0% identical to accession ID KJ496572, identified in GenBank as Diptera environmental sample. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611436 Diptera sp. water mite diet isolate 15252-BHL040517-GBD9158_8138-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACACTTTATTTTATTTTTGGAGCATGATCAGGAATAGTCGGAACTTCTTTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGATGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGAGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACTAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCACTTACACTATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KJ496572, identified in GenBank as Diptera environmental sample. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611437 Diptera sp. water mite diet isolate 15278-BHL040517-GBD5888_8788-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATCATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACACTATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID KU932128, identified in GenBank as Azelia zetterstedtii. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611438 Drosophila sp. water mite diet isolate 1920-BHL022317-GBD20166_13929-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACATTATATTTTATTTTTGGGACTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCTCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTAATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGAATACTACCCCCATCCCATA-CCCTTCTTCTGTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.7% identical to accession ID KJ841760, identified in GenBank as Scaptodrosophila sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611439 Drosophila sp. water mite diet isolate 1951-BHL022317-GBD29705_15976-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCCTTAAGAATGCTTATTCGGGCAGAACTAGGACGACCCGGGACCTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCTCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTCGGAAATTGATTAGTTCCTCTAATACTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTAACCCTTCTACTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.3% identical to accession ID KJ841760, identified in GenBank as Scaptodrosophila sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611440 Drosophila sp. water mite diet isolate 1965-BHL022317-GBD24934_10584-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGATCTGGTATAGTGGGAACATCTTTAAAAATGTTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTAATGGAGATGACCAAATTTATAATGTGATTGTAACAGCTCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTA-CCCTACTACTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.5% identical to accession ID KJ841760, identified in GenBank as Scaptodrosophila sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611441 Drosophila sp. water mite diet isolate 1969-BHL022317-GBD10885_24151-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAGTTCGGACGACCCGGGA-CTTTTATTGGAAATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGGTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTACTACTAACAAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.2% identical to accession ID EU493613, identified in GenBank as Drosophila paramelanica. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611442 Drosophila sp. water mite diet isolate 1975-BHL022317-GBD17720_23439-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCCTGATCTGGAATAGTGGGAACATCTTTAAGAATTCTTATTCGGGCAGAATTAGGACGACCCGGGA-CTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTTTTATAATTTTTTTCATAGTAATACCTATTCTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCTTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCAAACCCTACTACTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID EU493661, identified in GenBank as Drosophila kambysellisi. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611443 Drosophila sp. water mite diet isolate 1990-BHL022317-GBD17179_23456-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAACTCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATTTTTATTCGGGCAGAATTCGGACGACCCGGGACTTTTATTGGAGATGATCAAATTTATAATGTGATTGTAACAGCACACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTAACCCTACTACTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.4% identical to accession ID KJ841760, identified in GenBank as Scaptodrosophila sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611444 Drosophila sp. water mite diet isolate 1991-BHL022317-GBD27380_15671-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAACTAGGACGACCCGGGACCTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTATAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCAAACCCTACTACTAACAAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID KJ841760, identified in GenBank as Scaptodrosophila sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611445 Drosophila sp. water mite diet isolate 1995-BHL022317-GBD9717_20891-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACAACCAGGGTCATTTATTGGAGATGACCAAATTTATAATGTGATTGTTACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTCTAATACTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTGCCCCCATCCCTTACCCTACTACTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.6% identical to accession ID EU493613, identified in GenBank as Drosophila paramelanica. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611446 Drosophila sp. water mite diet isolate 2001-BHL022317-GBD10732_10224-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGTTTATTCGGGCAGAATTAGGACGACCCGGGTCTTTTATTGGAGATGATCAAATTTATAATGTGATTGTTACAGCACACGCATTTATTATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTTTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTA-CCCTTCTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.3% identical to accession ID KJ841760, identified in GenBank as Scaptodrosophila sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611447 Drosophila sp. water mite diet isolate 2026-BHL022317-GBD7398_17622-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCTTTGAGAATGTTTATTCGGGCAGAATTAGGACGCCCCGGGACTTTTATTGGAGATGATCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCATCACTTACCCTACTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.7% identical to accession ID KJ841760, identified in GenBank as Scaptodrosophila sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611448 Drosophila sp. water mite diet isolate 2035-BHL022317-GBD11202_19793-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGACTTGATCTGGAATAGTGGGCACTTCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCAGGGTCTTTTATTGGAGATGATCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATAATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTACCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCATCCCTTA-CCCTTCTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.5% identical to accession ID KJ841760, identified in GenBank as Scaptodrosophila sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611449 Drosophila sp. water mite diet isolate 2053-BHL022317-GBD15738_27403-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGACTTGATCTGGAATAGTGGGAACTTCTTTAAGACTGCTTATTCGGGCAGAATTAGGACGACCCGGGA-CTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCAGCCCTTACCCGACTTCTTGCAAGAGCAAGAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.6% identical to accession ID EU493613, identified in GenBank as Drosophila paramelanica. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611450 Drosophila sp. water mite diet isolate 2661-BHL072216-GBD16843_25579-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACTTTATATTTCATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.0% identical to accession ID DQ471590, identified in GenBank as Drosophila lacertosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611451 Drosophila sp. water mite diet isolate 3012-BHL032417-GBD6384_16032-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAATTTTATAATGTTGTAGTTACTGTACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATATTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.0% identical to accession ID AY750090, identified in GenBank as Drosophila lacertosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611452 Drosophila sp. water mite diet isolate 3650-BHL032417-GBD22458_6116-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATACATTATTTTTGGGGCGTGATCCGGAATAGTGGGAACTTCATTAACAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACCTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.6% identical to accession ID AY750090, identified in GenBank as Drosophila lacertosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611453 Drosophila sp. water mite diet isolate 5808-BHL032417-GBD22133_17549-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTTTAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID EU493661, identified in GenBank as Drosophila kambysellisi. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611454 Drosophila sp. water mite diet isolate 7017-BHL032417-GBD15516_23435-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATCGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTCTATTATAATTTTTTTTATAGTAATACCTATCTTAATTGGAGGATTTGGAAGTTGGTTATTATCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.0% identical to accession ID AY750090, identified in GenBank as Drosophila lacertosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611455 Drosophila sp. water mite diet isolate 7059-BHL032417-GBD11662_11423-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGGTTAATACCACTAATATTAGGAGCCCCTGATGTGGCTTTTCCACGAATAAATAATATAGGATTTTGATTATTACCCCCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID AY750090, identified in GenBank as Drosophila lacertosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611456 Drosophila sp. water mite diet isolate 7069-BHL032417-GBD27448_18024-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATACATTATTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTGGAGCAGAATTAGGACGACCCGGAGCTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATGTTAGGAGCCCCTGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTGCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.1% identical to accession ID AY750090, identified in GenBank as Drosophila lacertosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611457 Drosophila sp. water mite diet isolate 10214-BHL040517-GBD9271_8797-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGAGTACCAAATTTATAATGTAATTGTTACAGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTG--CTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.2% identical to accession ID JF416733, identified in GenBank as Stegana saigusai. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611458 Drosophila sp. water mite diet isolate 10309-BHL040517-GBD6029_23218-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTTGAGCTAAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAAATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTG--CTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 81.0% identical to accession ID JF416733, identified in GenBank as Stegana saigusai. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611459 Drosophila sp. water mite diet isolate 14558-BHL040517-GBD10027_3215-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACATTATATTTTATTTTCGGAGCTTGAGCGGGAATAGTAGGAACTTCTCTTAGTATTTTAATTCGAGCAGAATTAGGACATCCAGGTGCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTATAATTGGAGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTCCCCTCGAATGAATAATATAAGATTTTGACTTCTTCCCCC--CTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID AB669760, identified in GenBank as Drosophila pectinifera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611460 Drosophila sp. water mite diet isolate 14813-BHL040517-GBD27509_11752-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATTTTTGGAGCCTGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGATACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCGCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCACTAACACTATTATTAGCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID EU493627, identified in GenBank as Drosophila malerkotliana. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611461 Drosophila sp. water mite diet isolate 15057-BHL040517-GBD22411_24619-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTTTATTTTATTTTTGGAGCATGAGCAGGAATAGTCGGAACTTCTTTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTATAATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACACTATTATTAGCAAGAAGTATAGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID EU493627, identified in GenBank as Drosophila malerkotliana. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611462 Drosophila sp. water mite diet isolate 15110-BHL040517-GBD10708_2888-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATACAATATTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGACTGCTGATCCGAGCAGAATTAGGACGACCCGGAACTTTCCTTGGAGATGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCGTCACTTACACTATTATTAGTAAGAAGTAGAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.0% identical to accession ID EU493653, identified in GenBank as Drosophila eurypeza. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611463 Drosophila sp. water mite diet isolate 15168-BHL040517-GBD18677_25523-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACACTTTATTTTATATTTGGAGCATGAGCATGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAACTATGACACCCTGGATCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGATTTTGACTACTTCCTCCTTCACTAACACTATTATTAGTAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID EU493627, identified in GenBank as Drosophila malerkotliana. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611464 Erebidae sp. water mite diet isolate 5311-BHL032417-GBD9982_8332-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACATTAGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.1% identical to accession ID KC571061, identified in GenBank as Cyana meyricki. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611465 Eutrichota sp. water mite diet isolate 14322-BHL040517-GBD14975_9872-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACATTATATTTTATTTTCGGAACTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCGCCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTAATACCTATTATAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATGAATAATATAAGTTTTTGATTACTACCTCCTTCTCTTACCTTACTTTTAGTAAGCAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID GQ409325, identified in GenBank as Eutrichota paratunicata. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611466 Glyphodes sp. water mite diet isolate 8934-BHL032417-GBD27178_17651-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTTCTTTATATTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGAGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KM576860, identified in GenBank as Glyphodes pyloalis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611467 Glyptotendipes meridionalis water mite diet isolate 9277-BHL032417-GBD25279_13384-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACATTATATTTTATTTTTGGGGCACGATCAGGAATAGTTGGGACTTCTTTAAGAATGCTTATTCGAGCTGAACTAGGACAACCAGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACTGCACATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTATTTGGAGGGTTTGGAAATTGACTAGTTCCTTTAATATTGGGGGCCCCTGATATAGCTTTCCCGCGAATAAATAATATAAGTTTTTGACTATTACCTCCTTCTTTAACTCTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KP954649, identified in GenBank as Glyptotendipes meridionalis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611468 Glyptotendipes meridionalis water mite diet isolate 9303-BHL032417-GBD23282_8518-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACCTTATATTTTATTTTTGGGGCATGATCAGGAATAGTTGGGACTTCTTTTAGAATGCTTATTCGAGCTGAACTAGGACCACCAGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACTGCACATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTATTTGGAGGGTTTGGAAATTGACTAGTTCCTTTAATATTGGGGGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTGCTTTAACCCTTTTACTATCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KP954649, identified in GenBank as Glyptotendipes meridionalis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611469 Glyptotendipes senilis water mite diet isolate 6640-BHL032417-GBD20075_26030-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATATTGGCACATTATATCTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACGTCTTTAAGTATGCTAATTCGAGCAGAAATAGGACGACCTGGAACTTTTATTGGAGATGACCAGATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATATTTTTTTTTATAGTTATACCTATTTTAATTGGGGAATTTGGAAATTGATTAGTCCCTCTTATGCTGGGAGCTCCTGATAAGGCTTTCCCCCGAATAAATAATATAAATTCTTGGCTTCTCCCTCCTTCTTTAACTCTTCTTCTTTCTAGTTCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KP954645, identified in GenBank as Glyptotendipes senilis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611470 Glyptotendipes sp. water mite diet isolate 3486-BHL032417-GBD20951_25316-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATATTGGCACATTATATCTTATTTTTGGGGCTTGATCCGGAATAGCGGGAACGTCTTTAAGTATGCTAATTCGAGCAGAAATAGGACGACCTGGAACTTTTATTGGAGATGACCAGATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATATTTTTTTTTTTTATAGTTATACCTATTTTAATTGGGGAATTTGGAAATTGATTAGTCCCTCTTATGCTGGGAGCTCCTGATAAGGCTTTCCCCCGAATAAATAATATAAATTCTTGGCTTCTCCCTCCTTCTTTAACTCTTCTTCTTTCTAGTTCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KP954645, identified in GenBank as Glyptotendipes senilis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611471 Glyptotendipes sp. water mite diet isolate 3581-BHL032417-GBD16831_21432-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATATTGGCACATTATATCTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACGTCTTTAAGTATGCTAATTCGAGCAGAAATAGGACGACCTGGAACTTTTATTGGAGATGACCAGATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCGGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACT-TTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KP954645, identified in GenBank as Glyptotendipes senilis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611472 Glyptotendipes sp. water mite diet isolate 3596-BHL032417-GBD18008_24584-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATATTGGAACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGGGAATTTGGAAATTGATTAGTCCCTCTTATGCTGGGAGCTCCTGATAAGGCTTTCCTCCGAATAAATAATATAAATTCTTGGCTTCTCCCTCCTTCTTTAACTCTTCTTCTTTCTAGTTCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.7% identical to accession ID KP954645, identified in GenBank as Glyptotendipes senilis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611473 Glyptotendipes sp. water mite diet isolate 3662-BHL032417-GBD18564_19933-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATATTGGCACATTATATCTTATTTTTGGGGCTTGATCCGGAATAATGGGAACGTCTTTTAGTATGCTAATTCGAGTAGAAATAGGACGACCTGGAACTTTTATTGGAGATGACCAGATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGAATTTGGAAATTGATTAGTCCCTCTTATGCTGGGAGCTCCTGATAAGGCTTTCCCCCGAATAAATAATATAAAATCTTGGCTTCTACCTCCTTCTTTAACCCTACTTCTTTCTAGTTCAATAGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KP954645, identified in GenBank as Glyptotendipes senilis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611474 Glyptotendipes sp. water mite diet isolate 3850-BHL032417-GBD6904_5178-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATATTGGCACATTATATCTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACGTCTTTAAGTATGCTAATTCGAGCAGAAATAGGACGACCTGGAACTTTTATTGGAGATGACCAGATTTATAATGTTATTGTAACAGCTCACGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCAAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCTCTTACATTACTACTTTCAATTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KP954645, identified in GenBank as Glyptotendipes senilis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611475 Glyptotendipes sp. water mite diet isolate 3982-BHL032417-GBD14105_23681-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATATTGGAACACTATATTTTATTTTCGGGGCTTGATCCGGAATAGTGGGAACGTCTTTAAGTATGCTAATTCGAGCAGAAATAGGATGACCTGGAACTTTTATTGGAGATGACCAGTTTTATAATGTTAGTGTAACAGCTCACGCTTTTATTATATTTTTTTTTGTAGTTATACCTATTTTAATTGGGGAATTTGGATATTGATTAGTCCCTCTTATGCTGGGAGCTCCTGATAAGGCTTTCCCCCGAATAAATAATATAAATTCTTGGCTTCTCCCTCCTTCTTTAACTCTTCTTCTTTCTAGTTCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KP954645, identified in GenBank as Glyptotendipes senilis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611476 Glyptotendipes sp. water mite diet isolate 3987-BHL032417-GBD18023_24827-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATATTGGCACATTATATCTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACGTCTTTAAGTATGCTAATTCGAGCAGAAATAGGACGACCTGGAACTTTTATTGGAGATGACCAGATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATATATAATATAAGTTTTTGAGTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAAAGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KP954645, identified in GenBank as Glyptotendipes senilis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611477 Glyptotendipes sp. water mite diet isolate 4043-BHL032417-GBD14728_10669-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATATTGGAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGAGATGACCAGATTTATAATGTTATTGTAACAGCTCACGCTTTCATTATATTTTTTTTTATAGTTATACCTATTTTAATTGGGGAATTTGGAAATTGATTAGTCCCTCTTATGCTGGGAGCTCCTGATGAGGCTTTCCCCCGAATAAATAATACAAGTTTTTGATTATTACCCCCTTCATTAACT-TTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.1% identical to accession ID KP954645, identified in GenBank as Glyptotendipes senilis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611478 Glyptotendipes sp. water mite diet isolate 8996-BHL032417-GBD4161_12664-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACCTTATATTTATTTTTGGGGCATGATCAGGAATTGTTGGGACTTCTTTAAGAATGCTTATTCGAGCTGAACTAGGACGACCAGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACTGCACATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTATTTGGAGGGTTTGGAAATTGACTAGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.4% identical to accession ID KP954649, identified in GenBank as Glyptotendipes meridionalis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611479 Glyptotendipes sp. water mite diet isolate 9021-BHL032417-GBD16839_20530-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACCTTATATTTATTTTTGGGGCATGATCAGGAATAGTTGGGACTTCTTTAAGAATGCTTATTCGAGCTGAACTAGGACGACCAGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACTGCACATGCATCTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.4% identical to accession ID KP954649, identified in GenBank as Glyptotendipes meridionalis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611480 Glyptotendipes sp. water mite diet isolate 9202-BHL032417-GBD21946_16295-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACCTTATATTTATTTTTGGGGCATGATCAGGAATAGTTGGGACTTCTTTAAGAATGCTTATTCGAGCTGAACTAGGACGACCAGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACTGCACATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTTTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954649, identified in GenBank as Glyptotendipes meridionalis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611481 Glyptotendipes sp. water mite diet isolate 9236-BHL032417-GBD13358_16518-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTATTTGGAGGGTTTGGAAATTGACTAGTTCCTTTAATATTGGGGGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTCTTACCTCCTTCTTTAACTCTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KP954649, identified in GenBank as Glyptotendipes meridionalis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611482 Hydrachnidiae sp. water mite diet isolate 1749-BHL110116-GBD5425_12904-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAAATGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCGCTCACCTTACTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.1% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611483 Hydrachnidiae sp. water mite diet isolate 1923-BHL022317-GBD25391_7063-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGGAATTGATTAGTTCCTCTTATACT-AGAGGCTCCTGATATAGCATTCCTTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCATACCCTTCTTCTTTCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611484 Hydrachnidiae sp. water mite diet isolate 1959-BHL022317-GBD23392_25252-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCCTTTGGAGCATGATCCGGAGTAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTCTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.4% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611485 Hydrachnidiae sp. water mite diet isolate 2308-BHL072216-GBD7693_22354-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATACTTCGCTTTTGGGGCTTGATCAGGAATGGTGGGAGCAAGACTAAGAACTTTAATCCGTTTAGAATTAGGACAACCAGGAACTCTCCTAGGAAGAGACCAAATTTATAATACTATCGTAACAGCTCACGCCTTCGTTATAATTTTCTTTATAGTTATGCCAATAATAATTGGAGGATTCGGAAATTGACTAGTCCCATTGATAATTAGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGACTTTTACCCCCCTCTTTAACTCTTCT	Using NCBI BLASTN in June 2018, this sequence was 00.0% identical to accession ID MG773261, identified in GenBank as Lebertia quinquemaculosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611486 Hydrachnidiae sp. water mite diet isolate 3827-BHL032417-GBD15707_2287-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAGTTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAAAAAATAATATGAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAGTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.1% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611487 Hydrachnidiae sp. water mite diet isolate 3866-BHL032417-GBD5454_21266-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAGTTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAAACAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCATCTAATATTAGGAGCTCCGGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCACTTCTCTTACATTACTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611488 Hydrachnidiae sp. water mite diet isolate 5156-BHL032417-GBD14492_21104-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCATTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCTTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAG-TAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611489 Hydrachnidiae sp. water mite diet isolate 5375-BHL032417-GBD15659_19776-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACACCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCCTTTACCCCCGTCATTATCTTTACTTCTTTCTAGGTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.5% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611490 Hydrachnidiae sp. water mite diet isolate 5611-BHL032417-GBD12025_2232-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAGCCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTAATAATTTTTTTCATAGTAATACCAATAATAATTGGGGGGTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611491 Hydrachnidiae sp. water mite diet isolate 6537-BHL032417-GBD22468_10847-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACCGCTCATGCTTTCGTTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTATCCCCCTCTCCT--ACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611492 Hydrachnidiae sp. water mite diet isolate 7077-BHL032417-GBD6694_19189-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAGTTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTCTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.1% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611493 Hydrachnidiae sp. water mite diet isolate 10580-BHL040517-GBD12034_19293-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTATAGTTATGCCAATAATAATTGGAGGATTCGGAAATTGACTAGTCCCATTGATGATTAGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGACTTTTACCCCCCTCTTTAACTCTTCTACTATCTAGTTCTTTCACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG811666, identified in GenBank as Lebertia quinquemaculosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611494 Hydrachnidiae sp. water mite diet isolate 10861-BHL101516-GBD25075_8295-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATACTTCGCTTTTGGGGCTTGATCAGGAATGGTGGGAGCAAGACTAAGAACTTTAATCCGTTTAGAATTAGGACAACCAGGAACTCTCCTAGGAAGAGACCAAATTTATAATACTATCGTAACAGCTCACGCCTTCGTTATAATTTTCTTTATAGTTATGCCAATAATAATTGGAGGATTCGGAAATTGATTAGTACCTTTAATGTTAGGGGCCCCTGATATAGCCTTCCCGCGAATAAATAATATAAGATTTTGACTTCTCCCACCGTCTCTTTCTCTTCTTCTTTCTAATTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID MG811666, identified in GenBank as Lebertia quinquemaculosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611495 Insecta sp. water mite diet isolate 2683-BHL072216-GBD12475_20729-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACTGAATTAGGTCATCCTGAAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.6% identical to accession ID MF410860, identified in GenBank as Pterygota sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611496 Insecta sp. water mite diet isolate 5773-BHL032417-GBD12687_12403-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAGTTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGCTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCTTCTCTTACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.3% identical to accession ID MF410860, identified in GenBank as Pterygota sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611497 Insecta sp. water mite diet isolate 5840-BHL032417-GBD27057_7439-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCCTTTCCTCGAATAAATAACATAAGTTTCTGATTACTTCCTCCCTCTCTTTCTCTTCTTCTTTCAAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.0% identical to accession ID MF410860, identified in GenBank as Pterygota sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611498 Insecta sp. water mite diet isolate 13602-BHL040517-GBD13952_18749-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCATGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.7% identical to accession ID MF410860, identified in GenBank as Pterygota sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611499 Insecta sp. water mite diet isolate 13999-BHL040517-GBD6342_10800-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCAATAAGAATGCTTATCCGAACAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTTTGATATTAGGGACTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTACATTAACCTTACTTTTATCAAGATCAATAGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.0% identical to accession ID JN008918, identified in GenBank as Spilopsyllus cuniculi. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611500 Kiefferulus sp. water mite diet isolate 2525-BHL072216-GBD6920_11830-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTATCATAATTTTTTTCATAGTTATGCCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCCCTAATATTAGGAGCACCTGATATAGCTTTCCCGCGAATAAATAATATAAGCTTCTGACTTCTTCCCCCGTCTTTAACTCTCCTACTATCTAGATCAATAGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.0% identical to accession ID DQ648215, identified in GenBank as Kiefferulus brevibucca. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611501 Kiefferulus sp. water mite diet isolate 2631-BHL072216-GBD12770_9620-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATAAAGATATTGGAACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATAACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGGGGCTTTGGGAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGTTTTTGACTTTTACCACCCTCTTTAACTCTTTTACTTTCAAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.0% identical to accession ID DQ648215, identified in GenBank as Kiefferulus brevibucca. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611502 Lebertia quinquemaculosa water mite diet isolate 1117-BHL110116-GBD19638_4850-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATACTTCGCTTTTGGGGCTTGATCAGGAATGGTGGGAGCAAGACTAAGAACTTTAATCCGTTTAGAATTAGGACAACCAGGAACTCTCCTAGGAAGAGACCAAATTTATAATACTATCGTAACAGCTCACGCCTTCGTTATAATTTTCTTTATAGTTATGCCAATAATAATTGGAGGATTCGGAAATTGACTAGTCCCATTGATAATTAGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGACTTTTACCCCCCTCTTTAACTCTTCTACTATCTAGTTCTTTCACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID MG773261, identified in GenBank as Lebertia quinquemaculosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611503 Lebertia quinquemaculosa water mite diet isolate 9688-BHL032417-GBD26260_11318-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTATACTTCGCTTTTGGGGCTTGATCAGGAATGGTGGGAGCAAGACTAAGAACCTTAATCCGTTTAGAATTAGGACAACCAGGAACTCTCCTAGGAAGAGACCAAATTTATAATACTATCGTAACAGCTCACGCCTTCGTTATAATTTTCTTTATAGTTATGCCAATAATAATTGGAGGATTCGGAAATTGACTAGTCCCATTGATGATTAGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGACTTTTACCCCCCTCTTTAACTCTTCTACTATCTAGTTCTTTCACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID MG811666, identified in GenBank as Lebertia quinquemaculosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611504 Lebertia quinquemaculosa water mite diet isolate 10211-BHL040517-GBD12119_21140-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATACTTCGCTTTTGGGGCTTGATCAGGAATGGTGGGAGCAAGACTAAGAACTTTAATCCGTTTAGAATTAGGACAACCAGGAACTCTCCTAGGAAGAGACCAAATTTATAATACTATCGTAACAGCTCACGCCTTCGTCATAATTTTCTTTATAGTTATGCCAATAATAATTGGAGGATTCGGAAATTGACTAGTCCCATTGATGATTAGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGT	Using NCBI BLASTN in June 2018, this sequence was 98.0% identical to accession ID MG811666, identified in GenBank as Lebertia quinquemaculosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611505 Lebertia quinquemaculosa water mite diet isolate 11390-BHL101516-GBD20691_4390-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATACTTCGCTTTTGGGGCTTGATCAGGAATGGTGGGAGCAAGACTAAGAACTTTAATCCGTTTAGAATTAGGACAACCAGGAACTCTCCTAGGAAGAGACCAAATTTATAATACTATCGTAACAGCTCACGCCCTCATTATAATTTTCTTTATAGTTATGCCAATAATAATTGGAGGATTCGGAAATTGACTAGTCCCATTGATAATTAGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGACTTTTACCCCCCTCTTTAGCTCTTCTACTATCTAGTTCTTTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID MG773261, identified in GenBank as Lebertia quinquemaculosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611506 Lebertia quinquemaculosa water mite diet isolate 11452-BHL101516-GBD6598_24293-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATACTTCGCTTTTGGGGCTTGATCAGGAATGGTGGGAGCAAGACTAAGAACTTTAATCCGTTTAGAATTAGGACAACCAGGAACTCTCCTAGGAAGAGACCAAATTTATAATACTATCGTAACAGCTCACGCCTTCGTTATAATTTTCTTTATAGTTATACCAATAATAATTGGAGGATTCGGAAATTGACTAGTCCCATTGATGATTAGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGACTTTTACCCCCCTCTTTAACTCTTCTACTATCTAGTTCTTTCACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID MG811666, identified in GenBank as Lebertia quinquemaculosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611507 Lebertia quinquemaculosa water mite diet isolate 11646-BHL101516-GBD18625_20931-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATACTTCGCTTTTGGGGCTTGATCAGGAATGGTGGGAGCAAGACTAAGAACTTTAATCCGTTTAGAATTAGGACAACCAGGGACTCTCCTAGGAAGAGACCAAATTTATAATACTATCGTAACAGCTCACGCCTTCGTTATAATTTTCTTTATAGTTATGCCAATAATAATTGGAGGATTCGGAAATTGACTAGTCCCATTGATAATTAGAGCTCCAGATATAGCATTCCCACGAATAAACAATATAAGATTTTGACTTTTACCCCCCTCTTTAACTCTTCTACTATCCAGTTCTTTCACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID MG773261, identified in GenBank as Lebertia quinquemaculosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611508 Lebertia quinquemaculosa water mite diet isolate 11739-BHL101516-GBD23141_4420-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATACTTCGCTTTTGGGGCTTGATCAGGAATGGTGGGAGCAAGACTAAGAACTTTAATCCGTTTAGAATTAGGACAACCAGGAACTCTCCTAGGAAGAGACCAAATTTATAATACTATCGTAACAGCTCACGCCTTCGTTATAATTTTCTTTATAGTTATGCCAATAATAATTGGAGGATTCGGAAATTGACAAGTCCCATTGATGATTAGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGACTTTTACCCCCCTCTTTAACTCTTCTACTATCTAGTTCTTTCACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID MG811666, identified in GenBank as Lebertia quinquemaculosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611509 Lebertia sp. water mite diet isolate 1730-BHL110116-GBD6014_19147-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGCGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCATGACTAAATAATTTAAGATTCTGACTACTACCACCATC	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611510 Lebertia sp. water mite diet isolate 1905-BHL022317-GBD5140_21015-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCATACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611511 Lebertia sp. water mite diet isolate 2011-BHL022317-GBD24484_18838-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCTTAATTCGACTTGAATTATGACAACCAGGCTCATTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTTGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGATTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611512 Lebertia sp. water mite diet isolate 2022-BHL022317-GBD6087_17461-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCAGGAATAATTGGAGCTAGATTAAGAATCCTAATTCGACTTGAATTAGGACAACCAGGCTCATTACTAGGAAATGATCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATATTAATTGGAGGTTTTGGAAACTGATTAGTTCCTCTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611513 Lebertia sp. water mite diet isolate 2052-BHL022317-GBD10852_23177-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCATTCATAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATTATAATTGGAGGATTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGACATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTCCTTCCCCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611514 Lebertia sp. water mite diet isolate 3568-BHL032417-GBD17035_7428-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAGTTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611515 Lebertia sp. water mite diet isolate 4983-BHL032417-GBD9613_22359-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAG-TAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611516 Lebertia sp. water mite diet isolate 5008-BHL032417-GBD24408_10837-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGAATAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAACTTACAATACAATTGTAACTGATCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611517 Lebertia sp. water mite diet isolate 5020-BHL032417-GBD12965_14011-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAATGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCTTTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611518 Lebertia sp. water mite diet isolate 5057-BHL032417-GBD24364_8280-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACATTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGTCTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAGTTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTA	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611519 Lebertia sp. water mite diet isolate 5149-BHL032417-GBD16878_17016-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCCCACTCCTAGGAAGTGACCAAATTTACAATAAAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCAATAATAATCAGAGCCCCAGAGATAGCTTTTCCACCAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611520 Lebertia sp. water mite diet isolate 5224-BHL032417-GBD20064_13868-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTC	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611521 Lebertia sp. water mite diet isolate 5406-BHL032417-GBD28359_19351-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAAATGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCATTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAACATAAGATTTTGATTATTACCACCTACTTTAACATTATTATTATCAAGAACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611522 Lebertia sp. water mite diet isolate 5532-BHL032417-GBD12443_25330-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTGCTTTTGGAGCATGATCAGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTATAATACAATTGTAACTGATCATGCTTTTGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAGTAATATAAGATTTTGACTTCTTCCTCCATCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611523 Lebertia sp. water mite diet isolate 5621-BHL032417-GBD9311_25551-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCTCGAATAAATAAAATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611524 Lebertia sp. water mite diet isolate 5636-BHL032417-GBD18715_3338-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCGTACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611525 Lebertia sp. water mite diet isolate 5653-BHL032417-GBD23946_14352-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCTTTAACTCTTCTTCTTACTTGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611526 Lebertia sp. water mite diet isolate 5664-BHL032417-GBD25180_21590-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCGCTAATTCTA	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611527 Lebertia sp. water mite diet isolate 6175-BHL032417-GBD11652_3094-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATTCGGAATAATTGGGGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611528 Lebertia sp. water mite diet isolate 6196-BHL032417-GBD6969_18480-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTATGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTATCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACCGATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTATCTCTTCTTCTTACTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611529 Lebertia sp. water mite diet isolate 6260-BHL032417-GBD8823_23611-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGAATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611530 Lebertia sp. water mite diet isolate 6554-BHL032417-GBD19319_8690-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACATTTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611531 Lebertia sp. water mite diet isolate 6993-BHL032417-GBD21595_10025-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAGTTGGAGCTAGATTAAGAACCCTAATTCGTCTTGAATTAGGACTGCCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATGATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611532 Lebertia sp. water mite diet isolate 7025-BHL032417-GBD28849_11838-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAGTTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCAATCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTGTACCCCCCTCTCTTACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611533 Lebertia sp. water mite diet isolate 7057-BHL032417-GBD4201_20145-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAGTTGGAGCTAGATTAAGAACCCTAATTCGAGTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTCCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTCTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611534 Lebertia sp. water mite diet isolate 7064-BHL032417-GBD6745_7171-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAGTTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACCT-TATTACTTTCAAG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611535 Lebertia sp. water mite diet isolate 7281-BHL032417-GBD23772_11118-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAGTTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACATTACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCAGCCTTAACTCTTCTGCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611536 Lebertia sp. water mite diet isolate 7463-BHL032417-GBD6836_12326-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAGTTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTATGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAAATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611537 Lebertia sp. water mite diet isolate 8472-BHL101416-GBD25749_9205-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611538 Lebertia sp. water mite diet isolate 8755-BHL101416-GBD15691_20096-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGAATTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTGACTGCTCATGCTTTCGTTATAATTTTCTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAAATGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611539 Lebertia sp. water mite diet isolate 9313-BHL032417-GBD10497_20931-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATACTTCGCTTTTGGGGCTTGATCAGGGATGGTGGGAGCAAGACTAAGAACTTTAATCCGTTTAGAATTAGGACAACCAGGAACTCTCCTAGGAAGAGACCAAATTTATAATACTATCGTAACAGCTCACGCCTTCGTTATAATTTTCTTTATAGTTATGCCAATAATAATTGGAGGATTCAGAAATTGACTAGTCCCATTGATAATTAGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG773261, identified in GenBank as Lebertia quinquemaculosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611540 Lebertia sp. water mite diet isolate 9767-BHL040517-GBD25517_15633-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATACTTCGCTTTTGGGGCTTGATCAGGAATGGTGGGAGCAAGACTAAGAACTTTAATCCGTTTAGAATTAGGACAACCAGGAACTCTCCTAGGAAGAGACCAAATTTATAATACTATCGTAACAGCTCACGCCTTCGTTATAATTTTCTTTATAGTTATGCCAATAATAATTGGAGGATTTGGAAATTGACTAGTCCCATTGATGATTAGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG811666, identified in GenBank as Lebertia quinquemaculosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611541 Lebertia sp. water mite diet isolate 9771-BHL040517-GBD19930_21813-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATACTTCGCTTTTGGGGCTTGATCAGGAATGGTGGGAGCAAGACTAAGAACTTTAATCCGTTTAGAATTAGGACAACCAGGAACTCTCCTAGGAAGAGACCAAATTTATAATACTATCGTAACAGCTCACGCCTTCGTTATAATTTTCTTTATAGTTATGCCAATAATAATTGGAGGATTCGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID MG811666, identified in GenBank as Lebertia quinquemaculosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611542 Lebertia sp. water mite diet isolate 12111-BHL040517-GBD25749_9205-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611543 Lebertia sp. water mite diet isolate 12394-BHL040517-GBD15691_20096-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGAATTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTGACTGCTCATGCTTTCGTTATAATTTTCTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAAATGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611544 Lebertia sp. water mite diet isolate 1893-BHL022317-GBD25885_20941-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTATTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAGTTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGAATTTGACTTCGTCCTCCATCCTTAACTCTACATCTATCAAGTTCCTTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611545 Lebertia sp. water mite diet isolate 1992-BHL022317-GBD2095_12788-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTACCAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGGGCCCCAGATATAGCTTTTCCACGAATAAATAATAAAAGATTTTGACTTCCTCCTCCCTCCTTAACTCTACTTCTATCAAGTTCCTTTACAGAAAAAGGAGCTGGAACCGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611546 Lepidoptera sp. water mite diet isolate 1610-BHL110116-GBD23313_13977-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTCTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCA--GTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.7% identical to accession ID KX827002, identified in GenBank as Ectropis obliqua. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611547 Lepidoptera sp. water mite diet isolate 8666-BHL101416-GBD4538_10381-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAACTTTATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCCGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.7% identical to accession ID KR780071, identified in GenBank as Kumasia kumaso. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611548 Lepidoptera sp. water mite diet isolate 8719-BHL101416-GBD21935_13144-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACTCTATACTTCATCTTAGGAGTTTGAGCTGGAATAATTGGAACTGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGTGATCAACTTTATAATACTCTAGTAACTGCTCATGCATTCCTAATAATTTTCTTTCTGGTTATACCAATATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.0% identical to accession ID KX011066, identified in GenBank as Graphium leechi. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611549 Lepidoptera sp. water mite diet isolate 8749-BHL101416-GBD6869_19943-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.1% identical to accession ID EU768948, identified in GenBank as Rhodoecia aurantiago. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611550 Lepidoptera sp. water mite diet isolate 10375-BHL040517-GBD8484_15908-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAGCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGATATTGACTTCTACCTTTAATATTAGGAGCCCCAGATATAGCTCTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.9% identical to accession ID AB158247, identified in GenBank as Agrioglypta itysalis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611551 Lepidoptera sp. water mite diet isolate 10429-BHL040517-GBD22636_15736-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.0% identical to accession ID AB158247, identified in GenBank as Agrioglypta itysalis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611552 Lepidoptera sp. water mite diet isolate 10848-BHL101516-GBD27887_17179-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCGTTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTAACTCTACTACGTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.9% identical to accession ID KM576860, identified in GenBank as Glyphodes pyloalis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611553 Lepidoptera sp. water mite diet isolate 10891-BHL101516-GBD19941_13947-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTACCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID KM576860, identified in GenBank as Glyphodes pyloalis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611554 Lepidoptera sp. water mite diet isolate 11108-BHL110116-GBD5720_13525-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTATAA---TACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCCTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 81.9% identical to accession ID KM576860, identified in GenBank as Glyphodes pyloalis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611555 Lepidoptera sp. water mite diet isolate 11136-BHL110116-GBD20546_5447-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.6% identical to accession ID KM576860, identified in GenBank as Glyphodes pyloalis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611556 Lepidoptera sp. water mite diet isolate 12305-BHL040517-GBD4538_10381-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAACTTTATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCCGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.7% identical to accession ID KR780071, identified in GenBank as Kumasia kumaso. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611557 Lepidoptera sp. water mite diet isolate 12358-BHL040517-GBD21935_13144-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACTCTATACTTCATCTTAGGAGTTTGAGCTGGAATAATTGGAACTGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGTGATCAACTTTATAATACTCTAGTAACTGCTCATGCATTCCTAATAATTTTCTTTCTGGTTATACCAATATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.0% identical to accession ID KX011066, identified in GenBank as Graphium leechi. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611558 Lepidoptera sp. water mite diet isolate 12388-BHL040517-GBD6869_19943-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.1% identical to accession ID EU768948, identified in GenBank as Rhodoecia aurantiago. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611559 Lepidoptera sp. water mite diet isolate 14414-BHL040517-GBD19253_7078-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTTATATTTGGAGCTTGAGCGGGAATAGTAGGAACTTCTCTTAGTATTTTAATTCGAGCAGAATTAGGACATCCAGGTGCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTTACATTACTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID EU768912, identified in GenBank as Heliocheilus ionola. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611560 Leptocera erythrocera water mite diet isolate 1043-BHL100916-GBD20187_13068-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATATTTGGAGCTTGAGCGGGAATAGTAGGAACTTCTCTTAGTATTTTAATTCGAGCAGAATTAGGACATCCAGGTGCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCGTGCTTTTGTAATAATTTTTTTATAGTAATACCTATTATAATTGGAGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATGAATAATATAAGTTTTTGATTACTACCTCCTTCTCTTACCTTACCTTTAGTAAGCAGTATACTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR394103, identified in GenBank as Leptocera erythrocera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611561 Leptocera erythrocera water mite diet isolate 15215-BHL040517-GBD21552_20985-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATATTTGGAGCTTGAGCGGGAATAGTAGGAACTTCTCTTAGTATTTTAATTCGAGCAGAATTAGGACATCCAGGTGCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTATAATTGGAGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATGAATAATATAAGTTTTTGATTACTACCTCCTTCTCTTACCTTACTTTTAGTAAGCAGTATACTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID MF838592, identified in GenBank as Leptocera erythrocera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611562 Leptocera sp. water mite diet isolate 14219-BHL040517-GBD25687_15237-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTGATCGGAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTATAATTGGAGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCCGATATAGCTTTCCCTCGAGTGAATAATATAAGTTTTTGATTACTACCTCCTTCTCTTACCTTACTTTTAGTAAGCAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KM909916, identified in GenBank as Leptocera erythrocera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611563 Leptocera sp. water mite diet isolate 14242-BHL040517-GBD8185_4040-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTATAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATGAATAATATAAGTTTTTGATTACTACCTCCTTCTCGTACCTTACTTTTAGTAAGCAGTATACTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KM961632, identified in GenBank as Leptocera erythrocera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611564 Leptocera sp. water mite diet isolate 14245-BHL040517-GBD26216_14808-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTATAATTGGAGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATGAATAATATAAGTTTTTGATTACTACCTCCTTCTCTTACCTTATTTTTAGTAAGCAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID MF836864, identified in GenBank as Leptocera erythrocera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611565 Leptocera sp. water mite diet isolate 14343-BHL040517-GBD6669_7352-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATATTTGGAGCTTGAGCGGGAATAGTAGGAACTTCTCTTAGTATTTTAATTCGAGCAGAATTAGGACATCCAGGTGCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTATAATTGGAGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATGAATATTATAAGTTTTTGATTACTTCCCCCTTCT-TTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KM904712, identified in GenBank as Leptocera erythrocera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611566 Leptocera sp. water mite diet isolate 14363-BHL040517-GBD13672_6905-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATATTTGGAGCTTGAGCGGGAATAGTAGGAACTTCTCTTAGTATTTTAATTCGAGCAGAATTAGGACATCCAGGTGCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTATAATTGGAGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATGAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR394103, identified in GenBank as Leptocera erythrocera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611567 Leptocera sp. water mite diet isolate 14367-BHL040517-GBD21037_4030-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTCGGTGCCTGATCAAGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTATAATTGGAGGGTTTGGAAATTTATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATGAATAATATAAGTTTTTGATTACTACCTCCTTCTCTTACCTTACTTTTAGTAAGCAATATACTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID MF836532, identified in GenBank as Leptocera erythrocera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611568 Leptocera sp. water mite diet isolate 14397-BHL040517-GBD13129_10244-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCGGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTATAATTGGAGGGTATGGAAATTGATTAGGTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATGAATAATATAAGTTTTTGATTACTACCTCCTTCTCTTACCTTACTTTTAGTAAGCAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID MF836864, identified in GenBank as Leptocera erythrocera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611569 Leptocera sp. water mite diet isolate 14446-BHL040517-GBD27751_14560-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACATCCAGGTACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTATAATTGGAGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTTGAATGAATAATATAAGTTTTTGATTACTACCTCCTTCTCTTACCTTACTTTTAGCAAGCAGTATACTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM961632, identified in GenBank as Leptocera erythrocera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611570 Leptocera sp. water mite diet isolate 14495-BHL040517-GBD20539_2954-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAATTAGGACATCCAGGTGCTTTAATTGGAAATGATCAAATTTATAATGTAATTGTTACAGCTTATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTATAATTGGAGGATTTGAAAATTGATTGGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCAAATGAATAATATAAGTTTTTGATTACTACCTCCTTCTCTTACCTTACTTTTAGTAAGCAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MF836344, identified in GenBank as Leptocera erythrocera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611571 Leptocera sp. water mite diet isolate 14545-BHL040517-GBD11132_12346-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATATTTGGAGCTTGAGCGGGAATAGTAGGAACTTCTCTTAGTATTTTAATTCGAGCAGAAATAGGACATCCAGGTGCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTATAATTGGAGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATGAATAATATAAGTTTCTGATTACTTCCCCCATCACTTACATTACTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KM918163, identified in GenBank as Leptocera erythrocera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611572 Leucophenga sp. water mite diet isolate 862-BHL100916-GBD23353_16441-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACACAATTATTAGTAAGAAGTATAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID JX887648, identified in GenBank as Leucophenga sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611573 Leucophenga sp. water mite diet isolate 15010-BHL040517-GBD20268_26943-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACACTTTATTTTATTTTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACATCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCCTCACTAACACTATTACTAGCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID JX887648, identified in GenBank as Leucophenga sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611574 Leucophenga sp. water mite diet isolate 15061-BHL040517-GBD3133_20359-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACACTTTATTTTATATTTGGAGCATGAGCAGGTATAGTCGGAACTGCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGGGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACACTATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID JX887648, identified in GenBank as Leucophenga sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611575 Leucophenga sp. water mite diet isolate 15098-BHL040517-GBD18907_16331-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTACTGAATTAGGACATCCTGGAACTTTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGATTTTGACTACTTCCTCCTTCACTTACACTATTATTAGTAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID JX887648, identified in GenBank as Leucophenga sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611576 Limnophyes sp. water mite diet isolate 14447-BHL040517-GBD5168_18113-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACTTTATATTTTATTTTTGGAGCCTGATCTGGAATAATTGGAACCTCATTAAGAATTCTTATTCGAGCTGAATTAGGCCATTCAGGAACTTTAATCGGTGATGACCAAATTTATAACGTAATTGTAACTGTTCATGCTTTTGTTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGGGCACCAGACATAGCGTTCCCTCGTATAAACAATATAAGATTCTGGCTTTTACCCCCATCATTAACTCTCCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR292949, identified in GenBank as Limnophyes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611577 Limnophyes sp. water mite diet isolate 14456-BHL040517-GBD4960_9797-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTACTTTATATTTTATTTTTGGAGCCTGATCTGGAATAATTGGAACCTCATTAAGAATTCTAATTCGAGCTGAATTAGGCCATTCAGGAGCTTTAATCGGTGATGACCAAATTTATAACGTAATTGTAACTGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGGAATTGATTAGTGCCTTTAATGTTAGGGGCACCTGACATAGCGTTTCCTCGTATAAACAATATAAGATTCTGGCTTTTACCCCCATCATTAACTCTCCTTCTTTCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR292949, identified in GenBank as Limnophyes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611578 Macrocyclops sp. water mite diet isolate 10691-BHL040517-GBD17115_8667-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGACTTTGTATTTATTGGCAGGTGCTTGAGCGGGGTTAGTAGGAACTGGACTTAGAATGATTATTCGACTTGAGTTAGGTCAGCCGGGCAGCTTATTGGGTGATGATCAAATTTATAATGTAGTAGTAACTGCTCACGCATTTGTGATAATTTTTTTATAGTTATATCAATTTTAATTGGGGGATTTGGAAACTGGTTAGTTCCCCTAATACTAGGGTCTCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTTCTATTGCCCGCTTTAATCTTATTATTGGCTAGGGCCCTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID MF745282, identified in GenBank as Macrocyclops sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611579 Megascolecidae sp. water mite diet isolate 1471-BHL110116-GBD7086_22997-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTCTATACTTTATTTTAGGAGTCTGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTCTCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAACCTTACTAATATCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF017589, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611580 Megascolecidae sp. water mite diet isolate 1494-BHL110116-GBD21373_2936-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAATATCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTTTTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAATCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF017589, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611581 Megascolecidae sp. water mite diet isolate 1498-BHL110116-GBD4491_22509-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTCTTTACTTTATTTTAGGAGCATGAGCAGGAATAATTGGAACAGGGTTTAGAATACTAATTCGAACTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAATATTAATTGGAGGGTTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.3% identical to accession ID KF017589, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611582 Megascolecidae sp. water mite diet isolate 1565-BHL110116-GBD15030_10661-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTTTAGAATACTAATTCGAACTGAATTATCACAACCAGGATCATTCTTAGGAAGTGATCAACTTTATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.2% identical to accession ID KF205410, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611583 Megascolecidae sp. water mite diet isolate 1579-BHL110116-GBD25173_17785-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACATGGACTAGAATATTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGTGATCAACTTTATAACACCCTTGTTACTGCACATGCATTTTTAATAATTTTTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.2% identical to accession ID KF205410, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611584 Megascolecidae sp. water mite diet isolate 1709-BHL110116-GBD14700_25151-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTTTAGAATACTAATTCGAATTGAATTATCACACCCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTCTTGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTTGAGCTCCAGATATGGCTTTCCCACTACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.5% identical to accession ID KF205412, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611585 Megascolecidae sp. water mite diet isolate 1712-BHL110116-GBD20800_22081-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTTATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAATACCCTTGTTACTGCACATGCATTCTTAATAATTTTTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGAGATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTTCCACCATCTCTAACCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.8% identical to accession ID KF205412, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611586 Megascolecidae sp. water mite diet isolate 10263-BHL040517-GBD15668_24331-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGCTACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGGAGAGATCAACTTTATAATACTCTTGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTTCCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTATCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF017589, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611587 Megascolecidae sp. water mite diet isolate 10625-BHL040517-GBD8930_13231-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTCTATACTTTATCTTAGGAGCTTGAGCTGGAATAATTGGAACAGGATTTAGAATATTTATTCGAGTTGAATTATCTCAACCAGGATCATTCATAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCATAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGAGGATTTGGAAACTGACTTCCACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.2% identical to accession ID KF017589, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611588 Megascolecidae sp. water mite diet isolate 10801-BHL101516-GBD22820_12131-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGCATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCTCCAGATATAGCTTTCCCTCGAATAAATAACATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.0% identical to accession ID KF205412, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611589 Megascolecidae sp. water mite diet isolate 10907-BHL101516-GBD3233_20794-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTCAACAAATCATAAAGATATTGGCACTCTATATTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTGTTATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCCCCATCACTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 84.0% identical to accession ID KF205412, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611590 Megascolecidae sp. water mite diet isolate 10930-BHL101516-GBD9067_7637-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTCTTTACTTTATTTTAGGAGTTTGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTGCTACCACCATCACTAATCTTACTAATATCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF017589, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611591 Megascolecidae sp. water mite diet isolate 10990-BHL101516-GBD11821_12796-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAGCAGGGTCTAGAATACTTATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCCCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTTCTACCCCCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.3% identical to accession ID KF205412, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611592 Megascolecidae sp. water mite diet isolate 10997-BHL101516-GBD17411_3384-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTATATAACACCCTAGTAACTGCACATGCATTCTTAATAATTTACTTTCTCGTTATACCAGTATTTATTGGAGGATTTGGAAACTGATTACTACCTCTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCATCTCTAATCCTACTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF017589, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611593 Megascolecidae sp. water mite diet isolate 11023-BHL110116-GBD10560_22660-Lq76 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAGCAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGGTTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCCGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF017589, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611594 Megascolecidae sp. water mite diet isolate 11208-BHL110116-GBD27247_19543-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTCTATACTTTATTTTAGGAGCATGAGCAGGAATAATTGGAACAGGGTCTGGAATACTAATTCGAATTGAATTATCACCACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCTCCAGATATAGCCTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.6% identical to accession ID KF017589, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611595 Megascolecidae sp. water mite diet isolate 11223-BHL110116-GBD6089_17368-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTCTATACTTCATTTTAGGAGTATGAGCAGGAATGATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCATAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTTATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCTCGACTAAATAATATAAGATTCTGACTTCTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.2% identical to accession ID KF017589, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611596 Megascolecidae sp. water mite diet isolate 11398-BHL101516-GBD17595_3201-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTCAACAAATCATAAAGATATTGGCACACTATACTTAATTTTAGGAGCATGAGCAGGAATAATTGGAACAGGGACTAAAATACTAATTCGAATTGAATTAGCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACTCCCTAGTTACTGCACATGCATTCGTAATAATTTTTTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCCCCTTCTCTCATCTTACTACTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.2% identical to accession ID KF205412, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611597 Megascolecidae sp. water mite diet isolate 11418-BHL101516-GBD7345_13526-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACTCTATATTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGATTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCCCCATCACTAACCTTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.3% identical to accession ID KT429010, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611598 Megascolecidae sp. water mite diet isolate 11430-BHL101516-GBD2422_13201-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCGGGATCATTCTTAGGAAGAGATCAACTATATAATACCATTGTTACTGCACATGCATTCTTAATAATTTTTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF017589, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611599 Megascolecidae sp. water mite diet isolate 11591-BHL101516-GBD12868_22021-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGCATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATGACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTTTTTATTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCATTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF205971, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611600 Megascolecidae sp. water mite diet isolate 11608-BHL101516-GBD24506_5597-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTAGCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTTTTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCCCCCTCTCTTACCTTACTACTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.3% identical to accession ID KF205412, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611601 Megascolecidae sp. water mite diet isolate 11660-BHL101516-GBD24249_18628-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAATCAGGATCATTCTTAGGAAGAGATCAACTATATAACACAATAGTTACTGCACATGCATTTTTAATAATTTTTTTTCTTGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAACCCTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.6% identical to accession ID KF205412, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611602 Megascolecidae sp. water mite diet isolate 11694-BHL101516-GBD27808_15435-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGCACAGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAACCTTACTAATATCTTCATCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.2% identical to accession ID KF017589, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611603 Megascolecidae sp. water mite diet isolate 11891-BHL101516-GBD15277_18961-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTCTATACTTTATTTTCGGAGTATGAGCAGGAATAATTGGAACAGGGATTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTTTTCTTGTTATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTACAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF017589, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611604 Megascolecidae sp. water mite diet isolate 11937-BHL101516-GBD2701_18717-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTCAACAAATCATAAAGATATTGGCACTCTATACGTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTACTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGACTTTTACCCCCCTCTTTAACTCTTCTACTATCTAGTTCTTTCACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.9% identical to accession ID KF205412, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611605 Megascolecidae sp. water mite diet isolate 11952-BHL101516-GBD8884_6899-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTTTGAGCAGGAATAATTGGAACAGCGATTAGAATACTTATTCGAATTGAATTATCACAACCAGGACCATTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTGATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.0% identical to accession ID KF205412, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611606 Megascolecidae sp. water mite diet isolate 12006-BHL101516-GBD6979_15052-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTCTATACTTTATTTTAGGAGCCTGAGCAGGAATAATTGGAACAGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAAGATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.9% identical to accession ID KF017589, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611607 Megascolecidae sp. water mite diet isolate 12025-BHL101516-GBD3265_16024-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACATAATAGTTACTGCACATGCATTCTTAATAATTTTTTTCTTGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF017589, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611608 Megascolecidae sp. water mite diet isolate 13059-BHL040517-GBD18986_8183-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTCTAAACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGCTTCTAGAATATTAATTCGGATTGAATTATCACAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTTGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCTATTAGTTTCTACTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.9% identical to accession ID KF017589, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611609 Megaselia sp. water mite diet isolate 2276-BHL072216-GBD12129_26645-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTAGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATCTTAATTGGGGGATTTGGAAATTGACTTTTACCATTAATGCTTGGAGCACCAGATATAGCTTTCCCCCGAATGAATAATATAAGTTTTTGACTTCTTCCCCCATCTCTAACCCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KX774883, identified in GenBank as Megaselia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611610 Megaselia sp. water mite diet isolate 2359-BHL072216-GBD2504_14969-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACCTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCCCATGCTTTTATCATAATTTTTTTTATAGTTATACCTATCTTAATTGGGGGATTTGGAAATTGACTTTTACCATTAATGCTTGGAGCACCAGATATAGCTTTCCCCCGAATGAATAATATAAGTTTTTGACTTCTTCCCCCATCTCTAACCCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KX774883, identified in GenBank as Megaselia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611611 Megaselia sp. water mite diet isolate 2406-BHL072216-GBD15813_24073-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATATTTCACTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTAACAGCTCATGCTTTTATCATAATTTTTTTTATAGTTATACCTATCTTAATTGGGGGATTTGGAAATTGACTTTTACCATTAATGCTTGGAGCACCAGATATAGCTTTCCCCCGAATGAATAATATAAGTTTTTGACTTCTTCCCCCATCTCTAACCCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KX774883, identified in GenBank as Megaselia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611612 Megaselia sp. water mite diet isolate 2444-BHL072216-GBD21886_3339-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTTTATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACATCTTTAAGTATACTTATTCGTGCAGAATTAGGTCATCCAGGCACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCCCATGCTTTTATCATAATTTTTTTTATAGTTATACCTATCTTAATTGGGGGATTTGGAAATTGACTTTTACCATTAATGCTTGGAGCACCAGATATAGCTTTCCCCCGAATGAATAATATAAGTTTTTGACTTTTACCACCCTCTTTAACTCTTTTACTTTCAAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KX774883, identified in GenBank as Megaselia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611613 Megaselia sp. water mite diet isolate 2540-BHL072216-GBD13109_28417-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACACCCAGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCCCATGCCTTTATCATAATTTTTTTTATAGTTATACCTATCTTAATTGGAGGATTTGGAAATTGACTTTTACCATTAATTCTTGGAGCACCAGATATAGCTTTCCCCCGAATGAATAATATAAGTTTTTGACTTCTTCCCCCATCTCTAACCCTTCTTCTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KX774883, identified in GenBank as Megaselia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611614 Megaselia sp. water mite diet isolate 2637-BHL072216-GBD5831_13935-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTTTATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACATCTTTAAGTACACTTATTCGTGCAGAATTAGGTCATCCAGGCACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCCCATGCTTTTATCATAATTTTTTTTATAGTTATACCTATCTTAATTGGGGGATTTGGAAATTGACTTTTACCATTAATGCTTGGAGCACCAGATATAGCTTTCCCCCGAATGAATAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCA---GTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KX774883, identified in GenBank as Megaselia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611615 Megaselia sp. water mite diet isolate 2676-BHL072216-GBD6252_9068-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTTTATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGTATACTTATTCGTGCAGAATTAGGTCATCCAGGCACTTTTATTGGAGATGATCAAATTTATACTGTAATTTTTACAGCACATGCTTTTATCATAATTTTTTTTATAGTTATACCTATCTTAATTGTGGGATTTGGAAATTGACTATTACCATTAATGTTTGGAGCACCAGATATAGCTTTCCCCCGAATGAATAATATAAGTTTTTGACTTCTTCCCCCATCTCTAACCCTACTTCTTTCTAGTTCAATTGTAGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KX774883, identified in GenBank as Megaselia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW611616 Megaselia sp. water mite diet isolate 2554-BHL072216-GBD17680_4762-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGTGCAGAATTAGGTCATCCAGGCACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCCCATGCTTTTATCATAATTTTTTTTATAGTTATACCTATCTTAATTGGGGGATTTGGAAATTGACTTTTACCATTAATGCTTGGAGCACCAGATATAGCTTTCCCCCGAATGAATAATATAAGTTTTTGACTTCTTCCCCCATCTCTAACCCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KX774883, identified in GenBank as Megaselia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611617 Nais barbata water mite diet isolate 1438-BHL110116-GBD10601_24311-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAACTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611618 Nais barbata water mite diet isolate 3673-BHL032417-GBD16701_4895-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTGGGAAACTGATTACTTCCACTAATACTAGGTGCTTCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611619 Nais barbata water mite diet isolate 4240-BHL032417-GBD27860_9441-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTTTTTATTGGAGGATTCGGAAACTGATTACTTCCTCTAATACTAGGTGCTGCTGATATAGCATTCCCACGAATAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611620 Nais barbata water mite diet isolate 4961-BHL032417-GBD22810_24283-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAATATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCTATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611621 Nais barbata water mite diet isolate 5367-BHL032417-GBD26356_18808-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAACTATATAATACTCTTGTAACAGCACATGCTTTCTTAATAATTTTCTTCATAGTAATACCTGTATTAATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGGGCTGCTGATATAGCATTCCCACGAATAAATAATCTAAGATTTTGATTACTTCCACCATCATTAACTCTACTAATTTCTACTGCAGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611622 Nais barbata water mite diet isolate 5495-BHL032417-GBD27160_23162-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTATATCTTATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGATCAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCATAGTAATACCTGTTTTAATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGAATAAATAATCTAAGATTTTGATTACTTCCACCATCATTAACTCTACTAATTTCATCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611623 Nais barbata water mite diet isolate 5799-BHL032417-GBD12985_22019-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTCTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACTAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611624 Nais barbata water mite diet isolate 6670-BHL032417-GBD17365_2505-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACATCCAGGATCATTCCTTGGAAGAGATCAACTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCCGTCTTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611625 Nais barbata water mite diet isolate 7351-BHL032417-GBD22527_22607-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTACCAGCACATGCATTCTTAGTAATTTTCTTCTTAGTAATACCTGTATTAATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGTTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611626 Nais barbata water mite diet isolate 8511-BHL101416-GBD3810_15827-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGGTCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAAGTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611627 Nais barbata water mite diet isolate 11524-BHL101516-GBD26129_12632-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGTACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTATTGTAACAGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGAATAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATATCTACTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611628 Nais barbata water mite diet isolate 11538-BHL101516-GBD26672_8024-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCATTGGAAGAGATCAATTATATAATACTCTTGTAACAGCGCATGCATTCTTAATAATTTTTTTCATAGTAATACCTGTATTAATTGGAGGATTCGGAAACTGATTTCTTCCACTAGTACTAGGTGCTGCTGATATAGCATTCCCACGAATAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611629 Nais barbata water mite diet isolate 11543-BHL101516-GBD27742_16419-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTTTTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCGCTAATACTAGGAGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACATCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611630 Nais barbata water mite diet isolate 11550-BHL101516-GBD4302_15442-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGGTTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGAATAAATAATCTAAGATTCTGACTACTACCACCATCTCTAAGCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611631 Nais barbata water mite diet isolate 11551-BHL101516-GBD27810_18610-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGTTTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTATATTAATTGGAGGATTCGGAAACTGATTACTTCCTCTAATACTAGGTGCTGCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTGTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611632 Nais barbata water mite diet isolate 11556-BHL101516-GBD13489_4500-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGAGTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCGCGATTAAATAATCTAAGATTTTGATTACTTCCCCCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611633 Nais barbata water mite diet isolate 11559-BHL101516-GBD8969_18195-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTATTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAATAGATCAATTTTATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCATAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCTCTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611634 Nais barbata water mite diet isolate 11567-BHL101516-GBD10712_20948-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGGATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCATCTTAGTAATACCTGTATTTATTGGAGGATACGAAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATAAAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAAATCTACTAAATTCTACTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611635 Nais barbata water mite diet isolate 11574-BHL101516-GBD25067_4992-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCATAGTAATACCAGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGAGCTGCTGATATAGCATCCCCACGAATAAATAATCTAAGATTTTGATTACTTCCACTATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611636 Nais barbata water mite diet isolate 11665-BHL101516-GBD18629_4026-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTGATTCGCATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATCATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGATGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCAGTAATTCTACTAATTTCTTCAGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611637 Nais barbata water mite diet isolate 11699-BHL101516-GBD7252_23717-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTTGAACAAGATTACTAATTCTAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATCCTTAATAATTTTCTTCTTAGTAATACCTGGATTTATTGGAGGATTCGGAAACTGAGTACTTCCACTAATACTAGGTGCTGCTGATATAGCAGTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611638 Nais barbata water mite diet isolate 11711-BHL101516-GBD21339_14912-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCATAGTAATACCTGTATTAATTGGAGGATTTGGAAACTGACTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATATCTACAGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611639 Nais barbata water mite diet isolate 11714-BHL101516-GBD23337_26732-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAATAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTCCTGATATAGCATTCCCACGACTAAATAATCTAAGATTTTGATTACTTCCACCGTCATTAATTCTACTAAATTCTACTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611640 Nais barbata water mite diet isolate 12150-BHL040517-GBD3810_15827-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGGTCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAAGTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611641 Nais bretscheri water mite diet isolate 5124-BHL032417-GBD16782_26973-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTAATCTTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTCCTTCTTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID LN810267, identified in GenBank as Nais bretscheri. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611642 Nais bretscheri water mite diet isolate 6342-BHL032417-GBD25940_7048-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTAGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCATAGTAATACCTGTATTTATTGGAGGATTCGGAAATTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID LN810267, identified in GenBank as Nais bretscheri. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611643 Nais bretscheri water mite diet isolate 11523-BHL101516-GBD18689_2626-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTACTTGGAAGAGATCAATTTTATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTTTTCTTAGTAATACCTGTATTAATTGGAGGATTTGGAAACCGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAAGTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID LN810267, identified in GenBank as Nais bretscheri. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611644 Nais bretscheri water mite diet isolate 11585-BHL101516-GBD17819_21546-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTTACAGCACATGCATTCTTAATAATTTTCTTCCTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTACCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID LN810267, identified in GenBank as Nais bretscheri. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611645 Nais bretscheri water mite diet isolate 11615-BHL101516-GBD17477_6714-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGCACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTACCACCATCACTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID LN810267, identified in GenBank as Nais bretscheri. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611646 Nais bretscheri water mite diet isolate 11648-BHL101516-GBD21396_14936-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAATAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGCGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTTTTCTTAGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTACTTCCACTAATACTAGGAGCTGCTGATATAGCATTCCCACGAATAAATAATCTAAGATTTTGATTACTGCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID LN810267, identified in GenBank as Nais bretscheri. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611647 Nais bretscheri water mite diet isolate 11691-BHL101516-GBD8610_9774-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACGCTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCCCAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTTTTCTTAGTAATACCTGTATTTATTGGAGGATTTGGAAACTGATTACTACCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCCCCATCACTAATTCTACTAATTTCATCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID LN810267, identified in GenBank as Nais bretscheri. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611648 Nais pseudobtusa water mite diet isolate 5026-BHL032417-GBD8949_4873-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTCGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID LT905357, identified in GenBank as Nais pseudobtusa. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611649 Nais pseudobtusa water mite diet isolate 5217-BHL032417-GBD11043_17682-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACCAACACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTCTGACTACTACCACCTTCACTAATCCTATTGGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID LT905357, identified in GenBank as Nais pseudobtusa. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611650 Nais pseudobtusa water mite diet isolate 11446-BHL101516-GBD4343_15756-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTATATTTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACTAGATTACTTATTCGAATTGAACTATCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCAGTATTTATTGGAGGATTCGGTAACTGACTGCTTCCACTAATACTAGGTGCTGCCGATATAGCATTCCCACGATTAAACAATCTTAGATTTTGACTTCTTCCACCATCATTAATTCTATTAATTTCTTCTGCCGCTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID LT905357, identified in GenBank as Nais pseudobtusa. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611651 Nais pseudobtusa water mite diet isolate 11478-BHL101516-GBD14481_8236-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTATATTTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACTAGATTACTTATTCGAATTGAACTATCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACCCTTGTTACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGTAACTGACTGCTTCCACTAATACTAGGTGCTGCCGATATAGCATTCCCACGAATAAACAATCTAAGATTTTGACTACTACCGCCATCATTAATTCTATTAATATCTTCTGCCGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID LT905357, identified in GenBank as Nais pseudobtusa. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611652 Nais pseudobtusa water mite diet isolate 11560-BHL101516-GBD9948_14066-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTATATCTAATTTTAGGCGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGTAGAGATCACTTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCCTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAACCTAAGATTTTGACTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID LT905357, identified in GenBank as Nais pseudobtusa. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611653 Nais pseudobtusa water mite diet isolate 11607-BHL101516-GBD24498_24062-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACTAGATTACTAATTCGAATTGAACTATCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAACACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATGGCATTCCCACGACTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID LT905357, identified in GenBank as Nais pseudobtusa. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611654 Nais pseudobtusa water mite diet isolate 11730-BHL101516-GBD8616_3789-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTCAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTCCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCGGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID LT905357, identified in GenBank as Nais pseudobtusa. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611655 Nais pseudobtusa water mite diet isolate 11733-BHL101516-GBD13424_27355-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGTATCATTCCTTGGAATAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTACTACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCAACTAATACTAGGTGCTCCTGATATAGCATTCCCACGATTAAACAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID LT905357, identified in GenBank as Nais pseudobtusa. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611656 Nais sp. water mite diet isolate 5150-BHL032417-GBD9729_21631-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCGATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTATTACTAGGTGCTGCTGATATAGCATTCCTACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID LT905357, identified in GenBank as Nais pseudobtusa. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611657 Nais sp. water mite diet isolate 5158-BHL032417-GBD16072_14738-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATCTTAGGAGTTTGAACTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID LT905357, identified in GenBank as Nais pseudobtusa. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611658 Nais sp. water mite diet isolate 5164-BHL032417-GBD22817_5192-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTAGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID LT905357, identified in GenBank as Nais pseudobtusa. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611659 Nais sp. water mite diet isolate 5198-BHL032417-GBD17213_23882-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID LN810267, identified in GenBank as Nais bretscheri. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611660 Nais sp. water mite diet isolate 5261-BHL032417-GBD19225_11724-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATACTTCATTTTCGGTGCCCGATCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID LT905357, identified in GenBank as Nais pseudobtusa. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611661 Nais sp. water mite diet isolate 5377-BHL032417-GBD11440_17607-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTTGACCTAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATATTCTTGTAACAGCACATGCATTCTTAATAATTTTTTTCATAGTAATACCTGTATTAATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAACTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID LT905357, identified in GenBank as Nais pseudobtusa. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611662 Nais sp. water mite diet isolate 5475-BHL032417-GBD3458_18293-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTATAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTACTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611663 Nais sp. water mite diet isolate 5507-BHL032417-GBD14360_25378-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTCGGAAAATGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID LT905357, identified in GenBank as Nais pseudobtusa. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611664 Nais sp. water mite diet isolate 11537-BHL101516-GBD17895_29041-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATATGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611665 Nais sp. water mite diet isolate 11580-BHL101516-GBD18479_19182-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAAACAGGATCATTCTTAGGAGGAGATCAACTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTAGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID LT905357, identified in GenBank as Nais pseudobtusa. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611666 Nais sp. water mite diet isolate 11604-BHL101516-GBD16006_5039-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGAATACTAATTCGAATTGAACTCGCACAACCAGGATCATTCCTTGGAAGAGATCAAATATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTTTTTATTGGAGGATTCGGAAACTGATTACTTCCCCTAATACTAGGAGCTCCTGATATAGCATTCCCCCGATTAAATAATCTAAGATTTTGATTACTTCCCCCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611667 Neoptera sp. water mite diet isolate 2420-BHL072216-GBD21663_4326-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTCAACAAATCATAAAGATATTGGTTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAGCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTCTAATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGGTATGGCTTTTCCTCGTGTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTAGAAGGGCAGTTGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.3% identical to accession ID EU710809, identified in GenBank as Harpalus puncticeps. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611668 Neoptera sp. water mite diet isolate 5448-BHL032417-GBD3067_9465-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTGGCTTAGAATTTTAATTCGAGCAGAATTATGTCATGCGGGTTCTTTAATTGGAAATGATCAACTTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGACTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAG--CCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID EU877950, identified in GenBank as Sphaerius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611669 Neosilba sp. water mite diet isolate 12670-BHL040517-GBD8380_17757-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGACACCCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCAAGCACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID KR262649, identified in GenBank as Neosilba zadolicha. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW611670 Oligochaeta sp. water mite diet isolate 454-BHL040517-GBD5608_21761-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATCCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACGTAACAATTTAAGATTCTGACTACTACTACCCCCATCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611671 Oligochaeta sp. water mite diet isolate 478-BHL040517-GBD19947_16344-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAAATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTCATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611672 Oligochaeta sp. water mite diet isolate 577-BHL040517-GBD20415_14741-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATCAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAACACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGTTTATACCAGTATTAATTGGAGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCACACGACTTAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611673 Oligochaeta sp. water mite diet isolate 735-BHL072216-GBD20184_24333-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTCCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611674 Oligochaeta sp. water mite diet isolate 765-BHL040916-GBD3836_18928-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGTTAGAGATCAACTATCTAACTTCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTTATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAAGTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611675 Oligochaeta sp. water mite diet isolate 926-BHL100916-GBD11926_20446-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAACTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGGATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611676 Oligochaeta sp. water mite diet isolate 941-BHL100916-GBD27492_16258-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGTTGGAATAATTGGAACAGGATCTAGAATATTAATTCGGATTGAATTATCACAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACGCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTAGTTATACCAGTATTTATTGGTGGATTTGGAAAGTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCCCCTTCACTAACCCTATTGGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611677 Oligochaeta sp. water mite diet isolate 1108-BHL110116-GBD23786_10878-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGCGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGCATTGAATTCTCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611678 Oligochaeta sp. water mite diet isolate 1118-BHL110116-GBD7779_13019-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAGTTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCCCTAACCTTACTAACATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611679 Oligochaeta sp. water mite diet isolate 1128-BHL110116-GBD21010_25805-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTTGGTAGAGAACAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611680 Oligochaeta sp. water mite diet isolate 1133-BHL110116-GBD3661_16774-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTCGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGAGTAGTACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611681 Oligochaeta sp. water mite diet isolate 1137-BHL110116-GBD10434_14466-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633404, identified in GenBank as Slavina sp. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611682 Oligochaeta sp. water mite diet isolate 1143-BHL110116-GBD18517_9855-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACATGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAACATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATATCAGCAGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611683 Oligochaeta sp. water mite diet isolate 1144-BHL110116-GBD21725_24045-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGTTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCATAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTAATGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAACTTAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611684 Oligochaeta sp. water mite diet isolate 1146-BHL110116-GBD11847_12798-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGCGTCTAGAATACTAATTCGAATTGAATTATCGCAACCAGGATCATTCATAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCATAATAATTTTCTTTCTTGTAATACCAGTATTAAATGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611685 Oligochaeta sp. water mite diet isolate 1147-BHL110116-GBD8614_4197-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATACTTAGGAAGAAACAAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAAAACTTGTAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611686 Oligochaeta sp. water mite diet isolate 1149-BHL110116-GBD23562_22993-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAAATTAAGAAACTGACTACGACCACCATCTCTAAACTTACTAATTGCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611687 Oligochaeta sp. water mite diet isolate 1151-BHL110116-GBD10226_25722-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LN810268, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611688 Oligochaeta sp. water mite diet isolate 1156-BHL110116-GBD14218_27649-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTTTTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCTTCTCTAAACTTACTAATTTCTAGTGCAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611689 Oligochaeta sp. water mite diet isolate 1160-BHL110116-GBD25363_10538-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATATTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGTGATCAACTATATAACACACTAGTTACTGCACATGCATTTGTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.4% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611690 Oligochaeta sp. water mite diet isolate 1161-BHL110116-GBD28642_17265-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCATTCCCACGACCAAATAATTTAAGAGTCTGACAACTTCCACCATCTCAAAGCTTACTAATTTCTTCTGCAGCAGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611691 Oligochaeta sp. water mite diet isolate 1163-BHL110116-GBD10479_4594-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTCATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATGTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCAGCCCTAAACTTACTAAGTA-CTTCTGCAGCAGTAGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.7% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611692 Oligochaeta sp. water mite diet isolate 1165-BHL110116-GBD15717_15706-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCACCAGATATAGCCTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCAGCTCTAAACTTACGAATATCTTCGGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.4% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611693 Oligochaeta sp. water mite diet isolate 1166-BHL110116-GBD8433_15621-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTCTCCCACGACTAAATAATTTAAGATTCTGACTCCTACCACCATCTCAAATCTGACGAAGTTCTTCTGCAGCAGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611694 Oligochaeta sp. water mite diet isolate 1169-BHL110116-GBD27560_12957-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCATCTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACGAAATAATATAAGAATCTGACTACTACCACCATCTCTAATCTTACTAATTGCTTCTGCAGCAGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 86.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611695 Oligochaeta sp. water mite diet isolate 1173-BHL110116-GBD11235_20371-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTCATTTTAGGAGTCTGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACCTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611696 Oligochaeta sp. water mite diet isolate 1180-BHL110116-GBD23884_24325-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTTTGAGCAGGAATAATTGGAACTGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTTGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.7% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611697 Oligochaeta sp. water mite diet isolate 1188-BHL110116-GBD26647_17061-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTTATAATAATTTTTTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTTCTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 87.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611698 Oligochaeta sp. water mite diet isolate 1191-BHL110116-GBD14468_12071-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGCATGAGCAGGAATAATTGGAACTGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACATCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTTTTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611699 Oligochaeta sp. water mite diet isolate 1194-BHL110116-GBD22563_6751-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCGCTAACCATACAAAATTCTTCTGCAGCAGTAAAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611700 Oligochaeta sp. water mite diet isolate 1196-BHL110116-GBD7393_13269-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAGTACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTA-TTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611701 Oligochaeta sp. water mite diet isolate 1199-BHL110116-GBD17697_27770-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGCATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCATTGTTACTGCTCATGCATTTTTAATAATTTTCTTTCTAGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611702 Oligochaeta sp. water mite diet isolate 1200-BHL110116-GBD19807_21628-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTGAGGAGTATGAGCAGGAATAATGGGAACAGGGACTAGAATACTTATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACTCTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCATGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611703 Oligochaeta sp. water mite diet isolate 1202-BHL110116-GBD24268_6015-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGAACATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCTCATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCCCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAGAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611704 Oligochaeta sp. water mite diet isolate 1212-BHL110116-GBD25913_7929-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTGGTTACTGCACATGCATTCTTAATAGTTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGACTAGTACCACTAATACTTGGAGCACCAGATATGGCTTTCCCACGACAAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611705 Oligochaeta sp. water mite diet isolate 1220-BHL110116-GBD25995_10688-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGATCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACTCTAGTTACTGCACATGCTTTCTTAATAATTTTCTTTATTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611706 Oligochaeta sp. water mite diet isolate 1221-BHL110116-GBD24608_14235-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACCTAATCTTCGGAGTATGAGCAGGAATAATTGGAACCGGTACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACAACCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611707 Oligochaeta sp. water mite diet isolate 1226-BHL110116-GBD21850_26702-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGGGATCAATTATATAAAACCCTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTATTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCCCCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611708 Oligochaeta sp. water mite diet isolate 1240-BHL110116-GBD10598_4617-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTCGGAGTATGATCAGGAATAATTGGAACAGGGACTAGAGTACTAATTCGAATTGAATTATCACAACCAGGATCGTTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACACGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTACTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.8% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611709 Oligochaeta sp. water mite diet isolate 1242-BHL110116-GBD13921_27296-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGGGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTATTACCACTAATACTTGGAGCTCCAGATATTGCTTTCCCACGACTAAATAATTTAATATTCTGACTACTACCACCATCTCTAAACTTGCAAAATTCTTCTGCAGCAGGAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611710 Oligochaeta sp. water mite diet isolate 1245-BHL110116-GBD24286_20561-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATATTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGTTCTAGAATACTAATTCGAATTGAATTATCACAGCCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611711 Oligochaeta sp. water mite diet isolate 1246-BHL110116-GBD13306_15796-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACCCAATAATATAAGATTCTGACTACTACCAACATCTCGAATCTTACTAAGTACTTCTGCAGCAGTACAAAACGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611712 Oligochaeta sp. water mite diet isolate 1269-BHL110116-GBD28017_8726-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGTAACAGGTTCTAAAATACTAATTCGGATTGAATTATCACAACCTGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTTTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611713 Oligochaeta sp. water mite diet isolate 1271-BHL110116-GBD18280_2332-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATGCGAATTGAATTAACACAACCAGTATCAATCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGATCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCCCCATCTCTAATCTTGCTAATTTCTTCTGCAGCAGTAGAAAATGGCGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611714 Oligochaeta sp. water mite diet isolate 1275-BHL110116-GBD18230_19358-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTCTGAGCAGGAATAATTGGAACTGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGAACATTCTTAGGAAAAGATCAACTATATAACATCCTAGTTACTGCACACGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTCCCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTACTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.8% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611715 Oligochaeta sp. water mite diet isolate 1277-BHL110116-GBD17654_28582-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACGACCAGGATCATTCTTAGGTAGAGATCAACTATATAACACCCTTGTTACTGCTCATGCTTTCTTAATAATTTTTTTCCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611716 Oligochaeta sp. water mite diet isolate 1281-BHL110116-GBD26644_23125-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATACTTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAATCAGGATCATTCTTACGAAAAGATCAACTATATAACACCCTAGGTACTGCACATGCATTCTTAATACTTTTCTTTCTTGTACTACCAGTATTTATGGGAGGAATTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGAATCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611717 Oligochaeta sp. water mite diet isolate 1285-BHL110116-GBD17614_23884-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGCATGAGCAGGAATAATTGGAACTGCGTCTAGAATACTTATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAATACCCTAGTTACTGCACATGCATTTTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTCCCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611718 Oligochaeta sp. water mite diet isolate 1287-BHL110116-GBD10225_10607-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGCATGAGCAGGAATAATTGGAACTGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCTGATATGGCTTTCCCACGACTAAATAATATAAGATCCTGACTACTACCCCCATCTCTAACCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611719 Oligochaeta sp. water mite diet isolate 1292-BHL110116-GBD21432_25616-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGATCAGGAATAATTGGAACATGGT-CTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCATAGTTACTGCACATGCATTCGTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATATTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611720 Oligochaeta sp. water mite diet isolate 1295-BHL110116-GBD28024_22002-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGTATAATTGGAACAGGGTTTAGAATACTAATTCGAATTGAATTATGACAACCAGGATCATTCATAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGACTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.8% identical to accession ID KF021247, identified in GenBank as Amynthas morrisi. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611721 Oligochaeta sp. water mite diet isolate 1297-BHL110116-GBD15008_19287-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGGAACTGATTAGTACCACTAATACTTGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID LN810268, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611722 Oligochaeta sp. water mite diet isolate 1308-BHL110116-GBD16110_25545-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTTATTGGGGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCATTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCACTAACCTTACTAATATCTACTGCAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611723 Oligochaeta sp. water mite diet isolate 1314-BHL110116-GBD7671_6191-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTTATTTTAGGAGTATGATCAGGAATAATTGGAACTGCGACTAGAATACTTATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCACCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611724 Oligochaeta sp. water mite diet isolate 1319-BHL110116-GBD4154_17081-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGATCAGGAATAATTGGAATTTGTTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTATTAGGAAGAGATCAACTATATAACACACTAGTTACTGCTCATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611725 Oligochaeta sp. water mite diet isolate 1322-BHL110116-GBD22622_20353-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACAAATCATAAAGATATTGGCACTTTATACTTTATTTTTGGAGTATGAGCAGGAATAATTGGAACAGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTTTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCTCCAGATATAGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID KT716826, identified in GenBank as Amynthas morrisi. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611726 Oligochaeta sp. water mite diet isolate 1330-BHL110116-GBD18021_23361-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTGGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTGATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611727 Oligochaeta sp. water mite diet isolate 1333-BHL110116-GBD23531_22294-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCCGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTAGTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTATCCCACGACAAAATAATTTAAGATTCAGACTACGACCACCAACTCTAATCTTACAAAAATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611728 Oligochaeta sp. water mite diet isolate 1345-BHL110116-GBD24671_20457-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTTGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATATTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAGCACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611729 Oligochaeta sp. water mite diet isolate 1351-BHL110116-GBD10192_27969-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGCACTGGGTCTAGAATACTAATTCGAGTTGAATTATCACACCCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGGAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611730 Oligochaeta sp. water mite diet isolate 1352-BHL110116-GBD6563_4928-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATATTTTATTTTTGGAGTATGAGCAGGAATAATTGGAACAGCGACTAGAATACTAATTCGAATTGAATTAGCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATCCTGACTACTACCACCATCACTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611731 Oligochaeta sp. water mite diet isolate 1354-BHL110116-GBD8877_10073-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTGTATACTTTATTTTAGGAGTATGATCAGGAATAATGGGAACTTCGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGTGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG422806, identified in GenBank as Slavina appendiculata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611732 Oligochaeta sp. water mite diet isolate 1355-BHL110116-GBD17563_14726-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAGTTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCCTTCCCACGACTAAATAATATAAGATCCTGACTACTACCACCATCACTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611733 Oligochaeta sp. water mite diet isolate 1360-BHL110116-GBD27414_9643-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611734 Oligochaeta sp. water mite diet isolate 1363-BHL110116-GBD8483_7388-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGGGCTTGAGCAGGAATAATTGGAACTTGAATTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACATCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATCCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611735 Oligochaeta sp. water mite diet isolate 1367-BHL110116-GBD11871_23316-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTCGGAGTATGAGCAGGAATAATTGGAACAGGTACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGTAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTCCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGACATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611736 Oligochaeta sp. water mite diet isolate 1368-BHL110116-GBD25361_7001-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGCATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGAATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTGGTAATACCAGTATTTATTGGAGGATTTTGAAACTGATTAGTACCACTAATACTTGGAGCTCCACATATGGCTTTCCCACGACTAAAAAATTTAAGATTCTGACTATTACCAGCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611737 Oligochaeta sp. water mite diet isolate 1380-BHL110116-GBD26795_13914-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACACTATACTTAATTTTAGGAGGATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAAATCGAATAGAATTATCACAACCAGGATCACTCTTAGGAAGAGATCGACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGCAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACAAAATAAATTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCCTCTGCAGCAGTAGAAAATCGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG422806, identified in GenBank as Slavina appendiculata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611738 Oligochaeta sp. water mite diet isolate 1386-BHL110116-GBD7908_7912-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACATGGT-CTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGTAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATCGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGAGATGGCTTTCCCACGACTAAATAATATAAGATCCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611739 Oligochaeta sp. water mite diet isolate 1387-BHL110116-GBD8898_25993-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCGACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGAAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.1% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611740 Oligochaeta sp. water mite diet isolate 1390-BHL110116-GBD14427_25370-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATATTTTATTTTCGGAGCCTGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATATTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611741 Oligochaeta sp. water mite diet isolate 1391-BHL110116-GBD4984_7048-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGATCAGGAATAATTGGAACAGCGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGACCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTATTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATCCTGACTACTACCACCATCACTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611742 Oligochaeta sp. water mite diet isolate 1396-BHL110116-GBD22518_19496-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGCGTCTAGAATATTAATTCGAATTGAATTATCACAACCAGGATCATTCCTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCGTAATAATTTTCTTTATTGCAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCACTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611743 Oligochaeta sp. water mite diet isolate 1397-BHL110116-GBD19375_15826-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTCATTTTAGGAGCATGAGCAGGAATAATTGGAACTGGGATTAGAATATTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACATCCTTGTTACTGCACATGCATTTTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTGACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611744 Oligochaeta sp. water mite diet isolate 1398-BHL110116-GBD13597_13206-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACAAATCATAAAGATATTGGCACTCTATATTTAATTTTAGGAGTATGAGCAGGAATAATTGGGACAGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTTGTTACTGCACATGCATTTTTAATAATTTTCTTTATTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID KT716826, identified in GenBank as Amynthas morrisi. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611745 Oligochaeta sp. water mite diet isolate 1401-BHL110116-GBD2452_13421-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGTACTAGAATACTAATTCGAACTGAATTATGACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCTTTCTTAATAATTTTTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611746 Oligochaeta sp. water mite diet isolate 1406-BHL110116-GBD10478_14660-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTCTGAGCAGGAATAATTGGAACATGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCACTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCGTAATAATTTTCTTTATTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAAGTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611747 Oligochaeta sp. water mite diet isolate 1408-BHL110116-GBD15795_21952-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTCGGAGTATGAGCAGGAATAATTGGAACTGGGTTTAGAATACTTATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACATCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTTTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACGGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611748 Oligochaeta sp. water mite diet isolate 1411-BHL110116-GBD7834_11698-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGCCACTCTATACTTAATTTTAGGGATATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAAAATAAGATCCTGACTACCACCACCATCACTAATCTTACGAAAATCTTCTGCAGCAGTAGAAAAAGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611749 Oligochaeta sp. water mite diet isolate 1412-BHL110116-GBD25306_7237-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCCGGATCATTCCTAGGAAGAGATCAAATATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTCCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCCCTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATCCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611750 Oligochaeta sp. water mite diet isolate 1413-BHL110116-GBD15431_21703-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCATTCCCACGACTAAATAAAAAAAGATACTGAATACGACCACCATCGCTAAACTTACAGATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611751 Oligochaeta sp. water mite diet isolate 1428-BHL110116-GBD26607_8508-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAGCAGGGACTAGAATACTAATTCGAATTGAATTAAGACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACCCCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTCCCCACGACCAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.2% identical to accession ID KT716826, identified in GenBank as Amynthas morrisi. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611752 Oligochaeta sp. water mite diet isolate 1441-BHL110116-GBD9860_9997-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGTACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LN810268, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611753 Oligochaeta sp. water mite diet isolate 1443-BHL110116-GBD4086_15652-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAAATATATAACACCCTAGTTACTGCACATGCTTTCATAATAATTTTCTTTCTTGTAATACCAGTCTTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCCTTCCCACGACTAAATAATATAAGATTCTGAATACTACCACCATCTCTAACATTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611754 Oligochaeta sp. water mite diet isolate 1446-BHL110116-GBD9378_24686-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGCATTGAATTATCACCACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTAGATACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAATTTTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATATTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611755 Oligochaeta sp. water mite diet isolate 1449-BHL110116-GBD24905_15546-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATATTTAATTTTAGGAGTTTGAGCAGGAATAATTGGTACAGGTACTAGAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAGTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611756 Oligochaeta sp. water mite diet isolate 1450-BHL110116-GBD6380_15468-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGACTTGAATTATCACAACCAGGACCATTCTTAGGAAGAGATCAACTATATAACACCCTATTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCACCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611757 Oligochaeta sp. water mite diet isolate 1453-BHL110116-GBD24853_8937-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAGTTTTAGGAGTATGAGCAGGAATAATTGTAACAGGGACTGGAATACTAATTCGAATTGATTTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATCAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAAATTAAGATTCTGACTACTATCACCATCTCTAAACTTACTAATTTCTTCTGCAGCAGTAGAAAATGGCGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611758 Oligochaeta sp. water mite diet isolate 1454-BHL110116-GBD16118_12328-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.7% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611759 Oligochaeta sp. water mite diet isolate 1455-BHL110116-GBD3892_19642-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACATTGACTAGAATACTAATTCGGATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAAAACCCTAGTTACTTCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAGACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611760 Oligochaeta sp. water mite diet isolate 1456-BHL110116-GBD6603_14575-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCCGGAATAATTGGAACTGGGACTAGAATACTAATTCGAATTGAATTATCACAACCCGGATCATTCTTCGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611761 Oligochaeta sp. water mite diet isolate 1458-BHL110116-GBD9295_6315-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGCATGATCAGGAATAATTGGAACTCGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGTGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAAAACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTGTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611762 Oligochaeta sp. water mite diet isolate 1464-BHL110116-GBD2224_14571-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTCATTTTAGGAGTATGAGCAGGAATAATTGGAACTGCTCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCTTTTTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611763 Oligochaeta sp. water mite diet isolate 1467-BHL110116-GBD18189_11291-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTATATAACATCCTTGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCATCAGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611764 Oligochaeta sp. water mite diet isolate 1468-BHL110116-GBD23852_24885-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTTGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACTCTAGTTACTGCACATGCATTTGTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611765 Oligochaeta sp. water mite diet isolate 1472-BHL110116-GBD2726_13934-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTTATTTTCGGAGCATGATCAGGAATAATTGGAACATGGT-CTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611766 Oligochaeta sp. water mite diet isolate 1473-BHL110116-GBD26816_15068-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTCTATACTTAATTTTAGGAGTATGAGCAGGAATAGTTGGAACAGGGCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAAATATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611767 Oligochaeta sp. water mite diet isolate 1475-BHL110116-GBD18547_26173-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATCTGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCT-CAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID LN810268, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611768 Oligochaeta sp. water mite diet isolate 1478-BHL110116-GBD25970_10820-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTCGGAGTATGAGCAGGAATAATTGGAACTGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACACTAGTTACTGCACATGCATTTTTAATAATTTTTTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611769 Oligochaeta sp. water mite diet isolate 1480-BHL110116-GBD23997_24738-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGCGCAGGATTAATTGGAACAGGGCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGAGATGGCTTTCCCACGACTAAAAAATTTAAGAAACTGACTACGACCACCATCTCTAATCGTACTAATGGCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611770 Oligochaeta sp. water mite diet isolate 1482-BHL110116-GBD26848_20102-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACATCATCCTTGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGACTACTAATTCGAATAGAACTAGCTCAACCAGGATCATTTCTAGGCAGAGATCAACTATATAACACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAAATTAAGATTCTGACTACTACCACCATCTCTAATCTTACGAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID MG423030, identified in GenBank as Dero obtusa. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611771 Oligochaeta sp. water mite diet isolate 1484-BHL110116-GBD25718_19374-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGTAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTATCTTA-TAATACCAGTAATTATTGGAGGATTTGGAAACTGATTAGTAACACTAATACTTGGAGCTCCAGATATGGCTGCCCCACGCCAAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTGCTAATTTCTTCTGCAGCAGTAGAAAGTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611772 Oligochaeta sp. water mite diet isolate 1485-BHL110116-GBD10060_5845-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATGCTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAGCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTTACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTGGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611773 Oligochaeta sp. water mite diet isolate 1486-BHL110116-GBD26484_17305-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCCATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCAAAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACGAAAAAAATTAAGAATCTGACTACGACCACCATCTCTAAACTGACAAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611774 Oligochaeta sp. water mite diet isolate 1487-BHL110116-GBD25348_7273-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACATGGT-CTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACATCCTAGTTACTGCACATGCATTCGTAATGATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611775 Oligochaeta sp. water mite diet isolate 1489-BHL110116-GBD29256_17279-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTCTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATGGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGATCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCAACGCTAAGCGGACGAAGGGCGGCGGCAGCAGGAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611776 Oligochaeta sp. water mite diet isolate 1490-BHL110116-GBD18785_10038-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTCTGAGCAGGAATAATTGGAACTGCGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACCAAATAATATAAGATTCTGACTACTACCACCATCACTAACCTTACTAATATCTGCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611777 Oligochaeta sp. water mite diet isolate 1491-BHL110116-GBD10155_8090-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGATCAGGAATAATTGGAACATGTACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGACATGGCTTTCCCACGACTAAATAACATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611778 Oligochaeta sp. water mite diet isolate 1492-BHL110116-GBD9046_8697-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTGTACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCGTAATAATTTTTCTTCTT-GTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCACTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611779 Oligochaeta sp. water mite diet isolate 1493-BHL110116-GBD8765_18076-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATATTTAATTTTAGGAGTTTGAGCAGGAATAATTGGTACAGGTACTAGAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID LN810268, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611780 Oligochaeta sp. water mite diet isolate 1495-BHL110116-GBD11635_6333-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCCCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611781 Oligochaeta sp. water mite diet isolate 1496-BHL110116-GBD8800_9960-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTTATTTTAGGAGTATGATCAGGAATAATTGGAACTGGCTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611782 Oligochaeta sp. water mite diet isolate 1497-BHL110116-GBD8112_6441-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGTACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACATCCTTGTTACTGCACATGCATTCTTAATAATTTTTTTTATTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.0% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611783 Oligochaeta sp. water mite diet isolate 1499-BHL110116-GBD11262_8428-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATACTTAATTTTTGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTTGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGACTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCCCCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611784 Oligochaeta sp. water mite diet isolate 1504-BHL110116-GBD9844_23838-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATGCTTAATTTTAGGAGTATGAGCCGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAAAGATCAACTATATAATACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTCCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611785 Oligochaeta sp. water mite diet isolate 1506-BHL110116-GBD12825_4927-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAGTCTATACGTAATTTTAGAAGTATGAGAAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTCAAGATTCTGACCACTACCACCATCTCCAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATCGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 84.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611786 Oligochaeta sp. water mite diet isolate 1509-BHL110116-GBD20177_3589-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGCCTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID LN810268, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611787 Oligochaeta sp. water mite diet isolate 1510-BHL110116-GBD20510_2768-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGATCAGGAATAATTGGAACATCTACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAAATATATAACACAATTGTTACTGCACATGCATTCTTAATAATTTTCTTTATTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611788 Oligochaeta sp. water mite diet isolate 1511-BHL110116-GBD9857_26632-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAGCAGGGACTAGAATACGAATTCGAATTGAATTATCACAACCAGGAGCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACTTGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTCTTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGCCTAAATAATTTAAGATTCTGACTACTCCCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633404, identified in GenBank as Slavina sp. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611789 Oligochaeta sp. water mite diet isolate 1512-BHL110116-GBD22306_13453-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACAAATCATAAAGATATTGGCACTCTATATTTTATTTTAGGAGTATGAGCAGGAGTAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAAACAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTATTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCCCTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATATCTTCTGCAGCAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.2% identical to accession ID KT716826, identified in GenBank as Amynthas morrisi. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611790 Oligochaeta sp. water mite diet isolate 1513-BHL110116-GBD17964_20349-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAGTTGAATTATCACAACCAGGAACATTCTTAGGAAATGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611791 Oligochaeta sp. water mite diet isolate 1514-BHL110116-GBD16754_22193-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGATCAGAAATAGTTGGAACATCGTCTAGAATACTTATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611792 Oligochaeta sp. water mite diet isolate 1516-BHL110116-GBD2450_15993-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTTTGAGCAGGAATAATTGGAACTTGTTTTAGAATACTAATTCGAATTGAATTAGCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACTCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.2% identical to accession ID KT716826, identified in GenBank as Amynthas morrisi. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611793 Oligochaeta sp. water mite diet isolate 1519-BHL110116-GBD10891_19189-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCAGTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATCTAAGATTCTGACCACGACCCCCATCTTCAACCTTACAAAAATCTTCTGCAGCAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 86.6% identical to accession ID MG422806, identified in GenBank as Slavina appendiculata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611794 Oligochaeta sp. water mite diet isolate 1520-BHL110116-GBD11338_13126-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGATCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACGATCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATACAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611795 Oligochaeta sp. water mite diet isolate 1521-BHL110116-GBD8862_25916-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTCGGAGCATGATCAGGAATAATTGGAACATGCTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTATTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCCCGAATAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.1% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611796 Oligochaeta sp. water mite diet isolate 1527-BHL110116-GBD18926_23494-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTATGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGAATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGACTTGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611797 Oligochaeta sp. water mite diet isolate 1530-BHL110116-GBD28287_10045-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGCATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACATCATAGTTACTGCACATGCATTCTTAATAATTTTCTTTATAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCCCCAGATATGGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611798 Oligochaeta sp. water mite diet isolate 1531-BHL110116-GBD14397_13324-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACTTTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACATCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCTGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTGCTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.4% identical to accession ID KU728850, identified in GenBank as Enchytraeus albidus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611799 Oligochaeta sp. water mite diet isolate 1532-BHL110116-GBD2225_17531-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGATCAGGAATAATTGGAACATGGT-CTAGAATACTAATTCGAATTGAATTATCACAACCCGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCCCTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAGATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611800 Oligochaeta sp. water mite diet isolate 1533-BHL110116-GBD18623_13528-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGATCAGGAATAATTGGAACAGCGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACATCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTAATTGGAGGAGCTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTAGTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.0% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611801 Oligochaeta sp. water mite diet isolate 1534-BHL110116-GBD23691_9775-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTCGGAGTATGATCAGGAATAATTGGAACATCGT-CTAGTATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTTGGAAGAGATCAACTCTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611802 Oligochaeta sp. water mite diet isolate 1538-BHL110116-GBD20266_10252-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGTTTTCCCACGACTAAATAATTTAAGATTCTGACTTCTACCACCATCACTAATTCTATTAGTATCATCCGCAGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611803 Oligochaeta sp. water mite diet isolate 1539-BHL110116-GBD27071_18985-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATATTTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTTTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCCCCATCACTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611804 Oligochaeta sp. water mite diet isolate 1540-BHL110116-GBD24337_14732-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCGACAAATCATAAAGATATTGGCACTCTATACTTCATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACAGCACATGCATTCTTAATAATTTTCTTCCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID MK047674, identified in GenBank as Nais communis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611805 Oligochaeta sp. water mite diet isolate 1542-BHL110116-GBD26592_12301-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGCTACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCTACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611806 Oligochaeta sp. water mite diet isolate 1543-BHL110116-GBD13345_1878-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGACTAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGAGTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAAACTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611807 Oligochaeta sp. water mite diet isolate 1544-BHL110116-GBD25939_6816-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAATTGATTTGTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTTTGACTACTACCACCTTCACTAATCTTATTAGTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611808 Oligochaeta sp. water mite diet isolate 1547-BHL110116-GBD15312_11977-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGCATGAGCAGGAATAATTGGAACATGGCTTAGAATATTAATTCGAATTGAATTATGACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACAGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611809 Oligochaeta sp. water mite diet isolate 1548-BHL110116-GBD23415_26954-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTATATAATATCCTAGTTACTGCACATGCATTTATAATAATTTTTTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.7% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611810 Oligochaeta sp. water mite diet isolate 1549-BHL110116-GBD21747_7677-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGATCAGGAATAATTGGAACTGGTCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCATAGTTACTGCACATGCACTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGGCTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611811 Oligochaeta sp. water mite diet isolate 1554-BHL110116-GBD3729_14504-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGGACTAGAATACTAATTCTGATTGAATTATCTCAACCAGGATCATTCTTAGGAAGAGATCAACTATATAATACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTGGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCATCACTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611812 Oligochaeta sp. water mite diet isolate 1555-BHL110116-GBD5303_8472-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTCGGAGTATGAGCAGGAATAGTTGGAACTGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCATAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTTCCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGAAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611813 Oligochaeta sp. water mite diet isolate 1556-BHL110116-GBD12663_11521-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTAATTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCCCTAACCTTACTAACATCTGCTGCAGCAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611814 Oligochaeta sp. water mite diet isolate 1558-BHL110116-GBD19543_10664-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGTACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCCTAGTTACTGCCCATGCATTCTTAATAATTTTTTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCCCTAATACTTGGAGCTCCAGACATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCCCCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611815 Oligochaeta sp. water mite diet isolate 1559-BHL110116-GBD7483_10127-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCT-CAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID LN810268, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611816 Oligochaeta sp. water mite diet isolate 1560-BHL110116-GBD19126_24246-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTATGAGCTGGAATAATTGGAACAGGGACTAGAATATTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAATACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTGGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTACTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAGTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611817 Oligochaeta sp. water mite diet isolate 1561-BHL110116-GBD12485_8189-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGATCAGGAATAATTGGAACTGCGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGTGATCAACTATATAACATCCTAGTTACTGCACATGCTTTCATTATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611818 Oligochaeta sp. water mite diet isolate 1562-BHL110116-GBD17072_4006-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAAGAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCATTATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCATTATTTATGGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGATCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCCCCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGCGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 85.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611819 Oligochaeta sp. water mite diet isolate 1563-BHL110116-GBD18148_17635-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTTTATACTTTATTTTAGGAGCATGATCAGGAATAATTGGAACTTGTTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACATCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCACTAACCTTACTAATATCTTGTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.8% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611820 Oligochaeta sp. water mite diet isolate 1564-BHL110116-GBD11219_15932-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTCGGAGTATGAGCAGGAATAATTGGAACAGCGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCATAATAATTTTTTTTCTAGTAATACCAGTATTGATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633404, identified in GenBank as Slavina sp. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611821 Oligochaeta sp. water mite diet isolate 1566-BHL110116-GBD21302_2600-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTTTGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCCTTGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACAACTACCACCATCTCTAATCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611822 Oligochaeta sp. water mite diet isolate 1567-BHL110116-GBD7887_13830-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTTGTTATACCAGTATTTATTGGAGGATTTGGAAACTGACTACTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCATCTCTAATCCTAATAGTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611823 Oligochaeta sp. water mite diet isolate 1568-BHL110116-GBD14183_24718-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCCTTCTTAGGAAGAGATCAACTATATAACGGCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTATTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCACTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611824 Oligochaeta sp. water mite diet isolate 1569-BHL110116-GBD4246_20762-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCACAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACCCTAGTTACTGCACATGCATTCCTAATAATTTTCTTTCTTGTTATACCAGTATTTATTGGAGGATTTGGAAACTGACTACTACCACTAATACTTGGAGCACCAGATATGGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCATCTCTAATCCTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611825 Oligochaeta sp. water mite diet isolate 1570-BHL110116-GBD22152_16328-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGCATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAAATTTATAACATCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCCCTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCCCCATCTCTAATCTTACTAATTTCTTCTGCATCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611826 Oligochaeta sp. water mite diet isolate 1571-BHL110116-GBD17710_5268-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTCTTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGATCTCCAGATATGGCTTTCCCACGCCTTAATAATTTAAGATTCTGACTACTCCCCCCATCTCTAATCTTGCTAATTTCTTCTGCAGCAGTAGAAAATGGCGCTGGCACAG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611827 Oligochaeta sp. water mite diet isolate 1572-BHL110116-GBD19952_23182-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTTTATATTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAAATATATAATATCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611828 Oligochaeta sp. water mite diet isolate 1573-BHL110116-GBD22321_25030-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGTACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCGTAATAATTTTCTTTATTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCACTAACCTTACTAATATCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611829 Oligochaeta sp. water mite diet isolate 1574-BHL110116-GBD19095_3684-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGATCAGGAATAATTGGAACATGGT-CTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCAATCTTAGGAAAAGATCAAATATATAACACACTAGTTACTGCACATGCATTTTTAATAATTTTCTTTCTTGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCCCCATCACTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611830 Oligochaeta sp. water mite diet isolate 1576-BHL110116-GBD9662_23945-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTCATTTTCGGAGTATGAGCAGGAATAATTGGAACTGGGCTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCCCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAACTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611831 Oligochaeta sp. water mite diet isolate 1577-BHL110116-GBD15812_21120-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGTTCTAGAATACTAATTCGAATTGAATTATCACACCCAGGCTCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTGGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCGCGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611832 Oligochaeta sp. water mite diet isolate 1578-BHL110116-GBD5534_9016-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTCATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGACTAGAATACTAATTCGAATTAAATTATCACAACCAGGATCATCTATAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611833 Oligochaeta sp. water mite diet isolate 1580-BHL110116-GBD21144_7345-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGCACATGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCACTAATCTTACTAATACCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611834 Oligochaeta sp. water mite diet isolate 1581-BHL110116-GBD16561_16213-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTTCGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAAATATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCATTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611835 Oligochaeta sp. water mite diet isolate 1582-BHL110116-GBD25826_22649-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGTACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGATATCAAATATATAAAACCCTAGTTACTGCACATGGATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTGCCCACGACTAAATAATTTAAGAATCTGAACACTACCCCCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611836 Oligochaeta sp. water mite diet isolate 1584-BHL110116-GBD27425_20744-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACATTGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTATTAGGAAAAGATCAACTTTATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTATTGTAATACCAGTATTTATTGGAGGATTTGGAAAATGATTAGTACCACTAATACTTGGAGCTCCAGAAATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCCCCATCACTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611837 Oligochaeta sp. water mite diet isolate 1585-BHL110116-GBD28291_16970-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGCCTAGAATATTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTTTATAACACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTTCCACCATCTCTAATCTTACTAATCTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611838 Oligochaeta sp. water mite diet isolate 1587-BHL110116-GBD9544_3239-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAATGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTTATAATTTTTTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGACTAGTACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGACTAAATAACATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGCAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611839 Oligochaeta sp. water mite diet isolate 1591-BHL110116-GBD20315_25450-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTCAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTACTACCACTAATACTTGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 88.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611840 Oligochaeta sp. water mite diet isolate 1593-BHL110116-GBD19712_18198-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGTTCTAGAATACTAATTCGAATTGAATTATTACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCTTTCTTAATAATTTTCTTCATTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTAGTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611841 Oligochaeta sp. water mite diet isolate 1594-BHL110116-GBD6541_19903-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTCGGAGCATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACACCCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTTTTTATTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAACATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCAGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611842 Oligochaeta sp. water mite diet isolate 1596-BHL110116-GBD25166_11285-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGACTAGAATATTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTATTACCACTAATACTTGGAGCTCCAGATATGGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCGTCTCTAAACTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611843 Oligochaeta sp. water mite diet isolate 1597-BHL110116-GBD16492_11346-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTATTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAAAATAAGATTCTGACTACTACCACCATCTCTAAAATTACTAATATCAAGAGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611844 Oligochaeta sp. water mite diet isolate 1598-BHL110116-GBD25185_5020-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATATTTGGAACAGGCCCTAGAATACTAATTCGAATTAAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAAAAAATTAAGATTCTGACTACTACCACCAGCTCTAAACTGACTAATTTCTTCTGCAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611845 Oligochaeta sp. water mite diet isolate 1599-BHL110116-GBD9961_16138-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTTGGAGTATGATCAGGAATAGTTGGAACTTCGATTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCACCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611846 Oligochaeta sp. water mite diet isolate 1601-BHL110116-GBD11835_9061-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACAAATCATAAAGATATCGGCACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATCTTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.8% identical to accession ID KT716826, identified in GenBank as Amynthas morrisi. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611847 Oligochaeta sp. water mite diet isolate 1602-BHL110116-GBD28591_14304-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAGTTGGAACAGGGTTTAGAATACTAATTCGAGTTGAATTATGACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGGGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID EF089357, identified in GenBank as Limnodrilus hoffmeisteri. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611848 Oligochaeta sp. water mite diet isolate 1603-BHL110116-GBD21497_6833-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGATCTGGAATAATTGGAACAGGTACTAGAATACTTATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACCAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCCGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.2% identical to accession ID KT716826, identified in GenBank as Amynthas morrisi. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611849 Oligochaeta sp. water mite diet isolate 1606-BHL110116-GBD18105_13267-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAGTTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTTGTACCATTAATACTTGGAGCTCCAGATATAGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCCTACTAGTTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611850 Oligochaeta sp. water mite diet isolate 1607-BHL110116-GBD15694_26064-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTTTGAGCAGGAATAATTGGAACATCATCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGACATGGCTTTTCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.9% identical to accession ID KT716826, identified in GenBank as Amynthas morrisi. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611851 Oligochaeta sp. water mite diet isolate 1608-BHL110116-GBD13909_9973-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTTTGAGCAGGAATAATTGGAACTTGGACTAGAATACTTATTCGAATTGAATTATCACAACCAGGAACATTCTTAGGAAGTGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTCATTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611852 Oligochaeta sp. water mite diet isolate 1614-BHL110116-GBD27864_10909-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAAATATATAACACCCTAGTTACTGCACATGCATTCTTTATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCTCCAGATATAGCTTTCCCTCGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCCTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.4% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611853 Oligochaeta sp. water mite diet isolate 1616-BHL110116-GBD16983_25854-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATATTTTATTTTAGGAGTATGAGCAGGAATAGTTGGAACAGGTTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTATTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAGTACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611854 Oligochaeta sp. water mite diet isolate 1618-BHL110116-GBD13681_17280-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATCTTAGGAGTTTGAGCAGGAATAATTGGAACAGGGACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAACACCCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAACTGACTACTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611855 Oligochaeta sp. water mite diet isolate 1620-BHL110116-GBD27160_18715-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTCGGAGCATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGAACATTCTTAGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCTTTTTTAATAATTTTTTTCTAGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTTCCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID KY633404, identified in GenBank as Slavina sp. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611856 Oligochaeta sp. water mite diet isolate 1621-BHL110116-GBD22299_4995-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTCATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATCGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAAATATATAACACCATTGTTACTGCTCATGCATTCTTAATAATTTTCTTACTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611857 Oligochaeta sp. water mite diet isolate 1624-BHL110116-GBD18582_11848-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTATTATAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGGAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611858 Oligochaeta sp. water mite diet isolate 1625-BHL110116-GBD25995_10373-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTTTTATAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCCCCATCTCTAACCTTACTACTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611859 Oligochaeta sp. water mite diet isolate 1626-BHL110116-GBD17952_17099-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGAATTAAATTATCACAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGAGGATTTGGAAACTGACTACTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCATCACTAATCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.6% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611860 Oligochaeta sp. water mite diet isolate 1627-BHL110116-GBD25712_8560-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGGATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAATGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATAGCTTTCCCTCGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611861 Oligochaeta sp. water mite diet isolate 1635-BHL110116-GBD28066_12792-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTCATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAATGATCAACTATATAACACCATAGTTACTGCACATGCATTCTTAATAATTTTCTTTATTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTCCCACTAATACTAGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611862 Oligochaeta sp. water mite diet isolate 1638-BHL110116-GBD22605_26912-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAATACTCTTGTTACTGCACATGCATTTTTAATAATTTTCTTTCTTGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611863 Oligochaeta sp. water mite diet isolate 1639-BHL110116-GBD6167_16206-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATACAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTACCACAACCAGGATCATTCATAGGAAGGGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCGCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611864 Oligochaeta sp. water mite diet isolate 1642-BHL110116-GBD23248_13731-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611865 Oligochaeta sp. water mite diet isolate 1643-BHL110116-GBD8898_17025-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACTACTACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611866 Oligochaeta sp. water mite diet isolate 1649-BHL110116-GBD18198_20039-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGAACATTCTTAGGAAAAGATCAACTATATAATACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.4% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611867 Oligochaeta sp. water mite diet isolate 1656-BHL110116-GBD11360_3027-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGATCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTATTGTTATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611868 Oligochaeta sp. water mite diet isolate 1663-BHL110116-GBD27240_10978-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACCCCCTAGTTACTGCACATGCATTTTTAATAATTTTCTTACTTGTAATACCAGTATTAAATGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611869 Oligochaeta sp. water mite diet isolate 1664-BHL110116-GBD27311_19919-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGAACATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGATACTGATTAGTACCACTAATACTTGGAGCTCCAGATACGGCTTTCCCACGAAAAAATAAATTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCCTCTGCAGCAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611870 Oligochaeta sp. water mite diet isolate 1665-BHL110116-GBD16735_14258-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTCTACCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611871 Oligochaeta sp. water mite diet isolate 1668-BHL110116-GBD10822_14592-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGCATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACACTTGTTACTGCACATGCATTCGTAATAATTTTTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.8% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611872 Oligochaeta sp. water mite diet isolate 1675-BHL110116-GBD19611_21039-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGGGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAAATGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.5% identical to accession ID LN810268, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611873 Oligochaeta sp. water mite diet isolate 1681-BHL110116-GBD24486_10492-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACATGGACTAGAATACTAATTCGAATTGAACTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTCCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611874 Oligochaeta sp. water mite diet isolate 1682-BHL110116-GBD10959_24419-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTTGTTCTAGAATACTAATTCGAATTGAATTCTCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGAAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.0% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611875 Oligochaeta sp. water mite diet isolate 1686-BHL110116-GBD21176_15349-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAGTTGGAACTGCGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTTATAATTTTTTTTATAGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611876 Oligochaeta sp. water mite diet isolate 1687-BHL110116-GBD21137_11597-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID JQ519820, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611877 Oligochaeta sp. water mite diet isolate 1688-BHL110116-GBD22201_12480-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTATAGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACGAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTATTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611878 Oligochaeta sp. water mite diet isolate 1689-BHL110116-GBD13330_25256-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGCGACTGGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTATAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCCCCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611879 Oligochaeta sp. water mite diet isolate 1691-BHL110116-GBD8054_7357-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAGTTGGAACAGGGACTAGACTACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCACCAGATATGGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCCCCATCACTAATCCTACTAATTGCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611880 Oligochaeta sp. water mite diet isolate 1692-BHL110116-GBD19316_20107-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTATTAATAATTTTCTTTCATA-TAAAACCAGTATTTGTTGGAGGATTTGGAAACTGATTAGGACCACTAATACTTGGAGCTCCAGATAAGACCTTCCCACGACTAAATAATTTAAGATTCTGACCACTACCACCATCTCTAAACTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611881 Oligochaeta sp. water mite diet isolate 1694-BHL110116-GBD28546_14587-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTTTTAATTGGAGGATTTGGAAACTGATTATTACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCATCTACAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611882 Oligochaeta sp. water mite diet isolate 1695-BHL110116-GBD27013_22949-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTAGCAAAACCAGGATCATTCTTAGGAAGAGATCAACTATATACCATCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTATTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCGTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATATCTTCTTCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611883 Oligochaeta sp. water mite diet isolate 1697-BHL110116-GBD17182_28517-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACAAATCATAAAGATATTGGCACTCTATATTTAATTTTAGGAGCATGAGCAGGAATAATTGGAACAGGGATTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACATCCTAGTTACTGCACATGCATTTTTAATAATTTTCTTTCTTGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID KT716826, identified in GenBank as Amynthas morrisi. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611884 Oligochaeta sp. water mite diet isolate 1698-BHL110116-GBD26931_22283-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGGATACTAATTCGAATTGAATTACCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGTAGCTCCAGATATGGCTTTCCCACGACAAAATAATTTAAGATTCTGACTACTACCGGCATCTCTAATCTTACTAATTGCTTCTGCAGCAGTAGAAGATGGAGCTGAAGCAG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611885 Oligochaeta sp. water mite diet isolate 1699-BHL110116-GBD10072_4535-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGCATGAGCAGGAATAATGGGAACATGGT-TTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAATACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTGTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611886 Oligochaeta sp. water mite diet isolate 1700-BHL110116-GBD23382_10820-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACAAATCATAAAGATATTGGCACTCTATATTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAAAGATCAACTTTATAACACCCTTGTTACTGCACATGCATTTTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.8% identical to accession ID KT716826, identified in GenBank as Amynthas morrisi. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611887 Oligochaeta sp. water mite diet isolate 1701-BHL110116-GBD7595_4007-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGTACTAGAATACTAATTCGAATTAAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATGGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.0% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611888 Oligochaeta sp. water mite diet isolate 1702-BHL110116-GBD7810_12501-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACAAATCATAAAGATATTGGCACTTTATATTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGCGTTTAGAATACTAATTCGACTTGAATTATCACAACCAGGCTCATTCTTAGGAAGAGATCAACTATATAACACCCTTGTTACTGCACATGCTTTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.9% identical to accession ID KT716826, identified in GenBank as Amynthas morrisi. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611889 Oligochaeta sp. water mite diet isolate 1703-BHL110116-GBD11135_11769-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTGGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCATAATAATTTTTTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAAAAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611890 Oligochaeta sp. water mite diet isolate 1705-BHL110116-GBD21218_17087-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGTACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTCGGAAGCGATCAACTATATAACACACTAGTTACTGCACATGCATTCGTAATAATTTTCTTTCTAGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611891 Oligochaeta sp. water mite diet isolate 1707-BHL110116-GBD15925_9346-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGATCAGGAATAGTTGGAACATCGT-TTAGAATACTTATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACGCCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611892 Oligochaeta sp. water mite diet isolate 1708-BHL110116-GBD24223_16170-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACATGTACTAGAATACTAATTCGAATTGAATTAGCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTATTGTAATACCAGTATTAATTGGAGGCTTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCCCCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611893 Oligochaeta sp. water mite diet isolate 1710-BHL110116-GBD17775_7779-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCCCAACCAGGATCCTTCTTAGGAAGAGATCAACTATATAATACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTCCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCACCAGATATGGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTGCATCGGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611894 Oligochaeta sp. water mite diet isolate 1711-BHL110116-GBD7827_17116-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAGATAATATAAGATACTGACTACAACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGAAGAAAAAGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611895 Oligochaeta sp. water mite diet isolate 1713-BHL110116-GBD20932_12871-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTCGGAGTTTGAGCAGGAATAATTGGAACTGCGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTTGTTACTGCACATGCATTTTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATTTAAGATTCTGACTACTACCACCATCACTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611896 Oligochaeta sp. water mite diet isolate 1717-BHL110116-GBD11735_15821-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGGACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTAATACCAGTATTTATTGGAGGATTTGGAAACTGACTTGTACCACTAATACTTGGAGCACCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.4% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611897 Oligochaeta sp. water mite diet isolate 1721-BHL110116-GBD24246_23173-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATGCTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCAACAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611898 Oligochaeta sp. water mite diet isolate 1723-BHL110116-GBD17188_23845-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTTATTTTAGGAGCATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACGCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAATTTTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611899 Oligochaeta sp. water mite diet isolate 1724-BHL110116-GBD18263_15094-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611900 Oligochaeta sp. water mite diet isolate 1726-BHL110116-GBD9981_7218-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACGTCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCATTCCCACGAATAAATAATATAAGATTCTGATTACTACCACCATCTCTAACCTTACTAATATCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611901 Oligochaeta sp. water mite diet isolate 1727-BHL110116-GBD18585_23151-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCCGGAATAATTGGAACTGCGTTTAGAATACTTATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAACACTTGGAGCTCCTGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.3% identical to accession ID KT716826, identified in GenBank as Amynthas morrisi. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611902 Oligochaeta sp. water mite diet isolate 1728-BHL110116-GBD24414_12885-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTTTACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATCCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACCACGACCACCAACGCCGATCTTACAAAAATCTTCTGCAGCAGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.8% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611903 Oligochaeta sp. water mite diet isolate 1729-BHL110116-GBD10033_12186-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGATCAGGAATAATTGGAACTTGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTCATTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTTCTAATCTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611904 Oligochaeta sp. water mite diet isolate 1732-BHL110116-GBD18664_4961-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTTGGAGCATGATCAGGAATAATTGGAACTGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGACCAACTATATAATACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.8% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611905 Oligochaeta sp. water mite diet isolate 1733-BHL110116-GBD23840_21596-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGAGATGACTTTCCCACGACTAAATAAATTAAGAAACTGACTACTACCACCAGCTCCAAACTTACAAATGTCTTCTGCAGCAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611906 Oligochaeta sp. water mite diet isolate 1737-BHL110116-GBD16258_29086-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTTATTTTAGGAGTTTGAGCAGGAATAATTGGAACTGGTTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGAACATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTACACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCACCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611907 Oligochaeta sp. water mite diet isolate 1739-BHL110116-GBD11576_23073-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTTCGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAAATATATAACACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611908 Oligochaeta sp. water mite diet isolate 1741-BHL110116-GBD24399_21893-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTATTTTTAGGAGTGTGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACATCCAGGATCATTCTTTGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTACAGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611909 Oligochaeta sp. water mite diet isolate 1742-BHL110116-GBD20423_25161-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAAATATATAACATACTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID GU014006, identified in GenBank as Megascolecidae sp. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611910 Oligochaeta sp. water mite diet isolate 1745-BHL110116-GBD2755_17385-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATATTTTATTTTAGGAGTATGAGCAGGAATAATTGGCACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGAATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCACTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611911 Oligochaeta sp. water mite diet isolate 1746-BHL110116-GBD27566_16000-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTATTAGGAAGAGATCAAATATATAACCCCATAGTTACTGCACATGCATTCTTAATAATTTTTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611912 Oligochaeta sp. water mite diet isolate 1748-BHL110116-GBD16654_8649-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTTTATACTTTATTTTTGGAGCATGATCAGGAATAATTGGAACTTCGTTTAGAATACTAATTCGAATTGAATTAGCACAACCAGGATCATTCTTAGGAAGTGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.9% identical to accession ID MG422806, identified in GenBank as Slavina appendiculata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611913 Oligochaeta sp. water mite diet isolate 1750-BHL110116-GBD22505_25772-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGATTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTGATTTCTTCTACAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611914 Oligochaeta sp. water mite diet isolate 1751-BHL110116-GBD16705_12350-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGGTCATTCTTAGGAAGAGATCAACTATATAACACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCCTACTAGTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611915 Oligochaeta sp. water mite diet isolate 1756-BHL110116-GBD13404_13876-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGAACATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCATTATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTTGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTACAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611916 Oligochaeta sp. water mite diet isolate 1757-BHL110116-GBD19970_15649-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCATTCCCACGAATAAAAAAAATAAGAAAATGACTACTACCGCAATCTCTAAACTGACAAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611917 Oligochaeta sp. water mite diet isolate 1814-BHL011116-GBD10254_3807-Ldc73 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCTGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCACTAATCCTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611918 Oligochaeta sp. water mite diet isolate 1819-BHL011116-GBD28401_15293-Ldc73 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAGCTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTACTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTACAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611919 Oligochaeta sp. water mite diet isolate 1821-BHL011116-GBD16625_11676-Ldc73 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTATTAATAATTTTCTTTCTTGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTGCTACCACCATCTCTAACCTTATTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611920 Oligochaeta sp. water mite diet isolate 1822-BHL011116-GBD29282_12599-Ldc73 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATATCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCAACTCTAACCTTACTAATTTCTTCTGGAGCAGTAGAAAATGGAGCTGAAACA	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611921 Oligochaeta sp. water mite diet isolate 1866-BHL072216-GBD19144_8169-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGACATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.9% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611922 Oligochaeta sp. water mite diet isolate 1974-BHL022317-GBD7255_20351-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATGCTTGGGGCACCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCTATCCCTTACCCTTCTTCTTTCAAGATCAGTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.5% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611923 Oligochaeta sp. water mite diet isolate 2559-BHL072216-GBD5962_23321-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACCGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAAATATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAATATTCTGACTACTCCCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611924 Oligochaeta sp. water mite diet isolate 2811-BHL032417-GBD25523_23757-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTTTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATTATTCCTAGGAAGAGATCGACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAATATTTATTGGAGGATTTGGAAATTGAATTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611925 Oligochaeta sp. water mite diet isolate 2914-BHL032417-GBD19936_15146-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTATTACTTGGATCACCAGATATAGCTCTCCCACGAATTAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611926 Oligochaeta sp. water mite diet isolate 3110-BHL032417-GBD12902_23958-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTAGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGATCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611927 Oligochaeta sp. water mite diet isolate 3137-BHL032417-GBD2255_18772-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACCCTATACTTAATTTTAGGAGTTTGAGCCGGAATAATTGGAACCGGAACTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTCCTAGGGAGAGATCAGCTATATAACACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATGGCCTTCCCACGACTTAACAATATAAGATTTTGACTTCTACCACCTTCACTAATCCTACTGGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611928 Oligochaeta sp. water mite diet isolate 3680-BHL032417-GBD4512_19458-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACCCTATACTTAATTTTAGGAGTTTGAGCCGGAATAATTGGAACCGGAATTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTCCTAGGGAGAGATCAGCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATGGCCTTCCCACGACTTAACAATTTAAGATTTTGACTTCTACCACCTTCACTAATCCTACTGGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611929 Oligochaeta sp. water mite diet isolate 3842-BHL032417-GBD15313_27668-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGATGGATTTGGAAATTGACTTCTACCTCTAATACTTGTAGCACCAGATATAGCTTTCCCACCCCTTAACAATATAAGATTCTGACTACTCCCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 86.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611930 Oligochaeta sp. water mite diet isolate 3858-BHL032417-GBD26938_23469-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATAAACAATTTAAGATTCTGACTACTACCACCTTCACTAAACCGATTAGTTTCTTCTACAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611931 Oligochaeta sp. water mite diet isolate 4153-BHL032417-GBD3915_12385-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCCACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACTAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAATATTTTGACTTCTACCACCTTCACTAATCCTACTAGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611932 Oligochaeta sp. water mite diet isolate 4162-BHL032417-GBD8195_10981-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGTTCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCATACGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAAATTCTGACTACTACCACCTTCACTAATCCCATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611933 Oligochaeta sp. water mite diet isolate 4313-BHL032417-GBD19948_3105-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACCCTATACTTAATTTTAGGAGTTTGAGCCGGAATAATTGGAACCGGAACTAGAATATTAATTCGGGTTGAATTAGCTCAACCAGGATCATTCCTAGGGAGAGATCAGCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTTTAGTTATACCAGTATTTACTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATGGCCTTCCCACGACTTAACAATTTAAGATTTTGACTTCTACCACCTTCACTAACCCTACTGGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611934 Oligochaeta sp. water mite diet isolate 4540-BHL032417-GBD24566_5684-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCTTAATAATTTTTTTTCTGGTTTTACCAGTATTTATTGATGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611935 Oligochaeta sp. water mite diet isolate 4615-BHL032417-GBD27116_21137-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATATTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTATATAATACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTTATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611936 Oligochaeta sp. water mite diet isolate 4700-BHL032417-GBD10273_16812-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAGATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATT---ATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.5% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611937 Oligochaeta sp. water mite diet isolate 4934-BHL032417-GBD11043_2753-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGAAATAATTGGAACAGGGACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTACCAATATAAGATTCTGACTTCTACCACCTTCACTAAACCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611938 Oligochaeta sp. water mite diet isolate 4952-BHL032417-GBD4395_14161-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTGGGAAGAGATCAACTATGTAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATATGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATTCTGACTACTACCACCTCCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611939 Oligochaeta sp. water mite diet isolate 4958-BHL032417-GBD6318_23266-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACTACCACCTTCACTAATCCTATTGGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611940 Oligochaeta sp. water mite diet isolate 4962-BHL032417-GBD14725_24798-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACCCTATACTTAATTTTAGGAGTTTGAGCCGGAATAATTGGAACCGGAACTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTCCTAGGGAGAGATCAGCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATGGCCTTCCCACGACTTAACAATTTAAGATTTTGACTTCTACCACCTTCACTAATCCTACTGGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 87.2% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611941 Oligochaeta sp. water mite diet isolate 4974-BHL032417-GBD15524_20857-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCATGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAGTTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.7% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611942 Oligochaeta sp. water mite diet isolate 4993-BHL032417-GBD12712_5540-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCCACCTCTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LN810268, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611943 Oligochaeta sp. water mite diet isolate 5031-BHL032417-GBD10293_18726-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTGTTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATACATTTTTAATAATTTTTTTCTTATTAACACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCA--AGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.5% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611944 Oligochaeta sp. water mite diet isolate 5049-BHL032417-GBD28016_17903-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGCTTGAGCTGGAATAATTGGAACATGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCATAGGAAGAGATCAACTTTATAATACTCTAGTAACTGCACATGCATTTCTTATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTGGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611945 Oligochaeta sp. water mite diet isolate 5052-BHL032417-GBD18795_18053-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGATACCAACTATATAATACCTTAGTTACTGCGCATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGTTTTTGAATTCTCCCCCCATCTTTAACTCTTCTTCTT---TCTAGTTCATTTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611946 Oligochaeta sp. water mite diet isolate 5054-BHL032417-GBD24065_21595-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGTTTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTATACCCTCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.1% identical to accession ID LN810268, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611947 Oligochaeta sp. water mite diet isolate 5074-BHL032417-GBD9250_20681-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTATATTTTATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID LN810267, identified in GenBank as Nais bretscheri. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611948 Oligochaeta sp. water mite diet isolate 5075-BHL032417-GBD16037_12441-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGCTTGAGCTGGAATAATTGGAACAGGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTTTATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTTCTGGTTATACCAATATTTATTGGTGGATTTGGAAATTGATTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611949 Oligochaeta sp. water mite diet isolate 5076-BHL032417-GBD9526_22010-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCTTTCATAATAATTTTCTTTCTTGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611950 Oligochaeta sp. water mite diet isolate 5078-BHL032417-GBD5195_12762-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTTGTAACTACACATGCATTCCTAATAATTTTTTTTCTAGTGATACCAGTATTTATTGGAGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTGGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611951 Oligochaeta sp. water mite diet isolate 5084-BHL032417-GBD10772_8451-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATTCTTGGAGCTCCAGATATGGCTTTCCCACAACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611952 Oligochaeta sp. water mite diet isolate 5091-BHL032417-GBD7541_15646-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAGTTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCTTTCCCACGATTAAATAATATAAGTTTTTGGTTTTTACCCCCGTCATTA--TCT-TTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611953 Oligochaeta sp. water mite diet isolate 5100-BHL032417-GBD17077_8898-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611954 Oligochaeta sp. water mite diet isolate 5101-BHL032417-GBD9271_12716-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGTACAGGATCAAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTTTATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGGTTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTGGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611955 Oligochaeta sp. water mite diet isolate 5103-BHL032417-GBD18622_16298-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCAATCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGATGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCATCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.8% identical to accession ID KY633407, identified in GenBank as Specaria josinae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611956 Oligochaeta sp. water mite diet isolate 5107-BHL032417-GBD14469_17278-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGCTCTAGAATCTTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGATATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGATGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCCCCTTCACTAATCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611957 Oligochaeta sp. water mite diet isolate 5108-BHL032417-GBD20442_22818-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACCCTATACTTATTTTTAGGAGTTTGAGCCGGAATAATTGGAACCGGAACTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTCCTAGGGAGAGATCAGCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTATAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCAATTGGTTTCTTCTGCTGCCGTAGGAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611958 Oligochaeta sp. water mite diet isolate 5109-BHL032417-GBD23978_5336-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATAATCTAGTAACTGCACATGCATTTCTAATAATTTTCTTTATAGTTATACCAATATTAATTGGTGGATTTGGAAATTGACTTCAACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611959 Oligochaeta sp. water mite diet isolate 5110-BHL032417-GBD10657_6483-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGAAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACTTTCTTTAACATTATTATTATCAGGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.3% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611960 Oligochaeta sp. water mite diet isolate 5114-BHL032417-GBD4568_23176-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATATTTTATTTTCGGAGCTTGAGCTGGAATAATTGGAACAGGAACTAAAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611961 Oligochaeta sp. water mite diet isolate 5117-BHL032417-GBD13018_9089-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTCAGGAGTTTGAGCTGGAATAATTGGAACAGGTACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCATTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTATCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611962 Oligochaeta sp. water mite diet isolate 5143-BHL032417-GBD15096_18995-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTCGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.7% identical to accession ID LN810267, identified in GenBank as Nais bretscheri. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611963 Oligochaeta sp. water mite diet isolate 5146-BHL032417-GBD27048_15882-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGAACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAATACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGACTAGTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCATCTCTAATCCTACTAATTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611964 Oligochaeta sp. water mite diet isolate 5148-BHL032417-GBD25635_13157-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGATCAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATGATTTTCTTTCTGGTTATACCAGTATTAATTGATGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.4% identical to accession ID LN810267, identified in GenBank as Nais bretscheri. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611965 Oligochaeta sp. water mite diet isolate 5167-BHL032417-GBD23425_14449-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACTGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTTCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTAGAGCACCAGATATAGCTTTCCCTCGACTAAACAATATAAGATTCTGATTACTACCCCCTTCTCTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611966 Oligochaeta sp. water mite diet isolate 5172-BHL032417-GBD16142_19750-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTATACTTAATTTTAGGAGTTTGAGCCGGAATAATTGGAACCGGAACTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTCCTAGGGAGAGATCAGCTATATAATACTCTAGTAACTGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.0% identical to accession ID LT905357, identified in GenBank as Nais pseudobtusa. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611967 Oligochaeta sp. water mite diet isolate 5181-BHL032417-GBD14803_4890-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACCCTATACTTAATTTTAGGAGTTTGAGCCGGAATAATTGGAACCGGAACTAGAATATTAATTCGGATTGAATTAGCTCAACCAGTATCATTCCTAGGGAGAGATCAGCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTTTAGTTATACCGGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTGATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACATTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611968 Oligochaeta sp. water mite diet isolate 5187-BHL032417-GBD7457_8232-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCATGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGAATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAGTTGAATTCTACCTTTAATACTTGGGGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTT---ATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611969 Oligochaeta sp. water mite diet isolate 5189-BHL032417-GBD3900_15031-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACCCTATACTTAATTTTAGGAGTTTGAGCCGGAATAATTGGAACCGGAACTAGAATATTAATTCGGATTAAATTAGCTCAACCAGGATCATTCCTAGGGAGAGATCAGCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTTTAGTTATACCAGTATTTAATGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATGGCCTTCCCACGACTTAACAATTTAAGATTTTGACTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611970 Oligochaeta sp. water mite diet isolate 5194-BHL032417-GBD23772_18142-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGGCTATTAATTCGTATTAAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGAGCACCAGATATGGCCTTCCCACGACTTAACAATTTAAGATTTTGACTTCTACCACCTTCACTAATCCTACTGGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGAAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611971 Oligochaeta sp. water mite diet isolate 5201-BHL032417-GBD14842_10550-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTGCTGCACATGCATTTTTAATAATTTTTTTCTTAGTAACACCAGTTTTTATCGGAGGATTTGGAAAATGACTTCTACCTCTAATACTTGGAGCACCAGATATGGCCTTCCCACGACTTAACAATTTAAGATTTTGACTTCTACCACCTTCACTAACCCTACTGGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.1% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611972 Oligochaeta sp. water mite diet isolate 5218-BHL032417-GBD7451_15750-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTTTGAGCAGGAATAATTGGAACAGGGACTAGAATATTAATTCGAATTGAATTATCTCAACCAGGATCATTCTTAGGAAGAGATCAACTATGTAACACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCCCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611973 Oligochaeta sp. water mite diet isolate 5235-BHL032417-GBD4160_21667-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACCCTATACTTAATTTTAGGAGTTTGAGCCGGAATAATTGGAACCGGAACTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTCCTAGGGAGAGATCAGCTATATAATACTCTAGTAACTGTACATGCATTCCTAATAATCTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGATTTCTACCTCTAATACTTGGATCACCAGATATGGCCTTCCCACGACTTAACAATTTAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.2% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611974 Oligochaeta sp. water mite diet isolate 5241-BHL032417-GBD9600_2777-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGAAAGGGATCAACTATATAATAATCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGATGGATTTGGAAATTGACTTCTATCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTGAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611975 Oligochaeta sp. water mite diet isolate 5244-BHL032417-GBD12701_21862-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGAAACTAGAATATTAATTCGGAATGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAGTTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATTACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611976 Oligochaeta sp. water mite diet isolate 5257-BHL032417-GBD12434_20527-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTGTATAATACCTTAGTTACTGCACATGCAATTTTAATAATTTTTTTCTTAGTAACACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTCCACTAATCCTATTGGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.1% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611977 Oligochaeta sp. water mite diet isolate 5258-BHL032417-GBD26147_10061-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTTTGACTTCTTCCCCCCTCTTTAACTCGTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611978 Oligochaeta sp. water mite diet isolate 5259-BHL032417-GBD15003_27539-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCTATATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCCCCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCTCTAACCCTATTAGTTTCTTCAACAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611979 Oligochaeta sp. water mite diet isolate 5264-BHL032417-GBD6421_16768-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTTGGAGTTTGAGCTGGAATAATTGGAACAGGACCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTCCTAGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTATCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAGGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611980 Oligochaeta sp. water mite diet isolate 5270-BHL032417-GBD27760_11286-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTACTAGGAAGAGATCAACTTTATAATACTCTTGTTACTGCACATGCATTTCTAATAATTTTTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCTATTGGTTTCTTCTGCTGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611981 Oligochaeta sp. water mite diet isolate 5276-BHL032417-GBD11668_26251-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAAAACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGATGGATTTGGAAATTGACTTCTACCTTTAATATTAGGAGCCCCAGATATAGCTTTTACTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611982 Oligochaeta sp. water mite diet isolate 5283-BHL032417-GBD7684_13400-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATATTTAATCTTAGGAGTTTGAGCTGGAATAATAGGAACAGGAACTAGAATATTAATACGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTAGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGTACCAGATATGGCCTTCCCACGACTTAACAATTTAAGATTTTGACTTCTACCACCTTCACTAATCCTACTGGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611983 Oligochaeta sp. water mite diet isolate 5301-BHL032417-GBD20079_18735-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCAGGAATAATTGGAACCGGAACTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTCCTAGGGAGAGATCAGCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGGTATGGCCTTCCCACGACTTAACGATTTAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611984 Oligochaeta sp. water mite diet isolate 5314-BHL032417-GBD23850_21839-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACCCTATACTTAATTTTAGGAGTTTGAGCCGGAATAATTGGAACCGGAACTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTCCTAGGGAGAGATCAGCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCGTTTTAGTTATACCAGTATTTATTGGTGGATATGGAAATTGACTTCTACCTCTAATACTTGGGGCACCTGATTTAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611985 Oligochaeta sp. water mite diet isolate 5315-BHL032417-GBD7301_14358-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTATCTCATCCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCCTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAAAACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTTTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID |JQ19820, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611986 Oligochaeta sp. water mite diet isolate 5317-BHL032417-GBD14802_25483-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTTTACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCTTTTCTAATAATTTTTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCGTCACTAACCCTATTAGCATCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611987 Oligochaeta sp. water mite diet isolate 5321-BHL032417-GBD24523_5139-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTTTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAATCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGTACATGCATTCCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATGGCCTTCCCACGACTTAACAGTTTAAGATTTTGACTTCTACCACCTTCACTAATCCTACTGGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611988 Oligochaeta sp. water mite diet isolate 5323-BHL032417-GBD7341_10888-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCATGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTCATTGGAGGATTTGGAAGTTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCA--AGTAGAATAGCGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611989 Oligochaeta sp. water mite diet isolate 5332-BHL032417-GBD25943_21908-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTATGAGCTGGAATAATTGGAACAGGGACTAGGATATTAATTCGAATTGAATTATCACAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTAATACCAGTATTTATTGGTGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611990 Oligochaeta sp. water mite diet isolate 5342-BHL032417-GBD18091_16895-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACCCTATACTTAATTTTAGGAGTTTGAGCCGGAATAATTGGAACCGGAACTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTCCTAGGGAGAGATCAGCTATATAATACTCTAGTGACTGCACATGCATTCCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTAATACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.2% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611991 Oligochaeta sp. water mite diet isolate 5354-BHL032417-GBD23402_9826-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTTTATAATACTCTAGTAACTGCTCATGCATTTCTAATAATTTTTTTCCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTACTACCTCTAATACTTGGTGCACCAGATATAGCTTTCCCACGAATAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611992 Oligochaeta sp. water mite diet isolate 5365-BHL032417-GBD4730_8077-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACT	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611993 Oligochaeta sp. water mite diet isolate 5366-BHL032417-GBD18655_24250-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATATTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGACCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTTGTAACTGCACATGCATTTCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATAAACAACATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTATCTTGTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611994 Oligochaeta sp. water mite diet isolate 5368-BHL032417-GBD21091_22344-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAAGAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAAAGACCAACTATATAATACCGTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611995 Oligochaeta sp. water mite diet isolate 5383-BHL032417-GBD26010_11545-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACTGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTTGGAAGAGATCAACTTTATAATACTCTAGTAACTGCACATGCATTCCTTATAATTTTTTTTCTGGTTATACCAATTTTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCTCTAACCCTATTGGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW611996 Oligochaeta sp. water mite diet isolate 5384-BHL032417-GBD23957_22810-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGCGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAACACCAGTTTTTATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTA--TCT-TTACTTCTATCTAGTCCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611997 Oligochaeta sp. water mite diet isolate 5385-BHL032417-GBD15229_22321-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTTGTAACTGCACATGCATTCCTAATAATTTTCTTTCTAGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATATTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCTATTAGTATCTACTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611998 Oligochaeta sp. water mite diet isolate 5386-BHL032417-GBD14020_26528-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGTAATAATTGGAACAGGGACTAGAATACTAATTCGAATAGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTATAGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACCACTACCACCATCTCTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW611999 Oligochaeta sp. water mite diet isolate 5390-BHL032417-GBD22033_19049-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTCATGGTTATACCATTATTAATTGGAGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTGGTTTCTACTACAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612000 Oligochaeta sp. water mite diet isolate 5393-BHL032417-GBD17946_19892-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGATCATCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATAAGGCCTTCCCACTACTTAACAATTTAAGATTTTGACTTCTACCACCTTCACTAATCCTACTGGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612001 Oligochaeta sp. water mite diet isolate 5396-BHL032417-GBD21695_17754-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACTGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGAACATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTCCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCGGATATAGCTTTCCCACGAATAAACAATATAAGATTCTGACTACTACCCCCTTCTCTAACCCTATTGGTTTCTTCTGCAACCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612002 Oligochaeta sp. water mite diet isolate 5402-BHL032417-GBD23870_13444-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGATGGGTTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCCCCATCACTATTTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612003 Oligochaeta sp. water mite diet isolate 5410-BHL032417-GBD20848_6996-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGATCTGGAATAATTGGAACAGCTACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAGGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGATGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGACATAGCTTTCCCACGACTAAACGATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612004 Oligochaeta sp. water mite diet isolate 5413-BHL032417-GBD24228_22396-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTAAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGAGGATGTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTAGGCTTTTACCCCCGTCA-TTATCTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 81.6% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612005 Oligochaeta sp. water mite diet isolate 5417-BHL032417-GBD12144_25724-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTTTATAATACTCTTGTAACTGCACATGCATTCCTAATAATTCTTTTTCTGGTTATACCAGTATTAATTGATGGATTTGGAAATTGACTTTTGCCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612006 Oligochaeta sp. water mite diet isolate 5420-BHL032417-GBD24320_25790-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACATCAACTACAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTTGGAAGAGATCAACTATATAAAACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAATTTTTATTGGAGGATTTGGAAGTTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612007 Oligochaeta sp. water mite diet isolate 5426-BHL032417-GBD15642_14552-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCATGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAGTTGAATTCTACCTTTAATACTTGGGGCACCTGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCCTTAACTCTTCTTCTT---TCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612008 Oligochaeta sp. water mite diet isolate 5427-BHL032417-GBD20037_13136-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACTGGATCTAGAATATTAATTCGGATTAAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCTTTCCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCCCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCTACTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612009 Oligochaeta sp. water mite diet isolate 5430-BHL032417-GBD6843_10532-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACAATATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAGTTAAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATGATTTTATTCTTAGTAATACCTGTATTAATTGGAGGATTCGGAAACTGATTACTTCCAGTAATACTAGGTGCTGCTAATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.7% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612010 Oligochaeta sp. water mite diet isolate 5432-BHL032417-GBD4950_12665-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGATCTGGAATAATTGGAACATGACCTAGAATATTGATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAGGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTTCTGGTTATACCAGTATTTATTGATGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCCCCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612011 Oligochaeta sp. water mite diet isolate 5435-BHL032417-GBD29261_18829-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGATGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAAGCCGAGGAGGGGCGGCGGCGGCCGGAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612012 Oligochaeta sp. water mite diet isolate 5440-BHL032417-GBD5196_16865-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATATTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTTTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGATTACTACCACCTTCACTAACCCTATTGGTATCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612013 Oligochaeta sp. water mite diet isolate 5443-BHL032417-GBD19562_9558-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGATCTGGAATAATTGGAACATGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGAGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCCTTCCCACGACTAAACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCCATTGGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612014 Oligochaeta sp. water mite diet isolate 5445-BHL032417-GBD24277_5006-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTAATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCTTCTCTAATCCTACTAATTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.1% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612015 Oligochaeta sp. water mite diet isolate 5446-BHL032417-GBD18314_28174-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACCCTATACTTAATTTTAGGAGTTTGATCCGGAATAATTGGAACCGGAACTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTCCTAGGGAGAGATCAGCTATATAATACTCTAGTAACTGCTCATGCATTCCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTTTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCCCGACTAAACAATTTAAGATTCGGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612016 Oligochaeta sp. water mite diet isolate 5447-BHL032417-GBD12556_24398-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCACAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATAATCTAGTAACTGCACATGCATTCTTAATAATTTTCTTTCTTGTTATACCAGTATTTATTGATGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCTTCTCTAATCCTATTAGTTCCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612017 Oligochaeta sp. water mite diet isolate 5457-BHL032417-GBD5684_24389-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGCTTGAGCTGGAATAATTGGAACAGGAATTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTACTAGGAAGAGATCAACTATATAATACTCTTGTAACTGCACATGCATTTCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGATGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612018 Oligochaeta sp. water mite diet isolate 5460-BHL032417-GBD24503_25759-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTCCTGGTTATACCAGTATTTATTGGTGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612019 Oligochaeta sp. water mite diet isolate 5462-BHL032417-GBD4596_12919-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATATTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGATTTAGAATATTAATTCGGCTTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTTGTAACTGCACATGCATTCCTAATAATTTTTTTTATGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTGTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATAAACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCTATTGGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612020 Oligochaeta sp. water mite diet isolate 5469-BHL032417-GBD10239_15182-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATAATCTCGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGATGGATTTGGAAATTGACTTCTACCACTAATACTTGGAGCACCTGATGTAGCTTTCCCACGAATAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612021 Oligochaeta sp. water mite diet isolate 5472-BHL032417-GBD20636_3142-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAAATAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAGTTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGACTTTGACTATTACCCTCGTCATTAACTTTACTTCTTTC--TAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.2% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612022 Oligochaeta sp. water mite diet isolate 5478-BHL032417-GBD25865_19770-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACCCTATACTTAATTTTAGGAGTTTGAGCCGGACTAATTGGAACCGGAACTAGAATATTAATTCGGATTGACTTAGCTCAACCAGGATCATTCCTAGGGAGAGATCAGCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATGGCCTTCCCACGACTTAACAATTTAAGTTTTTGACTTCTCCCCCCATCTTTAACCCTACTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612023 Oligochaeta sp. water mite diet isolate 5481-BHL032417-GBD26085_22785-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACCCTATACTTAATTTTAGGAGTTTGAGCCGGAATAATTGGAACCGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGGAGAGATCAGCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACCTTATTGTTATCTAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612024 Oligochaeta sp. water mite diet isolate 5483-BHL032417-GBD3407_12908-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGAACAGGAACAAGACTAATAATTCGTATTGAATTAACCCATCCTGGAGCATTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTTTTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATGGCCTTCCCACGACTTAACAATTTAAGATTTTGACTTCTACCACCTTCACTAATCCTACTGGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612025 Oligochaeta sp. water mite diet isolate 5499-BHL032417-GBD14854_27613-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGGATTGAATTATCACAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGAGGATTTGGAAATTGACTACTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCATCTCTAATCCTATTGGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612026 Oligochaeta sp. water mite diet isolate 5538-BHL032417-GBD7493_6157-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGCCCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCATAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTTCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGATGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAAAATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612027 Oligochaeta sp. water mite diet isolate 5548-BHL032417-GBD23951_17665-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGCACAGGAACTAGAATTTTAATCCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCTTTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGATGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCATTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAAACCTATTAGTATCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612028 Oligochaeta sp. water mite diet isolate 5553-BHL032417-GBD17114_13401-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTATAATACTTGGAGCACCAGATATAGCTTTCCCACGACTGAACAATATAAGATTCTGACTGCTACCCCCGTCACTAACCCTGTTAGTATCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612029 Oligochaeta sp. water mite diet isolate 5560-BHL032417-GBD17538_22897-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACACGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612030 Oligochaeta sp. water mite diet isolate 5626-BHL032417-GBD21211_4206-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGAAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGACTTAACCCCTCCTGAAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGTGGCACCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612031 Oligochaeta sp. water mite diet isolate 5628-BHL032417-GBD3742_15168-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACACGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTATCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612032 Oligochaeta sp. water mite diet isolate 5640-BHL032417-GBD21239_14512-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGGTCATTCCTAGGAAAAGATCAACTATATAATACTCTAGTAACTGCACACGCATCCCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATAAACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCCATTAGTTTCTTGTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612033 Oligochaeta sp. water mite diet isolate 5681-BHL032417-GBD12704_11790-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACCGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTC---TTCTTCTATCTTGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612034 Oligochaeta sp. water mite diet isolate 5712-BHL032417-GBD17726_15122-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACTGGATTTAGAATATTAATTCGGATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACACGCATTCCTAATAATTTTTTTATGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGAATCTGACTACTACCCCCTTCACTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612035 Oligochaeta sp. water mite diet isolate 5754-BHL032417-GBD24548_5672-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTTCTGGTTTTACCAGTATTTATTGATGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGCCTTAACAATTTAAGATTCTGACTACTACCACCTTCACGAAACCTATTAGTATCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612036 Oligochaeta sp. water mite diet isolate 5811-BHL032417-GBD13523_20407-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGGTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAACAATTTTCTTTCTGGTTATACCAGTTTTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACATAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTGGTTTCGTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612037 Oligochaeta sp. water mite diet isolate 5818-BHL032417-GBD24393_24868-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCATAATATTTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCGGATATAGCTTTCCCCCGACTTAACAACTTAAGATTCTGACTACTACCACCTTCACTAATCTTATTGGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612038 Oligochaeta sp. water mite diet isolate 5983-BHL032417-GBD13671_19698-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAATTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAGCTGCCCATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612039 Oligochaeta sp. water mite diet isolate 6016-BHL032417-GBD15269_13688-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612040 Oligochaeta sp. water mite diet isolate 6127-BHL032417-GBD20094_17684-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGAATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACGATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAATATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612041 Oligochaeta sp. water mite diet isolate 6156-BHL032417-GBD9845_7401-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTTTACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTATTTATACCAGTATTTATTGATGGCTTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATACAGCTTTCACACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTATCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612042 Oligochaeta sp. water mite diet isolate 6275-BHL032417-GBD6534_11090-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACCCTATATTTAATTTTAGGACTTTGAGCCGGAATATTTGGAACCGGAACTAGAATATTAATTCGGCTTGAATTAGCTCAACCAGGATCATTCCTAGGGAGAGATCAGCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATGGCCTTCCCACGACTAAACAATTTAAGATTTTGACTTCTACCACCTTCACTAATCCTATTGGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612043 Oligochaeta sp. water mite diet isolate 6719-BHL032417-GBD20465_5941-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTGATCTTAGGAGTTTGAGCTGGAATAATTGCAACAGTAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612044 Oligochaeta sp. water mite diet isolate 6725-BHL032417-GBD13339_28170-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCATGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATACATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGACACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCA--AGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.9% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612045 Oligochaeta sp. water mite diet isolate 8389-BHL101416-GBD5608_21761-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATCCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACGTAACAATTTAAGATTCTGACTACTACTACCCCCATCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612046 Oligochaeta sp. water mite diet isolate 8406-BHL101416-GBD11952_9993-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTATTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTA--TCT-TTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.2% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612047 Oligochaeta sp. water mite diet isolate 8417-BHL101416-GBD16923_26155-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCCAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATGTGGCCTTCCCACGACTTAACAATTTAAGATTTTGACTTCTACCACCTTCACTAATCCTACTAGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612048 Oligochaeta sp. water mite diet isolate 8421-BHL101416-GBD20540_25164-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTCTACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAAAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTAGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTTCCACCTTCACTAATCCTATTAGTATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612049 Oligochaeta sp. water mite diet isolate 8425-BHL101416-GBD28894_16682-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAACTCATAAAGATATTGGCACTTTATACATTATTTTTGGAGCTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAGTTAACAATGTAAGATTCTGACTACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612050 Oligochaeta sp. water mite diet isolate 8430-BHL101416-GBD12928_2316-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTC-TTTATATTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.2% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612051 Oligochaeta sp. water mite diet isolate 8438-BHL101416-GBD26039_6135-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGATTGAGCTGGAATAATTGGAACAGGAACTAGAATATGAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAAATCAACTATATAATACTCTAGTAACTGCACATACATTCCTAATAATTTTCTTTCTGATTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAACTGGAA	Using NCBI BLASTN in June 2018, this sequence was 85.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612052 Oligochaeta sp. water mite diet isolate 8452-BHL101416-GBD19842_8454-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTCGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTCCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTGCTGTTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612053 Oligochaeta sp. water mite diet isolate 8456-BHL101416-GBD11634_16003-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGCTTGATCTGGAATAATTGGAACAGCATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTTGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATGCTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612054 Oligochaeta sp. water mite diet isolate 8467-BHL101416-GBD23140_8761-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACACTATACTTTATTTTTGGAGCTTGATCGGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.4% identical to accession ID KU728854, identified in GenBank as Mesenchytraeus antaeus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612055 Oligochaeta sp. water mite diet isolate 8469-BHL101416-GBD27103_11181-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGTACACTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTTGGAACAGGATCTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCTTTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612056 Oligochaeta sp. water mite diet isolate 8471-BHL101416-GBD23718_4471-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACCCTATACTTAATTTTAGGAGTTTGAGCCGGAATAATTGGAACCGGAACTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTCCTAGGGAGAGATCAGCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTTTTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATGGCCTTCCCACGACTTAACAATTTAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612057 Oligochaeta sp. water mite diet isolate 8474-BHL101416-GBD25676_11088-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTTGGAGTTTGAGCTGGAATAATTGGAACATGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGTGATCAAATATATAATACTCTAGTAACTGCACATGCATTTATAATAATTTTTTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612058 Oligochaeta sp. water mite diet isolate 8479-BHL101416-GBD28441_14433-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAGTTTAAGTTTTTGACTTTTACCCCCTTC-TTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.2% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612059 Oligochaeta sp. water mite diet isolate 8480-BHL101416-GBD16339_14074-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAATTATATAATACTCTAGTAACTGCTCATGCATTCCTAATAATTTTCTTTCTGATGATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATATTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612060 Oligochaeta sp. water mite diet isolate 8484-BHL101416-GBD14447_9157-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCATTCCCACGACTTAACAATATAAGATTCTGACTACTACCACCGTCATTAACCCTATTAGTATCTTCCGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612061 Oligochaeta sp. water mite diet isolate 8486-BHL101416-GBD18596_4335-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATATCATAAAGATATTGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTATCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATCGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTTACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612062 Oligochaeta sp. water mite diet isolate 8487-BHL101416-GBD9924_12161-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTAGCAATGAATTATCTCAATCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGGTTTCCCACGACTTAACAATTTAATATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612063 Oligochaeta sp. water mite diet isolate 8491-BHL101416-GBD6873_17749-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTCATCTTAGGAGCTTGAGCTGGAATAATTGGAACAGGACCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTTTATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTTCAGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATAAACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612064 Oligochaeta sp. water mite diet isolate 8502-BHL101416-GBD28887_18364-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGACCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTCTATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGTTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAAATTAAGATTCTGACTACTACCACCTGCACTAATCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612065 Oligochaeta sp. water mite diet isolate 8503-BHL101416-GBD27134_14970-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGAAACTAGAATATTAATTCGGATTGAATTATCCCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACTAGTATTTATTGGTGGATTTGGAAACTGACTTCTACCTCTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAA	Using NCBI BLASTN in June 2018, this sequence was 86.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612066 Oligochaeta sp. water mite diet isolate 8505-BHL101416-GBD19827_12298-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGATTTAGTATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAAAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTCTGGTTATACCAGTATTAATTGGAGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCTATTAGTATCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612067 Oligochaeta sp. water mite diet isolate 8507-BHL101416-GBD19741_21199-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTGTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTTCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCATTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTATGACTACGACCACCTTCACTAATCCTATTAGATTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612068 Oligochaeta sp. water mite diet isolate 8512-BHL101416-GBD16038_7532-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACCGGAACTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTCCTAGGGAGAGATCAGCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTATACCTCTAATACTTGGAGCACCAGATATGGCCTTCCCACGACTTAACAATTTAAGATTTTGACTTCTACCACCTTCACTAATCCTACTAGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.6% identical to accession ID AF534834, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612069 Oligochaeta sp. water mite diet isolate 8514-BHL101416-GBD5367_17994-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAACAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTCCTAATAATTTTCTTACTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.8% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612070 Oligochaeta sp. water mite diet isolate 8516-BHL101416-GBD16151_4126-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCTACTCTATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGGGCACCAGATATAGCTTTCCCATGCCTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612071 Oligochaeta sp. water mite diet isolate 8519-BHL101416-GBD27440_19537-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAACTCATAAAGATATTGGTACACTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAAGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTGATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTGCCCACGACTTAACAAGTTAAGATTCTGACTACTACCACCTTCACTAATCCGATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612072 Oligochaeta sp. water mite diet isolate 8522-BHL101416-GBD12624_11443-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCTGACGTAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTCTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612073 Oligochaeta sp. water mite diet isolate 8527-BHL101416-GBD23837_18309-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGCACTGGATTTAGAATATTAATTCGGCTTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTGGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612074 Oligochaeta sp. water mite diet isolate 8540-BHL101416-GBD17105_27331-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACATCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612075 Oligochaeta sp. water mite diet isolate 8541-BHL101416-GBD25887_24230-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAAATAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATACATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCATCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612076 Oligochaeta sp. water mite diet isolate 8551-BHL101416-GBD23374_24485-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGATTTTGAGCTGGAATAATTGGAACAGGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTTACTGCACATGCATTCCTAATAATTTTTTTCTGGTTGTACCAGTATTTATTGGTGGATTTGGAAATTGACTACTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTATCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612077 Oligochaeta sp. water mite diet isolate 8557-BHL101416-GBD26146_12792-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACTGGATCTACAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCATAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGACCTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612078 Oligochaeta sp. water mite diet isolate 8565-BHL101416-GBD26542_21489-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTCGAATATTCATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCATGACTTAACAATTTAAGTTTCTGACGTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612079 Oligochaeta sp. water mite diet isolate 8569-BHL101416-GBD5495_14441-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAAGTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGCTATACCAGTATTAATTGGTGGATTTGGAAATGGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTATCTTCTGCTGCCGTAGAAAATGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612080 Oligochaeta sp. water mite diet isolate 8576-BHL101416-GBD8092_19951-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACTGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTCTGGTTATACCAGTATTAATTGGAGGATTTGGAAACTGACTGCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCTCACGACTTAACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612081 Oligochaeta sp. water mite diet isolate 8579-BHL101416-GBD22506_6764-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCTTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATGGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCTTCATTAATCCTATTAGTGTCTGCTGCGGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612082 Oligochaeta sp. water mite diet isolate 8583-BHL101416-GBD11535_11578-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATTAACAATATAAGATTCTGATTCCTACCACCTTCACTAATCCTATTAGTTTCTTCGGCTGCCATAGAAACTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612083 Oligochaeta sp. water mite diet isolate 8586-BHL101416-GBD8200_23852-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTCGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCACAACCAGGATCATTCCTAGGAAGAGATCATCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTAATACCAGTATTTATTGGTGGATTTGGAAACTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCATCTCTAATCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612084 Oligochaeta sp. water mite diet isolate 8588-BHL101416-GBD22811_7892-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATTATAAAGATATTGGCACCCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTGGAATAATAATTCGGGTTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTACTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612085 Oligochaeta sp. water mite diet isolate 8590-BHL101416-GBD13281_20451-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTTTTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCATCAGATATAGCTTTCCCACGAATAAACAATATAAGATTCTGGCTAGTACCCCCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612086 Oligochaeta sp. water mite diet isolate 8592-BHL101416-GBD3766_11413-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAACAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTCTTGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCATCACTAATCCTATTAGTTTCAACTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612087 Oligochaeta sp. water mite diet isolate 8593-BHL101416-GBD3696_13945-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGACCATTCCTAGTAAGAGATCAACTATATAATACCCTAGTAACTGCACATGCATTCCTAATATTTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCATCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCGTCTGCTGCCGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612088 Oligochaeta sp. water mite diet isolate 8595-BHL101416-GBD19483_17289-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGTATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGATGTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCAAATCAGTTTCTTCTGCGGCCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 86.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612089 Oligochaeta sp. water mite diet isolate 8601-BHL101416-GBD15707_8785-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.2% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612090 Oligochaeta sp. water mite diet isolate 8603-BHL101416-GBD27645_22557-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGTACACTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGGTTGAATTATGTCAACCAGGATCATTTCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTTCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCATCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612091 Oligochaeta sp. water mite diet isolate 8604-BHL101416-GBD15403_27730-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAGCTTTATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTCTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCCGATATAGCTTTCCCACGGTTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612092 Oligochaeta sp. water mite diet isolate 8605-BHL101416-GBD24581_12357-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTATTTCTGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGC-TTCCCTACGACTTAACAATTGAAGATTCTGACTACTACCACCTACACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612093 Oligochaeta sp. water mite diet isolate 8606-BHL101416-GBD12675_3036-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAGTTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTACACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.5% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612094 Oligochaeta sp. water mite diet isolate 8607-BHL101416-GBD2149_15507-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTGGGAGTTTGAGCTGGAATAATTGGAACAGGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTTTATAATACTCTAGTAACTGCACATGCATTTCTAGTAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCCCCTTCTCTAACCCTATTAGTATCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612095 Oligochaeta sp. water mite diet isolate 8612-BHL101416-GBD15105_5518-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAAAATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612096 Oligochaeta sp. water mite diet isolate 8619-BHL101416-GBD22194_8239-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCTCTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCCCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTTCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGAAATAGCTTTCCCACGACTTAACAAATTAAGATTCTGACTACTACCACCTTCACTAAACCTATTAGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612097 Oligochaeta sp. water mite diet isolate 8623-BHL101416-GBD3586_18078-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTATCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTATCTCTAATACTTGGAGCACTAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACCACTACCACCTTCACCAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612098 Oligochaeta sp. water mite diet isolate 8626-BHL101416-GBD21609_22043-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGTACACTATACTTAATCTTAGGAGTTTGAGCCGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGACTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATTCTGACTACTATCACCTTCACTAATCCTATTAGTTTCTTCCGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612099 Oligochaeta sp. water mite diet isolate 8641-BHL101416-GBD18283_22705-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAGTCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAATTAGCATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTTGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCCACCTCTAATAGTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612100 Oligochaeta sp. water mite diet isolate 8643-BHL101416-GBD6168_14494-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGATCTGGAATAATTGGAACTGGCACTAGAATATTAATTCGGATTGAATTATCTCAACCTGGATCATTCCTAGGAAGTGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGAGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATATAAGATTCGGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612101 Oligochaeta sp. water mite diet isolate 8646-BHL101416-GBD15772_27980-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATCAAGATATTAGCACTCTATACTTAATCTTAGGAGATGGAGCTGGAATACTTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGTTCATTCCTAGGAAAAGATCAACTATATAGTACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACCTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATGAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612102 Oligochaeta sp. water mite diet isolate 8651-BHL101416-GBD10170_27433-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGGGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTTATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTTCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGACATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCATCACTAATCCTACTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.9% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612103 Oligochaeta sp. water mite diet isolate 8665-BHL101416-GBD28046_13410-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTGTACTTAATCTTAGGAGGTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATACAGCTTTCCCACGCCTTAACAATATAAGATTCTGACTACTCCCACCTTCACTAATCCAATCAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612104 Oligochaeta sp. water mite diet isolate 8677-BHL101416-GBD21323_8848-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGTACACTATACTTTATTTTTGGAGCTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTAAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAGCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACCTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTCCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612105 Oligochaeta sp. water mite diet isolate 8679-BHL101416-GBD23173_26869-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGTAACTAGAATATTAATTCGTATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAGTACTCTAGTTACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTTTTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATAATTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612106 Oligochaeta sp. water mite diet isolate 8693-BHL101416-GBD22236_23776-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGTATATTAATTCGGATTGAATTATCTCAACTAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTCCCCACGACATAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCAATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612107 Oligochaeta sp. water mite diet isolate 8698-BHL101416-GBD5728_10113-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCAACCAGGATCATTCCTAGGGAGAGAACAGCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTATAGTTATACTAGTATTTATTGGTGGATTTGGAAATTGACTTCTGCCTCTAATACTTGGAGCACCAGATATGGCCTTCCCATGACTTAACAATTTAAGATTTTGACTTCTACCCCCTTCACTAATCCTACTAGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.6% identical to accession ID KU728856, identified in GenBank as Mesenchytraeus hydrius. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612108 Oligochaeta sp. water mite diet isolate 8699-BHL101416-GBD26159_24107-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACATGTACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTTACTGCACATGCATTCCTAATAATTTTCTTTCTGGTGATACCAATATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCATTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTATCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612109 Oligochaeta sp. water mite diet isolate 8700-BHL101416-GBD27830_15967-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGATTTATCTCAACCAGGATCATTCATAGGAAGAGATCAACTTTATAATACTCTAGTAACTGCACATGCATTTCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCCCGACTTAACAATATAAGATTCTGACTACTACCACCTTCTCTAATCATATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612110 Oligochaeta sp. water mite diet isolate 8702-BHL101416-GBD25973_6406-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGCTTGATCTGGAATAATTGGAACATGAACTAGTATATTTATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAAATATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCGATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612111 Oligochaeta sp. water mite diet isolate 8709-BHL101416-GBD12707_14360-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGAAACAGGGACTAGAATATTAATTAGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATCGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAACATAAGATTCTGACTACTACCACCTTCTCTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612112 Oligochaeta sp. water mite diet isolate 8710-BHL101416-GBD15539_3197-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGAAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGGAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTCCCCCCTTCACTAATCCTATTATTTTCTTCAGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612113 Oligochaeta sp. water mite diet isolate 8721-BHL101416-GBD7167_19746-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATATTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAGCCAGGATCATTCCTAGGAAGGGATCAACTATATAATACTCCAGTAACTGCACATGCATTCCTATTAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTATCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612114 Oligochaeta sp. water mite diet isolate 8722-BHL101416-GBD19223_16682-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTCATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCCGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGTAAATTGACTTCTAACTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATTAACAATATAAGATTCTGACTACTACCACCTTCATTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612115 Oligochaeta sp. water mite diet isolate 8724-BHL101416-GBD21551_25282-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGTACACTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAATCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCATAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACTTCTACTACTAGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612116 Oligochaeta sp. water mite diet isolate 8728-BHL101416-GBD16288_16098-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTTTGAGCTGGAATAATTGGAACGGGGACTAGAATATTAATTCGGATTGAATTATCACAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTAATACCAGTATTTATTGGAGGATTTGGTAATTGACTACTACCTCTAATACTTGGAGTACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612117 Oligochaeta sp. water mite diet isolate 8733-BHL101416-GBD22728_18542-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTTGGTGTTTGATCTGGAATAATTGGAACTGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTTCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612118 Oligochaeta sp. water mite diet isolate 8736-BHL101416-GBD29404_17743-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAACCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTCCCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCATCACTAAGCCGAGGAGGGGCGGCGGCGGCCGGAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612119 Oligochaeta sp. water mite diet isolate 8741-BHL101416-GBD21015_20409-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGAATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGAATTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCATGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCGATTAGTATCTTCTGCTGCCGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612120 Oligochaeta sp. water mite diet isolate 8744-BHL101416-GBD4142_9881-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGTACACTATACTTTATTTTTGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAGTTCGGATTGAATTATATCAACCAGGATCATTCCTAGGAAGTGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATTCTGACTACTACCACCGTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612121 Oligochaeta sp. water mite diet isolate 8754-BHL101416-GBD13591_17105-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGCTTGAGCTGGCATAATTGGAACAGGATTTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACCGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGATCTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612122 Oligochaeta sp. water mite diet isolate 8757-BHL101416-GBD24813_11865-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTATAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACCCTAGTAACTGCACATACATTCCTAATAATTTTCTTTCTGATTATACCAGTATTTATTGGTGGATTTGGAAAATGACTTCTACCTCTAATACTTGGAGTACCAGATATAGCTTTCCCATGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612123 Oligochaeta sp. water mite diet isolate 8764-BHL101416-GBD21507_13108-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGTATATTGATTCGGATTGAATTATATCAACCAGGAGCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTTGTGGATGTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAAACCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612124 Oligochaeta sp. water mite diet isolate 8765-BHL101416-GBD26355_17759-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAAAGATCAACTATATAATACTATAGTAACTGCACATGCATTCCTTATAATTTTCTTTCTCGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTGTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612125 Oligochaeta sp. water mite diet isolate 8785-BHL101416-GBD5443_8657-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCTTTCCTAATAATTTTTTTTCTAGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCTCTAACCCTATTAGTTCCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612126 Oligochaeta sp. water mite diet isolate 8786-BHL101416-GBD22095_23532-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTTTGAGCAGGAATAATTGGAACAGGAACTAGAATATTAATTCGAATTGAATTATCTCAACCAGGATCATTCATAGGAAGAGATCAACTATATAATACTCTAGTTACTGCACATGCATTCCTAATAATTTTCTTTCTGGTAATACCAGTATTTATTGGAGGATTTGGAAATTGACTTCTACCACTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATAAACAATTTAAGATTCTGACTACTACCACCATCACTAATCCTATTAGTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.6% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612127 Oligochaeta sp. water mite diet isolate 8790-BHL101416-GBD15616_8461-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATACTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGAGGATTTGGAAACTGACTAGTACCTCTAATACTTGGAACTCCAGATATGGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAGTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612128 Oligochaeta sp. water mite diet isolate 8802-BHL101416-GBD3657_20837-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGATATCAACTTTATAATACTCTTGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACGAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTATCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612129 Oligochaeta sp. water mite diet isolate 8806-BHL101416-GBD27830_21839-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACACTATACTCTATTTTTGGAGCTTGTTCAGGAATACTAGGAACTTCTTTAAGTATATTAATTCGGATTAAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAGTACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.6% identical to accession ID KU728854, identified in GenBank as Mesenchytraeus antaeus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612130 Oligochaeta sp. water mite diet isolate 8813-BHL101416-GBD12786_10543-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCAATCTATACTTAATCTTAGGAGTTTGATCTGTAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAATGATCAACTATATAATACTTTAGTTACTGCACATGCATTCCTAATAATTTCCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACTAGATATAGCTTTTCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612131 Oligochaeta sp. water mite diet isolate 8816-BHL101416-GBD7510_13066-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGGGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCACCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.1% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612132 Oligochaeta sp. water mite diet isolate 8817-BHL101416-GBD7593_14146-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAGCAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATATCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACGACCCCCTTCACTAACCCTACTAGTATCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612133 Oligochaeta sp. water mite diet isolate 8819-BHL101416-GBD15833_26258-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATCTTCGGAGCTTGAGCTGGAATAATTGGAACAGGCACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTACTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATAAACAACATAAGATTCTGACTACTACCACCATCACTAACCCTATTAGTATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612134 Oligochaeta sp. water mite diet isolate 8820-BHL101416-GBD22773_5766-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACATGAACTAGAATATTTATTCGGAATGAATTATCTCAACCAGGATCATTCCTAGGAAAAGATCAACTTTATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGTATCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612135 Oligochaeta sp. water mite diet isolate 8829-BHL101416-GBD2985_14626-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTTTATACTTTATCTTTGGAGTTTGAGCTGGAATAATTGGAACTGGATCTAGAATATTAATTCGGATTAAATTATCTCAATCAGGATCATTCCTAGGAAGAGATCAACTTTATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612136 Oligochaeta sp. water mite diet isolate 8852-BHL101416-GBD4388_11584-Lq60 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.6% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612137 Oligochaeta sp. water mite diet isolate 8897-BHL032417-GBD3901_8736-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCATCTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612138 Oligochaeta sp. water mite diet isolate 9547-BHL032417-GBD9068_11473-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612139 Oligochaeta sp. water mite diet isolate 9551-BHL032417-GBD4804_17277-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAAACAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTTGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATATAAGATTCTGACCACTACCACCTTCACTAACCCTATTAGTTTCCTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612140 Oligochaeta sp. water mite diet isolate 9646-BHL032417-GBD26792_19139-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTACTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTAATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCCCCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAACCTTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612141 Oligochaeta sp. water mite diet isolate 9651-BHL032417-GBD14546_17102-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTTTTTATTGGTGGATTTGGAAATTGACTGCTTCCTCTAATACTCGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCTCTAACCCTATTAGTTTCTTCTACTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612142 Oligochaeta sp. water mite diet isolate 9720-BHL040517-GBD10098_4620-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTGTACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612143 Oligochaeta sp. water mite diet isolate 9768-BHL040517-GBD16608_21093-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCCGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACGAAATAATGTAAGATTATGACTACTACCCCCATCTCTAAGCTTACGAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612144 Oligochaeta sp. water mite diet isolate 9900-BHL040517-GBD17329_14524-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGGACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTCGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.2% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612145 Oligochaeta sp. water mite diet isolate 9915-BHL040517-GBD9667_19895-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATCCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.9% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612146 Oligochaeta sp. water mite diet isolate 9938-BHL040517-GBD12195_3491-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTACACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCGCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.9% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612147 Oligochaeta sp. water mite diet isolate 9953-BHL040517-GBD25598_17549-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCATGATCATTCATAGGAAAAGATCAACTATATAATACTCTAGTAACTTCACATGCATTCCTAATAATTTTCTTTCTAGTTATACCAGTATTTATTGGAGGCTTTGGAAATTGACTTCTACCTCTAATACTTGGTGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612148 Oligochaeta sp. water mite diet isolate 9955-BHL040517-GBD20873_5385-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGTACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTAGTTATACCAATATTAATTGGAGGATTTGGAAATTGACTACTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTACACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612149 Oligochaeta sp. water mite diet isolate 9960-BHL040517-GBD22827_26735-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTCGGAGCACCAGATATAGCTTTCCCACGACTTAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612150 Oligochaeta sp. water mite diet isolate 9974-BHL040517-GBD4845_18273-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAA---CCTTACTTTTATCGAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612151 Oligochaeta sp. water mite diet isolate 9980-BHL040517-GBD22738_24887-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.8% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612152 Oligochaeta sp. water mite diet isolate 10032-BHL040517-GBD13102_3285-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGATCTGGAATAATTGGAACAGGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTCCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATATAAGATTCTGACTGCTACCCCCTTCACTAACCCTATCAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612153 Oligochaeta sp. water mite diet isolate 10039-BHL040517-GBD14551_25793-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGCTTGAGCTGGAATAATTGGAACAGGATCTAGAATATTAATTCGGATTGAATTATCACAACCAGGATCATTCCTAGGAAGAGATCAACTTTATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTAGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTGCTACCACCTTCACTAACCCTATTAGTATCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612154 Oligochaeta sp. water mite diet isolate 10069-BHL040517-GBD15133_25827-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.8% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612155 Oligochaeta sp. water mite diet isolate 10076-BHL040517-GBD23768_12906-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACATGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTGTTTCTGGTTATACCAATTTTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTACTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612156 Oligochaeta sp. water mite diet isolate 10078-BHL040517-GBD27884_19688-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGAAACTAGTATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGTTCTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTCCCACCTACACCAATCCAAATAGTTTCTTCTGCTGCCGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612157 Oligochaeta sp. water mite diet isolate 10079-BHL040517-GBD19949_10662-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTCTCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTATAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTATCTAGTTCTTTAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 82.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612158 Oligochaeta sp. water mite diet isolate 10087-BHL040517-GBD20649_11052-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGCTTGAGCTGGAATAATTGGAACATGATTTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGTGATCAACTATATAATACTCTTGTAACTGCACATGCATTTCTAATAATTTTTTTTCTGGTTATACCAGTTTTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612159 Oligochaeta sp. water mite diet isolate 10102-BHL040517-GBD26773_17128-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTATTACCTCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612160 Oligochaeta sp. water mite diet isolate 10105-BHL040517-GBD20692_24341-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACATGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCTCATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCCCCAGACATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCCCCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612161 Oligochaeta sp. water mite diet isolate 10106-BHL040517-GBD12851_7208-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.2% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612162 Oligochaeta sp. water mite diet isolate 10115-BHL040517-GBD17798_15972-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAGTACTTGGGGCACCTGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTGCCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.5% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612163 Oligochaeta sp. water mite diet isolate 10124-BHL040517-GBD8557_22866-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACACTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCTCGACTAAACAATATAAGATTCTGACTACTTCCCCCTTCTCTAACCCTACTACTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612164 Oligochaeta sp. water mite diet isolate 10130-BHL040517-GBD15110_12475-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACTTGAACTAGAATATTAATTCGGATTGAATTATCTCAACTAGGAACATTCCTAGGAAGAGATCAACTATATAATATTCTAGTAACTGCACATGCATTTCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612165 Oligochaeta sp. water mite diet isolate 10131-BHL040517-GBD7474_18890-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAGTTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACCTTTAT--CAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.8% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612166 Oligochaeta sp. water mite diet isolate 10134-BHL040517-GBD11465_24630-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATATTTTATCTTTGGAGTTTGAGCTGGAATAATTGGAACAGCACCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTTCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTGTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612167 Oligochaeta sp. water mite diet isolate 10135-BHL040517-GBD13812_22894-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATAGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACTGGATCTAGAATATTTATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTTTATAATACTCTAGTAACTGCACATGCATTTCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTCCCCCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612168 Oligochaeta sp. water mite diet isolate 10151-BHL040517-GBD5619_19974-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATGATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LN810268, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612169 Oligochaeta sp. water mite diet isolate 10158-BHL040517-GBD22485_22004-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATATTTTATTTTAGGAGTTTGAGCTGGAATAATTGGAACAGGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGAACATTCCTAGGAAGAGATCAACTTTATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTTATGGTTATACCAGTTTTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612170 Oligochaeta sp. water mite diet isolate 10159-BHL040517-GBD7265_10753-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGGATATTAATTCGAGCTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.2% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612171 Oligochaeta sp. water mite diet isolate 10162-BHL040517-GBD23440_7542-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGGATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTTTATAATACTCTTGTAACTGCTCATGCATTCCTTATAATTTTTTTTCTAGTTATACCAATATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCCCCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612172 Oligochaeta sp. water mite diet isolate 10172-BHL040517-GBD16975_23996-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTTTGAGCTGGAATAATTGGAACAGGTACTAGAATATTAATTCGAATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTTACTGCACATGCATTCATAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTACTACCTCCAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.2% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612173 Oligochaeta sp. water mite diet isolate 10181-BHL040517-GBD19209_20015-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTCATCTTAGGAGTTTGATCTGGAATAATTGGAACAGGACCTAGAATATTAATTCGGATTGAATTATCTCACCCAGGATCATTCCTAGGAAAAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAATATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATATTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATCTAAGATTCTGACTACTACCCCCTTCACTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612174 Oligochaeta sp. water mite diet isolate 10185-BHL040517-GBD4923_7100-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAGGAGATCAACTTTATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTTATGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCCCCAGATATAGCTTTCCCACGACTTAACAATATAAGATTCTGACCACTACCCCCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612175 Oligochaeta sp. water mite diet isolate 10198-BHL040517-GBD28392_14995-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTCATCTTAGGAGCTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTTACTGCACATGCATTTCTAATAATTTTCTTTCTGGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612176 Oligochaeta sp. water mite diet isolate 10224-BHL040517-GBD22146_9536-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAGTTGGAACGGGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAAAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGGCTACTACCACCTTCTCTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612177 Oligochaeta sp. water mite diet isolate 10233-BHL040517-GBD26858_12514-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGCTTGAGCTGGAATAGTTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTTTATAATACTCTAGTAACTGCTCATGCATTCCTAATAATTTTTTTATGGCTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612178 Oligochaeta sp. water mite diet isolate 10241-BHL040517-GBD14933_27982-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTTTATATTTATTTTTGGAGTTTGAGCTGGAATAATTGGAACAGGAATTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTTGTAACTGCACATGCATTTCTAATAATTTTCTTTCTAGTTATACCAATATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612179 Oligochaeta sp. water mite diet isolate 10243-BHL040517-GBD23148_21936-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGGATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACTCTAGTTACTGCACATGCATTCCTAATAATTTTCTTTCTGGTAATACCAGTATTTATTGGAGGATTTGGAAATTGACTACTACCTCTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612180 Oligochaeta sp. water mite diet isolate 10248-BHL040517-GBD12733_21801-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612181 Oligochaeta sp. water mite diet isolate 10251-BHL040517-GBD29119_14185-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGATCTGGAATAATTGGAACAGCATCTAGCATATTAATTCGTATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTTCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGAGGATTTGGAAATGGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612182 Oligochaeta sp. water mite diet isolate 10255-BHL040517-GBD24978_15857-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAGCCTTTTTAGGATGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTAATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.1% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612183 Oligochaeta sp. water mite diet isolate 10259-BHL040517-GBD20083_24056-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCTCTCTATACTTCATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTTCTAATAATTTTTTTTCTGGTTATACCAGTATTTATTGGAGGATTTGGAAATTGACTGCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCCCCTTCTCTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612184 Oligochaeta sp. water mite diet isolate 10262-BHL040517-GBD23352_17368-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGATCTAGTATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTTCTTATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAACATAAAATTCTGACTACTACCCCCTTCACTAATCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612185 Oligochaeta sp. water mite diet isolate 10267-BHL040517-GBD25632_23269-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGTATAGGAACAAGACTATTAATTCGGCTTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGACTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KY633407, identified in GenBank as Specaria josinae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612186 Oligochaeta sp. water mite diet isolate 10268-BHL040517-GBD16382_17603-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTTTATACTTTATCTTAGGAGCTTGAGCTGGAATAATTGGAACATGATTTAGTATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTTGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTTCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATTAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612187 Oligochaeta sp. water mite diet isolate 10269-BHL040517-GBD14820_11502-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTACCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612188 Oligochaeta sp. water mite diet isolate 10279-BHL040517-GBD7609_16784-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACTGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTTGTAACTGCACATGCATTCCTAATAATTTTTTTTCTGGTTATACCAGTATTTATTGGAGGATTTGGCAATTGACTTCTACCTCTAATACTTGGAGCCCCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGTCTACTACCCCCTTCACTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612189 Oligochaeta sp. water mite diet isolate 10283-BHL040517-GBD19455_8061-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAATCATAAAGATATTGGCACTTTATACTTTATCTTTGGAGTTTGATCTGGAATAGTTGGAACAGGTACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTTATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612190 Oligochaeta sp. water mite diet isolate 10294-BHL040517-GBD7634_18450-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATCTTAGGAGTTTGAGCAGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LN810268, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612191 Oligochaeta sp. water mite diet isolate 10307-BHL040517-GBD21638_25309-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTGCCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612192 Oligochaeta sp. water mite diet isolate 10326-BHL040517-GBD6353_13292-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGCTTGAGCTGGAATAATTGGAACTGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCTCGACTTAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612193 Oligochaeta sp. water mite diet isolate 10331-BHL040517-GBD10945_12103-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCTGGAATAATTGGAACAGGGACTAGAATATTAATTCGGATTGAATTATCACAACCAGGATCATTCCTAGGAAGAGATCAACTATATAACACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTGGTAATACCAGTATTTATTGGAGGATTTGGAAACTGACTACTACCACTAATACTTGGAGCACCAGATATGGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCATCTCTAATCCTATTAGTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612194 Oligochaeta sp. water mite diet isolate 10334-BHL040517-GBD22635_18210-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACTGGATTTAGAATATTAATTCGGATTGAATTATCACAACCAGGATCATTCCTAGGAAGAGATCAACTTTATAATATTTTAGTAACTGCACATGCATTCCTAATAATTTTTTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAAACCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612195 Oligochaeta sp. water mite diet isolate 10341-BHL040517-GBD8376_19248-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCACAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCTTAATAATTTTCTTTCTGGTAATACCAGTATTTATTGGTGGATTTGGAAATTGATTACTACCTCTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCATCACTAATCTTACTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612196 Oligochaeta sp. water mite diet isolate 10345-BHL040517-GBD11113_21833-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTCTAGTTATACCAGTTTTTATTGGAGGATTTGGAAATTGACTTCTACCTTTAATACTCGGAGCACCAGATATAGCATTCCCACGACTAAACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCTATTAGTTTCTTCGGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612197 Oligochaeta sp. water mite diet isolate 10346-BHL040517-GBD20582_17193-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCTTAATAATTTTTTTCCTGGTTATACCAGTATTTATTGGAGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCATCCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTGCATCGGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612198 Oligochaeta sp. water mite diet isolate 10349-BHL040517-GBD12594_23739-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATATTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATGTAATACTCATGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCGCCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCAGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612199 Oligochaeta sp. water mite diet isolate 10351-BHL040517-GBD21434_4858-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTTTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACTGGAGCTAGAATATTAATTCGGATTAAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTCGGAGCACCAGATATAGCTTTCCCGCGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTATCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612200 Oligochaeta sp. water mite diet isolate 10363-BHL040517-GBD18280_25861-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGCTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAATTTTATAATACTCTAGTAACTGCACATGCTTTCTTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCACTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612201 Oligochaeta sp. water mite diet isolate 10367-BHL040517-GBD11065_7629-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTTCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTTCTAATAATTTTTTTCCTGGTAATACCAGTATTTATTGGAGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCATTCCCACGACTAAACAATATAAGATTTTGACTACTACCCCCATCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.6% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612202 Oligochaeta sp. water mite diet isolate 10369-BHL040517-GBD2893_16596-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACATGTACTAGAATATTAATTCGAGTTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTTACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGAGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCATTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612203 Oligochaeta sp. water mite diet isolate 10370-BHL040517-GBD24946_20222-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTTGGAGTTTGAGCTGGTATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGAGCATTCATAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612204 Oligochaeta sp. water mite diet isolate 10381-BHL040517-GBD7947_17983-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGAACACTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACATGAACTAGAATATTTATTCGGATTGAATTATCCCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAGTACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612205 Oligochaeta sp. water mite diet isolate 10391-BHL040517-GBD26841_8086-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGATCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAAATATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTAGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTAGGAGCACCAGATAGAGCTTTCCCTCGAATAAACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612206 Oligochaeta sp. water mite diet isolate 10403-BHL040517-GBD12178_4776-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCAGTCTATACTTAATCTTAGGAGTTTGAGATGGAATAATTGGAACAGGAACTGGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTAGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGAGACAGCTTTCCCACGCCTTAACAATATAAGATTCTGACTACTACCACCTTCACCAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATCGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612207 Oligochaeta sp. water mite diet isolate 10407-BHL040517-GBD17603_20034-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGCTTGAGCTGGAATAATTGGAACAGGAATTAGAATATTAATTCGGATTGAATTATCTCACCCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTTCCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGTCTAAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTCTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612208 Oligochaeta sp. water mite diet isolate 10408-BHL040517-GBD22275_27629-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATATTTTATCTTTGGAGCTTGAGCTGGAATAATTGGAACAGGTTCTAGAATATTAATTCGGCTTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCCCCTTCACTAATCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612209 Oligochaeta sp. water mite diet isolate 10411-BHL040517-GBD9936_4820-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACTGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTTGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTAATACCAGTATTTATTGGAGGATTTGGAAATTGACTTCTACCACTAATACTTGGAGCAGCAGATATAGCTTTCCCACGACTAAACAATCCAAGATTCTGACTACTACCACCATCACTAATCCTACTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612210 Oligochaeta sp. water mite diet isolate 10413-BHL040517-GBD20354_21461-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTTTATACTTTATCTTAGGAGCTTGAGCTGGAATAATTGGAACAGGAATTAGAATATTAATTCGGGTAGAATTATGTCAACCAGGATCATTCCTAGGAAAAGATCAACTTTATAATACTCTAGTAACTGCACATGCATTTCTAATAATTTTTTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612211 Oligochaeta sp. water mite diet isolate 10423-BHL040517-GBD5229_12009-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGCTTGAGCTGGAATAATTGGAACGGGACCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTTGTAACTGCACATGCATTTCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTTTGCCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAGACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612212 Oligochaeta sp. water mite diet isolate 10427-BHL040517-GBD10167_11733-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTTTGAGCTGGAATAATTGGAACAGGTACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCTTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTAATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCACTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTATTAGTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612213 Oligochaeta sp. water mite diet isolate 10435-BHL040517-GBD17481_4225-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGCATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTATTTCTGGTTATACCAGTATTAATTGGAGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCCCCAGATATAGCTTTCCCACGCCTTAACAATTTAAGATTCTGCCTACTCCCCCCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612214 Oligochaeta sp. water mite diet isolate 10441-BHL040517-GBD15566_18567-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGCTACTAGAATATTTATTCGGATTGAATTATCACAACCAGGATCATTCCTAGGTAAAGATCAACTATATAATACTCTAGTAACTGCACATGCTTTCCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612215 Oligochaeta sp. water mite diet isolate 10449-BHL040517-GBD3032_20730-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTAGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTTGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTAATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTAGGGGCACCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTT---TCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612216 Oligochaeta sp. water mite diet isolate 10450-BHL040517-GBD16012_24231-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGCATCTAGAATATTTATTCGGATTGAATTATCTCAACCAGGATCTTTCATAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATATAAGATTCTGACTACCACCACCTTCACTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612217 Oligochaeta sp. water mite diet isolate 10452-BHL040517-GBD14237_6882-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCCTCTTCTTTCTAGTTCATTT---GTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612218 Oligochaeta sp. water mite diet isolate 10469-BHL040517-GBD11594_15547-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGCTACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTACTAGGAAGCGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTATGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCCCCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612219 Oligochaeta sp. water mite diet isolate 10473-BHL040517-GBD5450_15993-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATAGAATTATCTCAACCAGGATCATTCCTAGGAAAAGATCAACTTTATAATACTCTAGTAACTGCACATGCATTTCTAATAATTTTTTTCTGGTTATACCAGTATTTATTGGAGGATTTGGAAATTGACTTCTACCTCTAATACTTGGGGCACCAGATATAGCTTTCCCACGACTTAACAATATAAGACTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612220 Oligochaeta sp. water mite diet isolate 10474-BHL040517-GBD21788_25006-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTTACTGCACATGCTTTTGTAATAATTTTTTTCTAGTTATACCAGTATTAATTGGAGGATTTGGAAGTTGACTTCTACCTCTAATATTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTATCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612221 Oligochaeta sp. water mite diet isolate 10483-BHL040517-GBD10708_17679-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAATTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCCAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTCTTTTTCTGGTTATACCAGTATTAATTGGAGGATTTGGAAATTGACTACTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTATCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612222 Oligochaeta sp. water mite diet isolate 10489-BHL040517-GBD16645_23030-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTTGGAGCTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTTATTCGGATTGAATTATCTCAACCAGGATCTTTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTTATAATAATTTTCTTCCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612223 Oligochaeta sp. water mite diet isolate 10493-BHL040517-GBD23036_13233-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCTCTCTATACTTTATCTTAGGAGTTTGATCTGGAATAATTGGAACAGGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCTCATGCATTCATAATAATTTTCTTTCTGGTAATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCAGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612224 Oligochaeta sp. water mite diet isolate 10494-BHL040517-GBD6837_23058-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGATCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCACCCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTTCTAATAATTTTTTTCTGGTTATACCAGTATTTATTGGAGGATTTGGAAATTGACCTCTACCTCTAATACTCGGAGCACCAGATATAGCATTCCCACGAATAAACAATATAAGATTCTGACTACTACCCCCGTCACTAACCCTATTAGTATCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612225 Oligochaeta sp. water mite diet isolate 10508-BHL040517-GBD15876_23379-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATATTTTATCTTCGGAGTTTGAGCTGGAATAATTGGAACTGGAACTAGAATATTTATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTCGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAA	Using NCBI BLASTN in June 2018, this sequence was 86.6% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612226 Oligochaeta sp. water mite diet isolate 10512-BHL040517-GBD18232_9343-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612227 Oligochaeta sp. water mite diet isolate 10527-BHL040517-GBD4711_10432-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATCTTCGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGTATATTAATTCGGATTGAATTATCTCACCCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAACATAAGATTCTGACTACTACCACCTTCTCTAACCCTATTAGTATCTACTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 8516% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612228 Oligochaeta sp. water mite diet isolate 10532-BHL040517-GBD6818_23055-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACTGGTACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACCTCTACCTCTAATATTCGGAGCACCAGATATAGCATTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCGTCACTAACCCTATTAGTATCTACTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612229 Oligochaeta sp. water mite diet isolate 10543-BHL040517-GBD27185_15831-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATATTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGTACTAGTATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGTGATCAACTATATAATACTCTAGTCACTGCACATGCATTTCTTATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTACTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612230 Oligochaeta sp. water mite diet isolate 10544-BHL040517-GBD13323_2036-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612231 Oligochaeta sp. water mite diet isolate 10545-BHL040517-GBD24364_20216-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGTTCAACTATATAACACTCTAGTTACTGCTCATGCATTTCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGAGGATTTGGAAACTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCTCTAATCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612232 Oligochaeta sp. water mite diet isolate 10551-BHL040517-GBD18433_27889-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGATCTGGAATAATTGGAACATCAACTAGAATATTAATTCGGGTTGAATTATCTCTACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCATAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGAGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATAAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612233 Oligochaeta sp. water mite diet isolate 10558-BHL040517-GBD23530_12261-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATATTTAATCTTAGGAGCTTGAGCTGGAATAATTGGAACAGGATCTAGAATATTAATTCGGATTAAATTATCTCAAACAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTTCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATATTCGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTATCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612234 Oligochaeta sp. water mite diet isolate 10566-BHL040517-GBD14250_13214-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTACTAGGAAGAGATCAACTATATAATACTCTTGTAACAGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCGCGACTAAACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCTACTAGTATCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612235 Oligochaeta sp. water mite diet isolate 10571-BHL040517-GBD16282_16756-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTCATCTTCGGAGTTTGAGCTGGAATAATTGGAACAGGCCCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAAATATATAATACTCTAGTAACTGCACATGCATTTCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTCGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCCTCACTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 86.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612236 Oligochaeta sp. water mite diet isolate 10578-BHL040517-GBD24310_13649-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTCGGAAGAGATCAACTATATAATACTCTAGTTACTGCACATGCATTTCTAATGATTTTTTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCATTCCCACGACTAAACAATATAAGATTCAGACTACTACCCCCGTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612237 Oligochaeta sp. water mite diet isolate 10583-BHL040517-GBD21260_21179-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGCTTGAGCTGGAATAATTGGAACAGGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTTTATAATACACTTGTAACTGCACATGCTTTTCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTATCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612238 Oligochaeta sp. water mite diet isolate 10585-BHL040517-GBD23368_16549-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTCGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612239 Oligochaeta sp. water mite diet isolate 10591-BHL040517-GBD12311_16259-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTCGGAGCACCAGATATAGCTTTCCCACGACTTAACAATATAAGATTTTGACTTTTGCCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612240 Oligochaeta sp. water mite diet isolate 10595-BHL040517-GBD20958_8924-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAGTTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTTCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGAGGATTTGGAAATTGAATTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGGCTACTACCACCATCACTAATCCTATTAGTTGCTTCGGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612241 Oligochaeta sp. water mite diet isolate 10596-BHL040517-GBD23866_4409-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGCTTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCTTTCCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTACTACCTCTAATACTGGGAGCACCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTATCTACTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612242 Oligochaeta sp. water mite diet isolate 10600-BHL040517-GBD15101_6718-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTTACTGCACATGCATTCCTAATAATTTTTTTTCTAGTTATACCAGTATTAATTGGAGGATTTGGAAATCGACTTCTACCTTTAATACTTGGAGCACCAGATATAGCATTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCGTCACTAACCCTATTAGTATCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612243 Oligochaeta sp. water mite diet isolate 10604-BHL040517-GBD6212_24984-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGCTTGAGCTGGAATAATTGGAACAGGCTCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTTATAATTTTCTTTCTGGTTATACCAGTATTAATTGGAGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCGTTCCCACGACTAAACAATTTAAGATTTTGACTACTACCACCTTCACTAACCCTATTAGTTTCTGCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612244 Oligochaeta sp. water mite diet isolate 10607-BHL040517-GBD14569_18452-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTTTATACTTTATCTTTGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTCCTGGTTATACCAGTATTAATTGGAGGATTTGGAAATTGACTTCTACCCCTAATACTCGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTATGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612245 Oligochaeta sp. water mite diet isolate 10612-BHL040517-GBD21246_10017-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATATTTGGAACAGGAACTAGAATACTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCTTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAACTGACTAGTACCACTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCAGACTACTACCACCATCACTAATCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612246 Oligochaeta sp. water mite diet isolate 10616-BHL040517-GBD11797_8490-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGACCTAGAATATTAATTCGTATCGAATTATCTCACCCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAAATTCTGATTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612247 Oligochaeta sp. water mite diet isolate 10623-BHL040517-GBD15149_27775-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCAGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCCCCAGACATAGCTTTCCCTCGAATAAACAATTTAAGATTCTGACTACTACCCCCGTCACTAACCCTATTAGTATCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612248 Oligochaeta sp. water mite diet isolate 10634-BHL040517-GBD24956_20824-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTTTATACTTTATTTTTGGAGCTTGAGCTGGAATAATTGGAACAGCATTTAGAATATTAATTCGGGTTGAATTATCTCAACCAGGATCATTCCTAGGAAAAGATCAACTATATAATACTCTAGTTACTGCACATGCTTTCCTAATAATTTTCTTTCTAGTTATACCAATATTAATTGGAGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTTCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612249 Oligochaeta sp. water mite diet isolate 10636-BHL040517-GBD21917_11150-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGTACAGGAACTAGAATATTTATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAACTGACTTCTACCTCTAATACTTGGAACACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCTATTAGCTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612250 Oligochaeta sp. water mite diet isolate 10647-BHL040517-GBD16168_20439-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTTTGAGCTGGAATAATTGGAACTGGTACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTTTATAATACTCTTGTAACTGCACATGCATTTCTTATAATTTTTTTCTAGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTACTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTACTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612251 Oligochaeta sp. water mite diet isolate 10649-BHL040517-GBD25987_8998-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCGGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCACAACCAGGATCATTCCTAGGAAGAGATCAACTTTATAATACTCTAGTTACTGCACATGCATTTGTAATAATTTTCTTTCTGGTTATACCAATATTTATTGGAGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCTATTAGTATCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612252 Oligochaeta sp. water mite diet isolate 10653-BHL040517-GBD25477_8412-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGATCTGGAATAATTGGAACAGGAATTAGAATATTAATTCGAATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTATAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATATAAGGTTCTGACTACTACCACCTTCACTAACCCTACTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612253 Oligochaeta sp. water mite diet isolate 10661-BHL040517-GBD6599_25524-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTTTATACTTCATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGCACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGACCATTCCTAGGAAGAGATCAACTTTATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATATTCGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTACAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612254 Oligochaeta sp. water mite diet isolate 10663-BHL040517-GBD8232_24565-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTTTGAGCAGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATAGTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTACTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.6% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612255 Oligochaeta sp. water mite diet isolate 10675-BHL040517-GBD10594_8657-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTCGGAGCTTGATCTGGAATAATTGGAACATGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTTCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTACTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTACTACAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612256 Oligochaeta sp. water mite diet isolate 10680-BHL040517-GBD21560_13204-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATATTTTGTTTTAGGAGCTTGAGCTGGAATAATTGGAACTGGGTCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTTCTGGTTATACCAATATTAATTGGTGGATTTGGAAATTGACTACTACCTCTAATACTCGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612257 Oligochaeta sp. water mite diet isolate 10681-BHL040517-GBD26442_11698-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACTGCACTTAGAATATTAATTCGGATCGAATTATCTCAAACCGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAATATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTACTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612258 Oligochaeta sp. water mite diet isolate 10684-BHL040517-GBD26642_7884-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGCTTGAGCTGGAATAATTGGAACAGGATTTAGAATATTTATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAAATTTATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTCCTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612259 Oligochaeta sp. water mite diet isolate 10688-BHL040517-GBD7904_9478-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGCTTGAGCTGGAATAATTGGAACAGCAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGAACATTCCTTGGAAGAGATCAAATATATAATACTCTAGTAACTGCACATGCTTTCCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATAAACAATATAAGATTCTGACTACTACCACCTTCTCTAACCCTACTAGTTTCTACTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612260 Oligochaeta sp. water mite diet isolate 10689-BHL040517-GBD17616_13650-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGCACTAGTATATTTATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTTGTAACTGCTCATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCTTCTCTAACCCTATTAGTTTCTTCTGCGGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612261 Oligochaeta sp. water mite diet isolate 10708-BHL101516-GBD23962_6340-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTCTTGTAGTACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTGATATCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612262 Oligochaeta sp. water mite diet isolate 10715-BHL101516-GBD9615_15076-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGTACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTTGTTACTGCTCATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTATCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612263 Oligochaeta sp. water mite diet isolate 10716-BHL101516-GBD10684_16120-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTTTGATTACTACCCCCATCTCTAACCTTACTACTTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LN810268, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612264 Oligochaeta sp. water mite diet isolate 10719-BHL101516-GBD10356_19065-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCCTGTAATACCAGTATTTATTGGAGGGTTTGGAAACTGATTAGTACCACTAATGCTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612265 Oligochaeta sp. water mite diet isolate 10722-BHL101516-GBD27616_9518-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTATACTTATTTTTAGGAGTATGAGCAGGAATAATTGGACCAGGGACTAGATTACTAATTCGACTTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGACCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612266 Oligochaeta sp. water mite diet isolate 10724-BHL101516-GBD7096_5529-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGACTACTAATTCGAATTGAATCATCACAACCAGGATCATTCTTAGGAAGAGACCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTGATTTCTTCTGCAGCAGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612267 Oligochaeta sp. water mite diet isolate 10727-BHL101516-GBD23293_24679-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATATTTGGAACAGGGACTAGAATACTAGTTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCCCCATGTCTAATCTTACTGATTTCTTCTGCAGCAGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612268 Oligochaeta sp. water mite diet isolate 10729-BHL101516-GBD8525_16227-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTATTGTAATACCAGTAATTATCGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCACCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTGCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612269 Oligochaeta sp. water mite diet isolate 10731-BHL101516-GBD22160_4942-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGATCAGGAATAATTGGAACAGGGTCTAGAATACTAGTTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCATAGTTCCTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAAGCTTACTGATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612270 Oligochaeta sp. water mite diet isolate 10732-BHL101516-GBD4203_20429-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTTGTACAGGGACTAGAATACTAATTCGAATTGAATTATCACATCCAGGATCATTCATAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTGCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCACCAGATATGGCATTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTATTAATTTCTTCTGCAGCAGTAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612271 Oligochaeta sp. water mite diet isolate 10733-BHL101516-GBD10346_5641-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGTGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAAATATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCCCCAGATATGGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612272 Oligochaeta sp. water mite diet isolate 10741-BHL101516-GBD24110_10085-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATTATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCACCAGATATGGCTTTCCCACGAATAAATAATTTAAGATTCTGACTACTACCACCGGCTCTAATCTTACTGATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612273 Oligochaeta sp. water mite diet isolate 10742-BHL101516-GBD6599_7217-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGATCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGACGAGAGCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612274 Oligochaeta sp. water mite diet isolate 10744-BHL101516-GBD21502_27969-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAAGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACACTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTGATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID KT716826, identified in GenBank as Amynthas morrisi. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612275 Oligochaeta sp. water mite diet isolate 10748-BHL101516-GBD22689_4589-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAAATATATAACTCCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAACTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATATCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612276 Oligochaeta sp. water mite diet isolate 10750-BHL101516-GBD9188_27148-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTATTTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTATTAATAATTTTCTTTCTTGTAATACCAATATTTATTGGAGGATTTGGAAAATGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTGATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612277 Oligochaeta sp. water mite diet isolate 10751-BHL101516-GBD20531_27912-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGAACATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCGGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTGATCTTACTAATTTCTTCTGCAACAGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612278 Oligochaeta sp. water mite diet isolate 10753-BHL101516-GBD18339_2961-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCCGGAATAATTGGAACAGGGACTAGAATACTCATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTCTATAACACCCTATTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGCGCTGGCACAG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612279 Oligochaeta sp. water mite diet isolate 10759-BHL101516-GBD19391_14879-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGATTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAATGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAACATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612280 Oligochaeta sp. water mite diet isolate 10761-BHL101516-GBD13661_28317-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGGCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTTTCTCTTCTTCTTTCTAGTTCAATTATTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612281 Oligochaeta sp. water mite diet isolate 10763-BHL101516-GBD20494_7084-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTTTAGAATACTAATTCGAATTGAATTATCACATCCAGGATCATTCTTAGGAAGAGATCAACTATATAACACTCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612282 Oligochaeta sp. water mite diet isolate 10771-BHL101516-GBD10541_10191-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGGCTAAATAATTTAAGATTCTGACTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612283 Oligochaeta sp. water mite diet isolate 10776-BHL101516-GBD23266_6449-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGTTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTAGTAATACCAGTATTTATTGGAGGGTTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612284 Oligochaeta sp. water mite diet isolate 10787-BHL101516-GBD21994_21301-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATATTTCATTTTTGGAGCTTGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAAGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTATATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTACAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612285 Oligochaeta sp. water mite diet isolate 10790-BHL101516-GBD22850_7366-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAGTTCGAATTGAATTATGACGACCAGGATCATTCTTAGGAAGTGATCAACTATATAACACCGTAGTTACTGCACATGCATTCTTAATAATTTTCTTCCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTGATTTCTTCTGCAGCAGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612286 Oligochaeta sp. water mite diet isolate 10791-BHL101516-GBD22200_10892-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAACACTTGGAGCTCCAGAGATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACAACCATCTCTAAACTTACTAAGCTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612287 Oligochaeta sp. water mite diet isolate 10793-BHL101516-GBD20985_7834-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATCGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCACACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.8% identical to accession ID LN810268, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612288 Oligochaeta sp. water mite diet isolate 10797-BHL101516-GBD13044_16672-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTCATTTTAGGGGTATGAGCAGGAATAATTGGAACTGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACAATAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCTGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612289 Oligochaeta sp. water mite diet isolate 10798-BHL101516-GBD28603_15343-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTCATTTTAGGAGTATGAGCCGGAATAATTGGAACAGGGACTCGAATACTAGTTCGAATTGAATTATCACAAACAGGATCATTCTTAGGGAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTGATTTCTTCTGCAGCAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612290 Oligochaeta sp. water mite diet isolate 10800-BHL101516-GBD10570_24170-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACCAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAAGAATTGGAAACTGATTAGTACCACTAATAATTAGAGCTCCAGATATGGCTTTCCCACGACTAAAAAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACCGATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612291 Oligochaeta sp. water mite diet isolate 10803-BHL101516-GBD17738_4372-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTTTTTATTGGAGGATTTGGAAACTGATTAGTACCACTAACACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTCCTACCACCATCTCTAATCTTCCTAATTTCTTCTGCAGCAGTACAAAATGGTGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612292 Oligochaeta sp. water mite diet isolate 10810-BHL101516-GBD24768_7752-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAGTTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATCTAACACCCTAGTTACTGAACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACGGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACGACCACCATCTATAATCTTACTGATTTCTTCTACAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612293 Oligochaeta sp. water mite diet isolate 10816-BHL101516-GBD15455_17804-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATATTTAATTTTAGGAGTATGAGCAGGAATAGTTGGAACTGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCCTTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCTTTCTTAATAATTTTTTTCCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612294 Oligochaeta sp. water mite diet isolate 10818-BHL101516-GBD8972_27053-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACATCCTAGTTACTGCCCATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCACTAAACTTACTAATATCTTCGGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612295 Oligochaeta sp. water mite diet isolate 10822-BHL101516-GBD6421_19299-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACCGGGACTAGAATACTAATTCGAATTGAATTACCACAGCCAGGATCATTCTTAGGAAGAGATCAACTATATAACGCCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCATCAGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612296 Oligochaeta sp. water mite diet isolate 10828-BHL101516-GBD11698_11433-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTCATTTTTGGGGCTTGATCAGGAATAATTGGAACAGGGACTAGAATACTAGTTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTGATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612297 Oligochaeta sp. water mite diet isolate 10831-BHL101516-GBD23787_16995-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATGTTAGGGGCCCCTGATATAGCCTTCCCGCGAATAAATAATATAAGATTTTGACTTCTCCCACCGTCTCTTGCTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.3% identical to accession ID KT429020, identified in GenBank as Amynthas moniliatus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612298 Oligochaeta sp. water mite diet isolate 10834-BHL101516-GBD5079_16675-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTACTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGACTAGTCCCACTAATACTTGGAGCTCCAGACATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTTCTACCCCCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612299 Oligochaeta sp. water mite diet isolate 10837-BHL101516-GBD17648_13024-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGCTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTCTTGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCTTTAATACTTGGAGCCCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTTCTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612300 Oligochaeta sp. water mite diet isolate 10839-BHL101516-GBD14914_2764-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTACACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGTATCATTCTTAGGAAGAGATCAACTATATAACACCCTACTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTCTTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGATCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612301 Oligochaeta sp. water mite diet isolate 10841-BHL101516-GBD23790_4020-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGATCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTTCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCCCTAACCTTACTAATTACTTCAGCAGCAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612302 Oligochaeta sp. water mite diet isolate 10843-BHL101516-GBD19748_3263-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTCGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCGCGACTAAATAATATAAGATTCTGACTATTACCACCATCTCTAATCTTACTAACTTCTGCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612303 Oligochaeta sp. water mite diet isolate 10847-BHL101516-GBD27877_12406-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGCATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAGTTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCATTCCCTCGACTAAACAATTTAAGATTCTGACTACTACCACCATCACTAATCTTACTGATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612304 Oligochaeta sp. water mite diet isolate 10856-BHL101516-GBD27671_8245-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGCATGAGCAGGAATAATTGGAACAGGCTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACCCACTAGTTACTGCACATGCATTCATAATAATTTTCTTTCTTGTAATACCAGTTTTTATTGGAGGATTTGGAAACTGATTAGTCCCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612305 Oligochaeta sp. water mite diet isolate 10863-BHL101516-GBD3625_18543-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGACTAGAATACTAGTTCGAATTGAATTATCACAACCCGGATCTTTCATAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAAACTTACTGATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612306 Oligochaeta sp. water mite diet isolate 10865-BHL101516-GBD26461_7145-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACGGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACTCCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATACTGACTACGACCACCAGCGCTAAACTTACTAATGTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612307 Oligochaeta sp. water mite diet isolate 10866-BHL101516-GBD18636_9013-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGATCAGGAATAATTGGAACTGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTTGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTATTGTAATACCAGTTTTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612308 Oligochaeta sp. water mite diet isolate 10871-BHL101516-GBD10999_22519-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTAATTTTAGGAGTATGAGCAGGTATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAACATCTTCTGCAGCAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612309 Oligochaeta sp. water mite diet isolate 10872-BHL101516-GBD20943_2814-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGACTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACAACTAAATAATATAAGATTCTGACTACTACCACCATCGCTAATCTTGCTGATTTCGTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612310 Oligochaeta sp. water mite diet isolate 10874-BHL101516-GBD22876_13857-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGAACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGCATTTATTGGAGGATTTGGAAACTGATTAGTACCCCTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCCCCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612311 Oligochaeta sp. water mite diet isolate 10876-BHL101516-GBD13486_17678-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAATCAGGATCATTCTTAGGAAGAGATCAACTATATAATACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGAATACTACCACCATCTCTAATCTTACTAATGGCTTCAGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612312 Oligochaeta sp. water mite diet isolate 10879-BHL101516-GBD6510_6680-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTTTTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAACTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATGGCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.6% identical to accession ID KT716826, identified in GenBank as Amynthas morrisi. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612313 Oligochaeta sp. water mite diet isolate 10882-BHL101516-GBD23038_18481-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGAACATTCTTAGGAAGAGATCCACTATATAACACTCTATTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTACCCCTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTGATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612314 Oligochaeta sp. water mite diet isolate 10888-BHL101516-GBD26241_11682-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGTACTAGAATACTAATTCGAATTGCATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAACTCCAGATATGGCTTTACCACGACTAAATAATTTAAGATTCTGACTGCTACCACCATCGCTAATCTTACGAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612315 Oligochaeta sp. water mite diet isolate 10890-BHL101516-GBD7074_7661-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATATTTTTTTTTAGGAGTTTGAGCAGGAATAATTGGAACTGGGTCTAGAATATTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACATCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTGATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612316 Oligochaeta sp. water mite diet isolate 10894-BHL101516-GBD27854_13332-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGAACATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTTTTAATAATTTTCTTTATAGTAATACCAATATTAATTGGAGGATCTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612317 Oligochaeta sp. water mite diet isolate 10905-BHL101516-GBD13019_16316-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGATCAGGAATAATAGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGTAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCTTCTCTAATCTTACTAATTTCTTCTGCAGCGGTAGAGAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612318 Oligochaeta sp. water mite diet isolate 10906-BHL101516-GBD26895_12349-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGGGATCAACTATACAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTGGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCCCCATCTCTAATCTTACTGATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612319 Oligochaeta sp. water mite diet isolate 10911-BHL101516-GBD24367_19524-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTTGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCCTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612320 Oligochaeta sp. water mite diet isolate 10912-BHL101516-GBD24290_6416-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGTAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612321 Oligochaeta sp. water mite diet isolate 10916-BHL101516-GBD26391_8814-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTCATTTTCGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCCAATATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTA-TAATACCAGTATCTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATGCTGACAACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATAGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612322 Oligochaeta sp. water mite diet isolate 10917-BHL101516-GBD12005_19223-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTATTTTCAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTATTTCGAATTGAATTATCACACCCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612323 Oligochaeta sp. water mite diet isolate 10918-BHL101516-GBD29124_13827-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTCGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGTAAGAGATCAACTATATAACACCCGAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGGATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACATGGAGCTCCAGATATGACTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGGAGTAGAAAAGGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612324 Oligochaeta sp. water mite diet isolate 10920-BHL101516-GBD13201_2478-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTTTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGACTTGAATTATCACAACCAGGATCATTCTTAGGAAGGGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAATCTTACTAGTTGCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612325 Oligochaeta sp. water mite diet isolate 10921-BHL101516-GBD4784_19501-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATATTTAATTTTAGGAGTTTGAGCAGGAATAATTGGTACAGGTACTAGAATATTAATTCGAGTTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LN810268, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612326 Oligochaeta sp. water mite diet isolate 10922-BHL101516-GBD13063_22589-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACGACCCCCAACGCTAACCTTACTAAAATCTTCTGCAGCAGTAGAAAATGGAGCTGAAACAG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612327 Oligochaeta sp. water mite diet isolate 10923-BHL101516-GBD6686_24572-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGTGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTGCAGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612328 Oligochaeta sp. water mite diet isolate 10924-BHL101516-GBD20345_5402-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGGGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCGTCTACGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.0% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612329 Oligochaeta sp. water mite diet isolate 10925-BHL101516-GBD14557_16796-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTATATAACACCCTAGTTACTGCTCATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAACATAAGATTCTGACTACTACCACCATCTCTAACCCTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612330 Oligochaeta sp. water mite diet isolate 10926-BHL101516-GBD8053_18805-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGATTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACATCATAGTTACTGCACATGCATTCATAATAATTTTCTTTATAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTCCCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612331 Oligochaeta sp. water mite diet isolate 10927-BHL101516-GBD5249_14989-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAGGATCAACTATATAACACCCTAGTTACTGCACATGCATTTATAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612332 Oligochaeta sp. water mite diet isolate 10928-BHL101516-GBD28442_13872-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAGTTGAATTATCACAACCAGGATCGTTCTTAGGAAAAGATCAAATATATAACACCCTAGTTACTGCACATGCTTTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTATCACCATCTCTAACCTTACTAATTTCTTCTGCATCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612333 Oligochaeta sp. water mite diet isolate 10929-BHL101516-GBD7873_18640-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATTCTACTAATTTCATCTGCAGCAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.0% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612334 Oligochaeta sp. water mite diet isolate 10931-BHL101516-GBD17824_27341-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATATTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCGTTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCCCATGCATTCTTAATAATTTTTTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCTCGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612335 Oligochaeta sp. water mite diet isolate 10932-BHL101516-GBD18117_12560-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTACACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTAGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCCCCATCTCTAACCTTACTAATTTCAACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612336 Oligochaeta sp. water mite diet isolate 10935-BHL101516-GBD14631_3919-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGCAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGATGATTTGGAAACTGGTTAGTACCCCTAATACTTGGAGCTCAAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGCGCTTGAAC	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612337 Oligochaeta sp. water mite diet isolate 10936-BHL101516-GBD27773_12837-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATGAGCAGGAATAGTTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACACTTGTTACTGCACATGCATTTTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCCTCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.9% identical to accession ID KY633404, identified in GenBank as Slavina sp. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612338 Oligochaeta sp. water mite diet isolate 10938-BHL101516-GBD23895_10796-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTCATTTTAGGAGTATGAGCCGGAATAGTTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTATTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAAGACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCGTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612339 Oligochaeta sp. water mite diet isolate 10939-BHL101516-GBD25574_21084-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGAACATTATTAGGAAGGGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCAGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612340 Oligochaeta sp. water mite diet isolate 10940-BHL101516-GBD14949_3706-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTGTTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGCCTAAAT-ATCTTAAGATTCTGCCTACTACCTCCATCTCTAATCTTGCTAATTTCTTCTGCAGCATTAGAAAATGGCGCTGGAACTGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KY633404, identified in GenBank as Slavina sp. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612341 Oligochaeta sp. water mite diet isolate 10941-BHL101516-GBD18172_7016-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCGTTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCCCCAGATATGGCTTTCCCACGACTAAAAAATTTAAAATTCTGACCACTACCACCATCTCTAATCCTAAGAAATTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612342 Oligochaeta sp. water mite diet isolate 10942-BHL101516-GBD10662_15234-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTTGGAGTATGAGCAGGAATAGTAGGAACAGGGCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGTGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612343 Oligochaeta sp. water mite diet isolate 10943-BHL101516-GBD20872_27839-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGTCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCAGTCTTAGGAAGAGATCAACTATATAACACTCTAGTTACTGCACATGCATTCATAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAAACTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612344 Oligochaeta sp. water mite diet isolate 10944-BHL101516-GBD9769_6202-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTTATTTTAGGAGTATGATCAGGAATAATTGGAACTGGTTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAATGGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCCCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCACTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.0% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612345 Oligochaeta sp. water mite diet isolate 10948-BHL101516-GBD24973_17695-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTAATATTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATTTAAGATTTTGACTACTACCCCCATCACTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.8% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612346 Oligochaeta sp. water mite diet isolate 10950-BHL101516-GBD24744_11060-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTTTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTTATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGGGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCCTCTCTAACCATACAAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612347 Oligochaeta sp. water mite diet isolate 10951-BHL101516-GBD6536_6688-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTTTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACATGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGGGATCAACTTTATAACACACTAGTTACTGCACATGCTTTCTTAATAATTTTTTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCCGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612348 Oligochaeta sp. water mite diet isolate 10953-BHL101516-GBD11883_13992-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTTGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGCTCATTCTTAGGAAGAGATCAACTATATAACATCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCACTAACCTTACTAATATCTACTGCAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612349 Oligochaeta sp. water mite diet isolate 10954-BHL101516-GBD10589_14150-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGCATTAGAATACTAATTCGATTTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAAATATATAACACTATAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTCGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612350 Oligochaeta sp. water mite diet isolate 10955-BHL101516-GBD12828_8347-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTCGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGAATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGAAATGGCTTTCCCACGACAAAAAAAATTAAGATTCTGACTACTACCACCATCACTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612351 Oligochaeta sp. water mite diet isolate 10956-BHL101516-GBD25856_12982-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCAAATTGAATTATCACAACCAGGATCACTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTGGTACCACTAATACTTGGAGCTCCAGAAATAGCTTTCCCACGACAAAATAATTTAAGATTCTGACTACTACCACCATCTCCAATCTTACTAAATTCTTCTGCATCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612352 Oligochaeta sp. water mite diet isolate 10958-BHL101516-GBD27538_15637-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACACTTGTTACTGCACATGCATTCTTAATAATTTTTTTTATAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCTTTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612353 Oligochaeta sp. water mite diet isolate 10959-BHL101516-GBD3558_17144-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGACGAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTATTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCTTACTGATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612354 Oligochaeta sp. water mite diet isolate 10961-BHL101516-GBD9657_25412-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTTGGAGTATGAGCAGGAATAATTGGAACTGGGATTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATATTTGGAGCTCCAGATATGACATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612355 Oligochaeta sp. water mite diet isolate 10962-BHL101516-GBD24820_6923-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGCATGAGCAGGAATAATTGGAACAGGGACTAGAATGCTAATTCGAATTGAATTATGACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACTCTTGTTACTGCACATGCATTTTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KT716826, identified in GenBank as Amynthas morrisi. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612356 Oligochaeta sp. water mite diet isolate 10963-BHL101516-GBD19306_15135-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTTTATACTTAATTTTCGGAGTATGAGCAGGAATAATTGGAACAGGGATTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGGGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTATAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATAGTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTGCTACCACCATCTCTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.4% identical to accession ID MG422806, identified in GenBank as Slavina appendiculata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612357 Oligochaeta sp. water mite diet isolate 10965-BHL101516-GBD11122_12161-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATATTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGCACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACGTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAAAATAAGAATCTGACTACTACCACCAGCTCTAAACTTACAAATGTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612358 Oligochaeta sp. water mite diet isolate 10966-BHL101516-GBD21264_22721-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGTGTCTAGAATGCTGATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTATAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCAGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612359 Oligochaeta sp. water mite diet isolate 10967-BHL101516-GBD15555_18710-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTTTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGGGATCAAATATATAACACCCTAGTTACTGCTCATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAACCTTACTAATATCTTCCGCACCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612360 Oligochaeta sp. water mite diet isolate 10969-BHL101516-GBD24407_15510-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGATCAGGAATAATTGGAACATGGTCTAGAATACTAATTCGAATTGAATTATGACAACCAGGATCATTCTTCGGAAGAGATCAACTATATAACACACTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID KT716826, identified in GenBank as Amynthas morrisi. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612361 Oligochaeta sp. water mite diet isolate 10971-BHL101516-GBD18728_6155-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACAAATCATAAAGATATTGGCACTCTATACTTCATTTTAGGAGTCTGATCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATCGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATACAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.2% identical to accession ID KT716826, identified in GenBank as Amynthas morrisi. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612362 Oligochaeta sp. water mite diet isolate 10972-BHL101516-GBD21545_5667-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGTACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACATACTAGTTACTGCACATGCATTCTTTATAATTTTCTTTCTTGTAATACCAGTTTTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612363 Oligochaeta sp. water mite diet isolate 10973-BHL101516-GBD7803_11270-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAACCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTTATTGGAGGGTTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCATTCCCACGAATAAATAATATAAGATTCTGACTACCACCACCATCACTAATCTTACTAATATCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612364 Oligochaeta sp. water mite diet isolate 10975-BHL101516-GBD11719_9307-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGACTTGAATTATCACAACCAGGCTCATTCTTCGGAAGGGATCAACTATATAACACCATAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.7% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612365 Oligochaeta sp. water mite diet isolate 10977-BHL101516-GBD23808_16465-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGGGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGAGATGGCTTTCCCACGACGAAATAATTTAAGATACTGACTACTACCACCAGCGCTAAACGTACTAATGTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612366 Oligochaeta sp. water mite diet isolate 10978-BHL101516-GBD4383_18039-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTTGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGAACATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATATTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCCCACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612367 Oligochaeta sp. water mite diet isolate 10979-BHL101516-GBD26171_16900-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAACGATATTGGCACTCTATATTTTATTTTTGGAGTATGAGCAGGAATAATTGGCACAGGGTCTAGAATACTAATTCGAATTAAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612368 Oligochaeta sp. water mite diet isolate 10980-BHL101516-GBD16800_4172-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCATTATCATTCTTAGGAAGGGATCTACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGAACCACTAATACTTGGAGCTCAAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGTGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612369 Oligochaeta sp. water mite diet isolate 10982-BHL101516-GBD26398_8623-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAACAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTACTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATGTTGACTTCTTCCACCTTCACTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.7% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612370 Oligochaeta sp. water mite diet isolate 10985-BHL101516-GBD20947_4782-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGTTACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGAATCATTCTTAGGAAGAGATCCACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTGCCCACGACTAAATAATATAAGATTCTGACTACGACCACCATCTCTAAACTGACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612371 Oligochaeta sp. water mite diet isolate 10986-BHL101516-GBD19540_14528-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGATCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTATTGTAATACCAGTATTAACTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCAGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612372 Oligochaeta sp. water mite diet isolate 10988-BHL101516-GBD10903_23819-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTTATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTCATAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCCTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612373 Oligochaeta sp. water mite diet isolate 10989-BHL101516-GBD11453_11602-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGGACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTTCCACGACTAAATAATTTAAGATTCTGACTATTACCACCATCTCTAACCTTACTAATTTCTTCAGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612374 Oligochaeta sp. water mite diet isolate 10992-BHL101516-GBD18264_13923-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGAATAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612375 Oligochaeta sp. water mite diet isolate 10993-BHL101516-GBD6729_21345-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGTACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGGGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCCCTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGGCTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612376 Oligochaeta sp. water mite diet isolate 10994-BHL101516-GBD9008_22850-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAGGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTCCTTGTTATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCTCGACTAAATAATATAAGATTCTGACTTCTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612377 Oligochaeta sp. water mite diet isolate 10998-BHL101516-GBD6316_10601-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTTATACCAGAATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTTCTACCGCCATCTCTAACCCTACTAATTTCATCTGTAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612378 Oligochaeta sp. water mite diet isolate 10999-BHL101516-GBD17599_29064-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACAAATCATAAAGATATTGGCACTTTATATTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGGGATCAACTATATAACATTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACGACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.2% identical to accession ID KT716826, identified in GenBank as Amynthas morrisi. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612379 Oligochaeta sp. water mite diet isolate 11000-BHL110116-GBD15249_3231-Lq74 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612380 Oligochaeta sp. water mite diet isolate 11011-BHL110116-GBD25099_9276-Lq75 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTACACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTGTTATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCTCCAGATATGGCTTTCCCTCGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612381 Oligochaeta sp. water mite diet isolate 11013-BHL110116-GBD10933_9333-Lq75 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTGATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCAGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612382 Oligochaeta sp. water mite diet isolate 11014-BHL110116-GBD4641_7863-Lq75 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACGCTAGTTACTGCACATGCATTCTTAATAATTTTATTTATTGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATAATTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTTTGACTACTACCCCCATCTCTAACATTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612383 Oligochaeta sp. water mite diet isolate 11024-BHL110116-GBD29051_12663-Lq76 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGAATTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTGTCCCACGACAAAATAATTTAAGAATCAGACTACGACCACCATCTCTAATCTTACTAATTTCTTCGGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612384 Oligochaeta sp. water mite diet isolate 11031-BHL110116-GBD24655_9975-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612385 Oligochaeta sp. water mite diet isolate 11048-BHL110116-GBD18596_3111-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LN810268, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612386 Oligochaeta sp. water mite diet isolate 11050-BHL110116-GBD12806_21379-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCCCTAATACTTGGAGATCCAGATATGGCTTTCCCACGACTAAATAATCTAAGATTCTGACTACTACCACCATCACTAAACTTACGAAGTACTTCGGCAGCAGTAGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612387 Oligochaeta sp. water mite diet isolate 11051-BHL110116-GBD29033_18824-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTCATTTTAGGAGTATGCGCAGGAATAATTGGCACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTGATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCATTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCGCTAATCTTACTAATTGCTGCGGCAGCAGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612388 Oligochaeta sp. water mite diet isolate 11060-BHL110116-GBD27286_20513-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCTCATGCATTCTTAATAATTTTCTTTATAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTCGGAGCTCCAGATTTGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAAACTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612389 Oligochaeta sp. water mite diet isolate 11069-BHL110116-GBD27142_18209-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGTAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTCTAGTAATACCAGTATTAATTGGAGGTTTTGGAAATTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCAGCAGCAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612390 Oligochaeta sp. water mite diet isolate 11071-BHL110116-GBD20845_8035-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTCGGAGTCTGAGCAGGAATAATTGGAACTGTTACTAGAATACTAATTCGAATCGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTTATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTGCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612391 Oligochaeta sp. water mite diet isolate 11072-BHL110116-GBD7037_5096-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTGTCCCACGAATAAATAATATAAGAGTTTGACTTCTTCCCCCCTCTTTAA-CACAGTTACTTTCA--AGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612392 Oligochaeta sp. water mite diet isolate 11075-BHL110116-GBD24657_5018-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGTAATAATTGTAACAGGTTCTAGAATACTAATTCGTATTGAATTATCACAACCAGGAGCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTTCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGTCAAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTGACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612393 Oligochaeta sp. water mite diet isolate 11092-BHL110116-GBD17106_14286-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACATGGT-CTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAAATATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATATTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAAACTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612394 Oligochaeta sp. water mite diet isolate 11097-BHL110116-GBD16650_16186-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTATTTCTTGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACAACCACCATCTCTAATCTTACAAATTTCTTCTGCAGCAGTAGAAAATGGTGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612395 Oligochaeta sp. water mite diet isolate 11102-BHL110116-GBD20639_5463-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAGTTGGAACAGGGACTAGAATACTAATTCGTATTGAATTAGCACACCCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCACTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGTTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612396 Oligochaeta sp. water mite diet isolate 11109-BHL110116-GBD5180_11539-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTTGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTGCCCACGACTAAAAAAATTAAGATACTGACTACGACCGCCAGCTCTAAACTTACAAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612397 Oligochaeta sp. water mite diet isolate 11111-BHL110116-GBD7924_19201-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACGAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCCAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCGCGAATAAATAACATAAGATTCTGACTACTACCACCATCACTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612398 Oligochaeta sp. water mite diet isolate 11112-BHL110116-GBD14572_3228-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGTATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCAATCTTAATAATTTTCTTTCTGGTAATACCATTCTTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTCTCCCACGACTAAATAATTTAAGATTCTGACTACTACCCCCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGCGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612399 Oligochaeta sp. water mite diet isolate 11114-BHL110116-GBD8717_25008-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTCATTTTAGGAGCATGAGCAGGAATAATTGGAACTGGGCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTCGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612400 Oligochaeta sp. water mite diet isolate 11116-BHL110116-GBD11385_7646-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACATGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGTTCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCTCATGCATTCTTAATAATTTTCTTTATTGTGATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTGTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612401 Oligochaeta sp. water mite diet isolate 11119-BHL110116-GBD18926_10426-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGGTTTGGAAACTGATTAGTACCACTAATACTTGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCACCATCATTAACTTTAT---TGTGATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.9% identical to accession ID LN810268, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612402 Oligochaeta sp. water mite diet isolate 11121-BHL110116-GBD29380_14809-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAGTTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTACCACAACCAGGATCATTCTTCGGAAAAGATCAACTATATAACACACTAGTTACTGCACATGCATTCGTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGGGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612403 Oligochaeta sp. water mite diet isolate 11123-BHL110116-GBD21371_4671-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATATTTTATTTTAGGAGTCTGAGCAGGAATAATTGGAACATGTTCTAGAATACTAATTCGAATTGAATTATCACAACCTGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612404 Oligochaeta sp. water mite diet isolate 11124-BHL110116-GBD11877_6412-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGAATAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 81.7% identical to accession ID KU728850, identified in GenBank as Enchytraeus albidus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612405 Oligochaeta sp. water mite diet isolate 11125-BHL110116-GBD2049_17201-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGTACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCATAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAACAATATAAGATTCTGACTGCTACCCCCATCACTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612406 Oligochaeta sp. water mite diet isolate 11128-BHL110116-GBD19750_22417-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTTTGACTACTACCACCATCTCTAACCTTACTAATATCTAGTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612407 Oligochaeta sp. water mite diet isolate 11129-BHL110116-GBD10027_18558-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCT-CTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID JQ519897, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612408 Oligochaeta sp. water mite diet isolate 11131-BHL110116-GBD8752_23191-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGCACTGCGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCCTTCTTAGGAAGAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCATTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612409 Oligochaeta sp. water mite diet isolate 11135-BHL110116-GBD21408_21795-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCTCATGCATTCTTAATAATTTTTTTTCTTGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGTGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCCTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612410 Oligochaeta sp. water mite diet isolate 11147-BHL110116-GBD11850_15161-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTCATTTTAGGAGTATGAGCAGGAATAATTGGAACTTGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTCCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCAACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612411 Oligochaeta sp. water mite diet isolate 11157-BHL110116-GBD25887_5908-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATGAGCAGGAATAGTTGGAACTGGTACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACTCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTACTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.3% identical to accession ID KY633404, identified in GenBank as Slavina sp. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612412 Oligochaeta sp. water mite diet isolate 11165-BHL110116-GBD18101_12146-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTGATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAACCTTACTAATATCTACTGCAGTAGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612413 Oligochaeta sp. water mite diet isolate 11169-BHL110116-GBD14360_9268-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGATCAGGAATAGTTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGCAGAGATCAATTATATAACACCCTAGTTACTGCACATGCATTCTTTATAATTTTCTTTATTGTAATACCAGTATTAATTGGAGGATTTGGAAAATGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAAGCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612414 Oligochaeta sp. water mite diet isolate 11170-BHL110116-GBD18755_4691-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAATGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTAGTAATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCCGATATAGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612415 Oligochaeta sp. water mite diet isolate 11174-BHL110116-GBD22152_25001-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAATATTAATTGGAGGATTTGGAAACTGACTAGTACCACTAATATTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAACATAAGATTTTGACTACTACCCCCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612416 Oligochaeta sp. water mite diet isolate 11177-BHL110116-GBD23567_7993-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGCACAGGGACTAGAATACTAATTCGACTTGAATTATCACACCCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATGCCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAATCTTACTAATATCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612417 Oligochaeta sp. water mite diet isolate 11184-BHL110116-GBD16943_24212-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTAAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGACATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCTCCGTCTATTTCTTTGCTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612418 Oligochaeta sp. water mite diet isolate 11186-BHL110116-GBD25013_17569-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACATTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTATAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCATTTCCTCGACTAAATAATATAAGATTCTGACTACTACCCCCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612419 Oligochaeta sp. water mite diet isolate 11189-BHL110116-GBD14351_7041-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGATCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGTAAGAGATCAACTACATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCCCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTGTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612420 Oligochaeta sp. water mite diet isolate 11192-BHL110116-GBD22621_14117-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGTATTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTAAATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATATTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612421 Oligochaeta sp. water mite diet isolate 11194-BHL110116-GBD12047_7576-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGATCAGGAATAATTGGAACTGGCACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTTATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTACAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612422 Oligochaeta sp. water mite diet isolate 11196-BHL110116-GBD25317_23878-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATATTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTATATAACACCCTTGTTACTGCTCATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCTCCAGATATAGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612423 Oligochaeta sp. water mite diet isolate 11201-BHL110116-GBD25099_21975-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACATGTTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAATACCCTAGTTACTGCACATGCTTTCTTTATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612424 Oligochaeta sp. water mite diet isolate 11206-BHL110116-GBD23569_20597-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTTGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTTGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATAGCATTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAAACTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.7% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612425 Oligochaeta sp. water mite diet isolate 11209-BHL110116-GBD18894_10016-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCTCAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCCCATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATGTGGCTTTCCCACGACTAAATGATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612426 Oligochaeta sp. water mite diet isolate 11212-BHL110116-GBD26355_7279-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTTGTTACTGCACATGCATTTTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAAAATAAGATTCTGACTACCACCACCATCTCCAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612427 Oligochaeta sp. water mite diet isolate 11213-BHL110116-GBD25171_22091-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATACTTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACCGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTAGTTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATAACTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612428 Oligochaeta sp. water mite diet isolate 11219-BHL110116-GBD24968_9785-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATAGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTTGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTTTTAATTGGGGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612429 Oligochaeta sp. water mite diet isolate 11222-BHL110116-GBD25658_11152-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTCATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAGGAGATCAACTATATAACACACTAGTTACTGCTCATGCATTTTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612430 Oligochaeta sp. water mite diet isolate 11225-BHL110116-GBD18841_18947-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACATCCTAGTTACTGCTCATGCATTTTTAATAATTTTTTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAAACTTACTAATTTCCACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612431 Oligochaeta sp. water mite diet isolate 11226-BHL110116-GBD10242_23149-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGATTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTTGTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCATCTGTAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612432 Oligochaeta sp. water mite diet isolate 11227-BHL110116-GBD5757_10255-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCACTTTTAATTGGAGGATTTGGAAACTGATTAGTACCCCTAATACTTGGAGCTCCAGATATAGCTTTCCCTCGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612433 Oligochaeta sp. water mite diet isolate 11230-BHL110116-GBD20624_19850-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGCTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTATTGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACATTACTAATTTCTTCAGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612434 Oligochaeta sp. water mite diet isolate 11234-BHL110116-GBD14690_8027-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGCTCATTCTTCGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTATTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCACTAACCTTACTAATATCATGAGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612435 Oligochaeta sp. water mite diet isolate 11235-BHL110116-GBD17133_17755-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGATCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAATATCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCCTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612436 Oligochaeta sp. water mite diet isolate 11239-BHL110116-GBD29167_15380-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGCATGAGCAGGAATAATTGGAACTGGGACTAGAATACTAATTCGAATTAAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAAACTTACTAATATCTTCTACAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612437 Oligochaeta sp. water mite diet isolate 11240-BHL110116-GBD4578_21886-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTTTTAATAATTTTTTTACTAGTAATACCAGTTTTTATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCACCAGATATGGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAGTTTCTTCGGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612438 Oligochaeta sp. water mite diet isolate 11241-BHL110116-GBD28415_12698-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAAATTTATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCCCCATCTCTAACCTTACTAATATCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612439 Oligochaeta sp. water mite diet isolate 11253-BHL110116-GBD23130_22188-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTCATTTTAGGAGTATGAGCAGGAATAATTGGAACATCGCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTTGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTATTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612440 Oligochaeta sp. water mite diet isolate 11258-BHL110116-GBD27408_17959-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTTATTCGAATTGAATTATCACAACCAGGATCTTTCTTAGGAAAAGATCAACTTTATAACACTCTAGTTACTGCACATGCTTTCTTTATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612441 Oligochaeta sp. water mite diet isolate 11259-BHL110116-GBD4387_13504-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTTGGAGTATGAGCAGGAATAATTGGAACATGTTCTAGAATACTAATTCGAGTTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612442 Oligochaeta sp. water mite diet isolate 11261-BHL110116-GBD6148_7484-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATATTTCATTTTTGGAGTATGATCAGGAATAATTGGAACATGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGGGCACCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTACTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612443 Oligochaeta sp. water mite diet isolate 11262-BHL110116-GBD14039_24651-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTTGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCGTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCATTCCCACGAATAAATAATTTAAGATTCTGACTACTACCACCATCTTTAACCTTACTAATATCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612444 Oligochaeta sp. water mite diet isolate 11266-BHL110116-GBD25413_24348-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGAACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAATACCCTAGTTACTGCACATGCATTTTTAATAATTTTTTTCCTTGTAATACCAGTATTTATTGGAGGATTTGGAAATTGATTAGTACCACTAATACTTGGAGCACCAGATATAGCATTCCCACGACTAAATAATATAAGATTCTGACTATTACCACCATCTCTAATCCTACTAATTGCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.0% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612445 Oligochaeta sp. water mite diet isolate 11267-BHL110116-GBD7838_9734-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTTGGAGTATGAGCAGGAATAATTGGAACTGGGCTTAGAATACTTATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACTCTAGTTACTGCACATGCATTCTTTATAATTTTTTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612446 Oligochaeta sp. water mite diet isolate 11269-BHL110116-GBD19979_18294-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATTAGCAGGAATAATTGGAACAGTGACTAGTATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATCACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTACTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTATCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACGAATTGCTTCTGCAGCAGTAGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612447 Oligochaeta sp. water mite diet isolate 11272-BHL110116-GBD12265_9450-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGATCAGGAATAATTGGAACATGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCACTAATCTTACTAATTTCGTGTGCAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612448 Oligochaeta sp. water mite diet isolate 11274-BHL110116-GBD20544_4088-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTGATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCCTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.8% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612449 Oligochaeta sp. water mite diet isolate 11276-BHL110116-GBD22330_20516-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCATAGTTACTGCACATGCATTCTTAATAATTTTCTTTATTGTAATACCAGTATTTATTGGAGGGTTTGGAAACTGATTAATACCACTAATACTTGGAGCTCCAGATATGGCTTTACCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAAACTTACTAAATTCTTCTGCAGCAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612450 Oligochaeta sp. water mite diet isolate 11280-BHL110116-GBD24271_5207-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTGGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAATAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCCCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612451 Oligochaeta sp. water mite diet isolate 11282-BHL110116-GBD26935_22185-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCTTTCTTAGGAAGAGATCAACTATATAATATCCTAGTTACTGCACATGCATTCATAATAATTTTTTTTCTAGTAATACCTGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612452 Oligochaeta sp. water mite diet isolate 11288-BHL110116-GBD16478_24889-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGCGTCTAGAATACTTATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTTTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTCTGACTACTACCCCCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612453 Oligochaeta sp. water mite diet isolate 11289-BHL110116-GBD23543_15990-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGATATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCAACTCTAATCTTACTAATTTCGTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612454 Oligochaeta sp. water mite diet isolate 11291-BHL110116-GBD10017_17407-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTACATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAGACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAAACTTACTAATTTCAACTGCAGCAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612455 Oligochaeta sp. water mite diet isolate 11297-BHL110116-GBD18199_24036-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGTTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAGGAGATCAAATATATAACACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAAACTTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612456 Oligochaeta sp. water mite diet isolate 11299-BHL110116-GBD21603_3908-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGTTCTAGAATACTTATTCGAATTGAATTATCACAACCAGGATCCTTCTTAGGAAGAGACCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCACCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612457 Oligochaeta sp. water mite diet isolate 11300-BHL110116-GBD13336_1800-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTTGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACGACCACCAGCACTAAACTTACTAATATCATCTGCAGCAGTAGAAAATGGAGCTGGAACCGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612458 Oligochaeta sp. water mite diet isolate 11304-BHL110116-GBD24692_12729-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTATTAGGAAGAGATCAACTATATAACACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCATTAATACTTGGAGCTCCAGATATAGCATTCCCACGACTAAATAATATAAGATTCTGACTATTACCCCCATCACTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612459 Oligochaeta sp. water mite diet isolate 11305-BHL110116-GBD23493_5059-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGATCAGGAATAATTGGAACATGTACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTATAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGACTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAACCTTACTAATTTCATGTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612460 Oligochaeta sp. water mite diet isolate 11307-BHL110116-GBD27237_10352-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGACTACTACCTCTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTATACAATTTAAGATTCTGACTACTACCACCATCACTAATCCTACTGGTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612461 Oligochaeta sp. water mite diet isolate 11311-BHL110116-GBD22594_18034-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGGATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACATTACTAATTTCTAGTGCAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612462 Oligochaeta sp. water mite diet isolate 11312-BHL110116-GBD9731_20774-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTTGGAGTATGAGCAGGAATAATTGGAACTGGTACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTCGGAAGAGATCAACTATATAACACCCTTGTTACTGCACATGCTTTTTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCGCGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.4% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612463 Oligochaeta sp. water mite diet isolate 11315-BHL110116-GBD27702_16619-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATCCTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTTTATAACACTCTAGTTACTGCACATGCATTCTTAATAATTTTTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCCCTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTATTACCCCCATCTCTAACCTTACTAATTTCTTCTGCAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612464 Oligochaeta sp. water mite diet isolate 11318-BHL110116-GBD27880_20860-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAATACCCTTGTTACTGCACATGCTTTCTTAATAATTTTCTTTCTTGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCATTCCCACGACTAAATAATTTAAGATTCTGACTACTACCCCCATCACTAATCTTACTAATATCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612465 Oligochaeta sp. water mite diet isolate 11321-BHL110116-GBD25936_9133-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACATGGT-CTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTTTTAATAATTTTCTTTATAGTAATACCAGTATTGATTGGAGGATTTGGAAACTGATTAGTACCACTAGTACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCATCAACAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612466 Oligochaeta sp. water mite diet isolate 11323-BHL110116-GBD18554_9265-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTACTTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCACACGACGAAATAACTTAAGATTCTGACTACGACCACCATCGCTAATCTTACAAATAGATTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612467 Oligochaeta sp. water mite diet isolate 11325-BHL110116-GBD17524_26028-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTTGGATTAGAATATTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAATATCCTTGTTACTGCACATGCATTTTTAATAATTTTTTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612468 Oligochaeta sp. water mite diet isolate 11326-BHL110116-GBD24364_18888-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTTATAATTTTTTTTCTTGTAATACCAATATTAATTGGAGGATTTGGAAACTGACTACTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCCCGACTAAATAACATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATATCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612469 Oligochaeta sp. water mite diet isolate 11327-BHL110116-GBD17048_25038-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCCATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCTTTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCGTCTCTAACCTTACTAATATCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612470 Oligochaeta sp. water mite diet isolate 11329-BHL110116-GBD25469_24155-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCCGGAATAATTGGAACTGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCGTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCCCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAAACTTACTAATTTCTACTGCATCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612471 Oligochaeta sp. water mite diet isolate 11331-BHL110116-GBD9568_4649-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTTGGAGTATGAGCAGGAATAGTTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTTTATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTTCTACCACCATCGCTAACCTTACTAATTTCTACTGCAGCTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612472 Oligochaeta sp. water mite diet isolate 11333-BHL110116-GBD26002_15693-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACACACAGGATCATTATTAGGAAGAGATCAACTTTATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612473 Oligochaeta sp. water mite diet isolate 11335-BHL110116-GBD14270_12262-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGAACATTCTTAGGAAATGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTAATACCACCATCTCTGACCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612474 Oligochaeta sp. water mite diet isolate 11336-BHL110116-GBD19695_24871-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACTCTAGTTACTGCACATGCATTCGTAATAATTTTCTTTCTAGTAATATCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTCACCTTACTACTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612475 Oligochaeta sp. water mite diet isolate 11339-BHL110116-GBD19448_16012-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACATTCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCCCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTACTTTCTAGTGCAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612476 Oligochaeta sp. water mite diet isolate 11340-BHL110116-GBD20596_11829-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTCTGAGCAGGAATAATTGGAACTGGGCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGAACATTCTTAGGAAGAGATCAACTTTATAACACCCTTGTTACAGCACATGCATTCTTAATAATTTTTTTTATTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612477 Oligochaeta sp. water mite diet isolate 11343-BHL110116-GBD8568_12237-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGCATGATCAGGAATAATTGGAACTGCGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAATACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612478 Oligochaeta sp. water mite diet isolate 11344-BHL110116-GBD2978_18779-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTAGCACACCCAGGATCATTCTTAGGAATAGATCAATTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612479 Oligochaeta sp. water mite diet isolate 11345-BHL110116-GBD15765_27649-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCTAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACTCTAGTTACTGCACATGCATTCTTAATAATTTTTTTCTAGTTATACCAGTTTTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612480 Oligochaeta sp. water mite diet isolate 11347-BHL110116-GBD20803_4462-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACATCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTATAGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTACTACAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.9% identical to accession ID KT429020, identified in GenBank as Amynthas moniliatus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612481 Oligochaeta sp. water mite diet isolate 11351-BHL110116-GBD23183_6766-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACTCTAGTTACTGCACATGCATTCTTAATAATTTTTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCCCTAATACTTGGAGCTCCAGACATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCCCCATCTCTAACCTTACCAATTTCTTCTGCAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.4% identical to accession ID GQ355375, identified in GenBank as Slavina appendiculata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612482 Oligochaeta sp. water mite diet isolate 11355-BHL110116-GBD23938_24701-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTCGGAGTATGAGCAGGAATAATTGGAACAGCGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGTGATCAACTTTATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTGCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612483 Oligochaeta sp. water mite diet isolate 11357-BHL110116-GBD9626_25510-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGTGATCAACTATATAACACCCTAGTTACTGCTCATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTTTTAATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTTTGACTACTACCCCCATCTTTAACCTTACTAATTTCTTCTGCAGCTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612484 Oligochaeta sp. water mite diet isolate 11361-BHL110116-GBD8714_25310-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGATCAGGAATAATTGGAACATGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTATATAACTCCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTATTGTAATACCAGTCTTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCCCCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612485 Oligochaeta sp. water mite diet isolate 11362-BHL110116-GBD15097_15546-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGTTCATTCTTAGGAAGAGATCAACTTTATAACATCCTTGTTACAGCACATGCTTTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612486 Oligochaeta sp. water mite diet isolate 11368-BHL110116-GBD28436_16525-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAATACCCTTGTTACTGCTCATGCATTTTTTATAATTTTTTTTATAGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612487 Oligochaeta sp. water mite diet isolate 11369-BHL110116-GBD20549_14220-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCT-CTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.8% identical to accession ID LN810268, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612488 Oligochaeta sp. water mite diet isolate 11370-BHL110116-GBD13537_16579-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGATCAGGAATAATTGGAACAGCGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGAACATTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCGCTAATACTTGGAGCACCAGATGTGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612489 Oligochaeta sp. water mite diet isolate 11371-BHL110116-GBD10330_28050-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAAAACCGTAGTTACAGCACGTGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTGAATGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCGTTCCCACGACTAAATAAAATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612490 Oligochaeta sp. water mite diet isolate 11376-BHL110116-GBD8965_16788-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTCTGAGCAGGAATAATTGGAACAGCGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTTTTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTGTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612491 Oligochaeta sp. water mite diet isolate 11378-BHL110116-GBD21325_21239-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTTATTTTAGGAGTATGATCGGGAATAATTGGAACTGGGATTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGTGATCAACTTTATAACACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.7% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612492 Oligochaeta sp. water mite diet isolate 11380-BHL110116-GBD4489_16604-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAAATTCTGACTACTACCACCATCTCTAACATTACTAATTTCTAGTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612493 Oligochaeta sp. water mite diet isolate 11381-BHL110116-GBD2467_13611-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATACAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTACTTCGAATTGAATTCTCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATATTTGGAGCTCCAGATATAGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612494 Oligochaeta sp. water mite diet isolate 11388-BHL101516-GBD24789_18123-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612495 Oligochaeta sp. water mite diet isolate 11389-BHL101516-GBD10962_15318-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACCCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGTTCTAAAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCGTTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTTAACTTACTAATTTCTTCAGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612496 Oligochaeta sp. water mite diet isolate 11391-BHL101516-GBD28658_18261-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATCTTAGGAGTTTGAGCAGGAATAATTGGAACAGGGACTAAAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACTCTAGTTACTGCACATGCATTCCTAATAATTTTCTTTCTGGTAATACCAGTATCTATTGGAGGATTTGGAAACTGACTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCATCACTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612497 Oligochaeta sp. water mite diet isolate 11392-BHL101516-GBD16090_28774-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAAAATACTAATTCGAATTGAATTATGACAACCAGGATCATTCATAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTTGTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612498 Oligochaeta sp. water mite diet isolate 11393-BHL101516-GBD19020_17719-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAAAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGAAAAGGCTTTCCCCCGAATAAATAAATTAAGATTCTGACTACTACCACCATCTCTAAACTTACTAATTTCTTCTGCGACAGTAGAAAAAGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612499 Oligochaeta sp. water mite diet isolate 11395-BHL101516-GBD15736_4701-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAAAATACTAATGCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGGTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTACTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCCCCATCTCTAATCTTACTACTTTCTTCTGCCGCAGTAGAAA	Using NCBI BLASTN in June 2018, this sequence was 86.6% identical to accession ID KY633404, identified in GenBank as Slavina sp. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612500 Oligochaeta sp. water mite diet isolate 11397-BHL101516-GBD6020_12001-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGATTAAAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTTTAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGACTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCGCCATCTCTAATCTTACTACTTTCTTCTACAGCAGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 85.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612501 Oligochaeta sp. water mite diet isolate 11399-BHL101516-GBD21445_6177-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTCATTTTAGGAGTCTGAGCAGGAATAATTGGAACATGTACTAAAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTATGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCGCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612502 Oligochaeta sp. water mite diet isolate 11401-BHL101516-GBD22833_23828-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAAAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATCTAAGATTCTGACCACTATCCCCCTCTCCAACCTTACTAATATCTTCTGCAGCATTAGAAAATGGCGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612503 Oligochaeta sp. water mite diet isolate 11405-BHL101516-GBD7934_14035-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTCATTTTAGGAGTCTGAGCAGGAATAATTGGAACAGGGATTAAAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCCCCATCTCTAACCTTACTAATTTCTACTGCAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612504 Oligochaeta sp. water mite diet isolate 11406-BHL101516-GBD16899_28566-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACCGGGACTAAAATACTAATTCGAATTGAATTGTCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACGGCCACCATCGCTAATCTTACTAAAAGCTTCTGCAGCAGTAGAAAATGGCGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612505 Oligochaeta sp. water mite diet isolate 11407-BHL101516-GBD23359_22923-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTTTGAGCAGGAATAATTGGTACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCACCAGATATAGCTTGCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAATCTTACTAATATCTTCTGCAGCAGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612506 Oligochaeta sp. water mite diet isolate 11408-BHL101516-GBD7521_10765-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAACTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCCTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCATTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612507 Oligochaeta sp. water mite diet isolate 11412-BHL101516-GBD9926_23774-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTATATAACACCCTAGTTACTGCTCATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTGCTACCACCATCACTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612508 Oligochaeta sp. water mite diet isolate 11413-BHL101516-GBD19034_5146-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGATCAGGAATAATTGGAACTGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTGGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612509 Oligochaeta sp. water mite diet isolate 11414-BHL101516-GBD25647_22301-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGAACTTTCTTAGGAAAAGATCAACTATATAACACACTAGTTACTGCACATGCATTTATAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTTCCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612510 Oligochaeta sp. water mite diet isolate 11415-BHL101516-GBD22235_21000-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTTTAAAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTTTATAATACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTATAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612511 Oligochaeta sp. water mite diet isolate 11416-BHL101516-GBD19614_6579-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGATCAGGAATAGTTGGAACTGCGTCTAGAATACTTATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTGGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAGTACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612512 Oligochaeta sp. water mite diet isolate 11417-BHL101516-GBD7913_8783-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCAGCTCTAACCTTACTAATTTCAACTGCAGCAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612513 Oligochaeta sp. water mite diet isolate 11422-BHL101516-GBD6745_5662-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTCTGAGAAGGAATAATTGGAACTGGGACTAAAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGCGATCAACTATATAACACCCTAGTTACTGCACATGCATTCATAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTTCCACTAATATTTGGAGCTCCAGATATGGCTTTTCCACGAATAAATAATATAAGATTCTGATTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612514 Oligochaeta sp. water mite diet isolate 11424-BHL101516-GBD20692_21686-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAAAATACTGATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATGAACTATATAACGCACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612515 Oligochaeta sp. water mite diet isolate 11426-BHL101516-GBD14049_8414-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACATCCTTGTTACTGCACATGCATTCTTAATAATTTTTTTCCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATATTAGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612516 Oligochaeta sp. water mite diet isolate 11427-BHL101516-GBD3940_21149-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCGGGATCATTCTTAGGAAAAGATCAACTATATAACACCATAGTTACTGCACATGCATTCTTAATAATTTACTTTATTGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCCCCATCTCTAATCTTACTACTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612517 Oligochaeta sp. water mite diet isolate 11428-BHL101516-GBD26146_23981-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAAAATACTAATTCGAATTGCATTATCACAACAAGAATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGTACATGCAATCTTAATAATTTTCTTTCTTGTAATACCAGTATGTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCAACTCCAAGCTTACTAATTACTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.1% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612518 Oligochaeta sp. water mite diet isolate 11429-BHL101516-GBD13423_3748-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTAACCCAACCAGGAGCCATCTGAGGAAGAGATCAACTATATAACACCTCAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTTTTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCCCCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID KY633404, identified in GenBank as Slavina sp. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612519 Oligochaeta sp. water mite diet isolate 11432-BHL101516-GBD18034_16849-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGCGTCTAGAATACTAATTCGACTTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCATAGTTACTGCACATGCATTCTTAATAATTTTCTTTATTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCACTAATCTTACTAATATCTCCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612520 Oligochaeta sp. water mite diet isolate 11433-BHL101516-GBD28875_13365-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTTTTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCCCCAGATATGGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATATCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.4% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612521 Oligochaeta sp. water mite diet isolate 11434-BHL101516-GBD4868_15803-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTATATAACATCCTTGTTACTGCACATGCATTCTTGATAATTTTTTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCACCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTACTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612522 Oligochaeta sp. water mite diet isolate 11435-BHL101516-GBD26221_21663-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAAAATACTAATTCGAATTGAATTATCACAACCAGAATCATTATTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTAATTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAAAAATTTAAGATGCAGACGACAACCACCATCTCTAAGCTTACTAATTACTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612523 Oligochaeta sp. water mite diet isolate 11436-BHL101516-GBD23074_5661-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAAAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATAGCTTTCCCGCGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAACCTTACTAATATCAACAGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612524 Oligochaeta sp. water mite diet isolate 11437-BHL101516-GBD26254_8322-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGATCAGGAATAATTGGAACAGGTTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGGGATCAACTTTATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATATTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTGTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612525 Oligochaeta sp. water mite diet isolate 11438-BHL101516-GBD9161_21004-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATATTTTATTTTAGGAGTCTGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTCCTACAGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612526 Oligochaeta sp. water mite diet isolate 11439-BHL101516-GBD12984_8248-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTCGGAGTATGATCAGGAATAATTGGAACTTGGCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGACTCTGACTACTACCACCATCTCTAACCTTACTAATTTCATGTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612527 Oligochaeta sp. water mite diet isolate 11440-BHL101516-GBD5983_7153-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATGTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTAATGGAGGATTTGGAAACTGGTTAGTACCACTAATACTTGGAACTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTTACTACTACCACCATCTCTAATCTTACTAATTACTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGGA	Using NCBI BLASTN in June 2018, this sequence was 85.7% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612528 Oligochaeta sp. water mite diet isolate 11442-BHL101516-GBD16832_11838-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCGCAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACAACCTAGTTACTGCACATGCATTATTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612529 Oligochaeta sp. water mite diet isolate 11444-BHL101516-GBD21568_16352-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGCGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACTCCCTAGTTACTGCACATGAATTCTTAATAATTTTCTTTCTGGTACTACCAGTATGTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAATATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612530 Oligochaeta sp. water mite diet isolate 11445-BHL101516-GBD23717_7752-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACATGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612531 Oligochaeta sp. water mite diet isolate 11450-BHL101516-GBD13211_8759-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612532 Oligochaeta sp. water mite diet isolate 11453-BHL101516-GBD2643_14017-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACATGAACTAGAATACTAATTCGAATCGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGACTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612533 Oligochaeta sp. water mite diet isolate 11454-BHL101516-GBD19989_5079-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTAATTTTAGGAGTTTGAGCAGGAATAATTGGTACAGGTACTAGAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612534 Oligochaeta sp. water mite diet isolate 11455-BHL101516-GBD20536_19779-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTTTTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCACTAAACTTACTAATGTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612535 Oligochaeta sp. water mite diet isolate 11458-BHL101516-GBD23814_10122-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAAATGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCAGCATCGCTAATCATACTAATTGCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612536 Oligochaeta sp. water mite diet isolate 11459-BHL101516-GBD7836_11812-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTATAATACTAATTCGACTTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGTAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612537 Oligochaeta sp. water mite diet isolate 11460-BHL101516-GBD10584_25784-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACCTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTCCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAAACTTACCAATCTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612538 Oligochaeta sp. water mite diet isolate 11462-BHL101516-GBD8160_23755-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGCGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAAATTTATAACACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCTTACTACTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612539 Oligochaeta sp. water mite diet isolate 11464-BHL101516-GBD12520_11162-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGCATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAATATCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612540 Oligochaeta sp. water mite diet isolate 11465-BHL101516-GBD24843_6478-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTTTGAGCAGGAATAATTGGAACAGGAACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGATATCAACTATATAATACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCACCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCCTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612541 Oligochaeta sp. water mite diet isolate 11466-BHL101516-GBD20024_21646-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTATAGTAATACCAATATTAATTGGAGGATTTGGAAACTGACTAGTACCACTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612542 Oligochaeta sp. water mite diet isolate 11467-BHL101516-GBD25577_7807-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATCGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACCACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTTATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCCCTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612543 Oligochaeta sp. water mite diet isolate 11468-BHL101516-GBD14914_13571-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACGGGGACTAGAATACTAATTCGAATTGAATTATCACAGCCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAACACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCAGCTCTAATCTTACAAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612544 Oligochaeta sp. water mite diet isolate 11470-BHL101516-GBD2452_19480-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGTAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGGTTTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTCGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACGACCACCATCTCTAACCTTACAAAAATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612545 Oligochaeta sp. water mite diet isolate 11471-BHL101516-GBD22707_8517-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGTACCAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATGACACCCTAGTTACTGCACACGCATTCATAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612546 Oligochaeta sp. water mite diet isolate 11473-BHL101516-GBD9222_8923-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGTTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTCCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCACTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612547 Oligochaeta sp. water mite diet isolate 11474-BHL101516-GBD13968_2187-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTCGGAGGATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCAAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTACTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGATCAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612548 Oligochaeta sp. water mite diet isolate 11477-BHL101516-GBD18511_6778-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGATCAGGAATAATTGGAACATCGCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACGCTAGTTACTGCACATGCACTCTTAATAATTTTCTTTCTTGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAAGTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612549 Oligochaeta sp. water mite diet isolate 11479-BHL101516-GBD2809_14032-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGACTAGTACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGGTTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612550 Oligochaeta sp. water mite diet isolate 11480-BHL101516-GBD13274_8111-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAACAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGACGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTGCCCACGACGAAATAATATAAGATTCTGACTACGACCACCATCTCTAAACTTACAAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612551 Oligochaeta sp. water mite diet isolate 11481-BHL101516-GBD5272_8065-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGCATGAGCAGGAATAATTGGAACAGCGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCATTATAATTTTCTTTCTTGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGACATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612552 Oligochaeta sp. water mite diet isolate 11482-BHL101516-GBD6109_20476-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTAATTTTAGGAGTTTGAGCAGGAATAATTGGTACAGGTACTAGAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGTTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.3% identical to accession ID KY633409, identified in GenBank as Stylaria lacustris. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612553 Oligochaeta sp. water mite diet isolate 11484-BHL101516-GBD16500_28414-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTAGCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCCTTGTTACTGCACATGCATTTGTAATAATTTTCTTTCTTGTAATACCAGTTTTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCCCCATCTCTAATCTTACTAATTCCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612554 Oligochaeta sp. water mite diet isolate 11485-BHL101516-GBD28080_13269-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCCCTAATACTTGGAGCCCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTATTACCCCCATCTCTAACCTTACTAATTTCTACTGCATCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612555 Oligochaeta sp. water mite diet isolate 11486-BHL101516-GBD28883_19589-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGACTAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTGAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGAGTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCTGCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612556 Oligochaeta sp. water mite diet isolate 11487-BHL101516-GBD4339_23443-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAAACAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAAGATTTGGAAACTTAATAGTACCACTAATACTTGGAGGTCCAGATAAGGCCTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612557 Oligochaeta sp. water mite diet isolate 11490-BHL101516-GBD27811_13454-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACTCTAGTTACTGCACATGCATTCCTAATAATTTTCTTTATAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTTCTACCACCATCTCTAATCCTACTAGTTTCTTCTGCAGCATTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.1% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612558 Oligochaeta sp. water mite diet isolate 11491-BHL101516-GBD13819_14096-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCATTCTT-GTAATAACAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGATTTCCCACGACTAAACAATATAAGAGTCTGACTACTACCACCATCTCCAATCTTGCCAATTTCGTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612559 Oligochaeta sp. water mite diet isolate 11494-BHL101516-GBD5809_8582-Lq80 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612560 Oligochaeta sp. water mite diet isolate 11509-BHL101516-GBD20346_25179-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCACCACCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612561 Oligochaeta sp. water mite diet isolate 11514-BHL101516-GBD11364_5879-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTCGGAGTATGAGCAGGAACAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCGTAATAATTTTCTTTATTGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612562 Oligochaeta sp. water mite diet isolate 11515-BHL101516-GBD21848_16598-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCCGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATCATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCATAATAATTTTCTTTATTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.4% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612563 Oligochaeta sp. water mite diet isolate 11516-BHL101516-GBD19510_9161-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGGTTTGGAAACTGACTAGTTCCATTAATACTCGGAGCCCCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612564 Oligochaeta sp. water mite diet isolate 11517-BHL101516-GBD25325_19703-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGTAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGGATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACAACTAAATAAATTAAGAATCTGACTACGACCACCATCTCTAAACTTACTAATTTCTTCTGCATCAGTAGAAAATGAAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612565 Oligochaeta sp. water mite diet isolate 11518-BHL101516-GBD23668_5399-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTCGGAGTATGAGCAGGAATAATTGGAACCGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACGAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACGACTACCACCATCTCTAATCTGACTAATATCTTCTGCGGCAGTAGAAAAGGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612566 Oligochaeta sp. water mite diet isolate 11519-BHL101516-GBD5610_18667-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGAAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACCCCTAAATAATTTAAGATCCTGACTCCTACCACCATCTCGAATCTTACTAAGTTCTTCTGCAGCAGGAGAAAACGGAGCTGCAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612567 Oligochaeta sp. water mite diet isolate 11522-BHL101516-GBD19976_17586-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGTTCTAGAATATTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGTATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.4% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612568 Oligochaeta sp. water mite diet isolate 11528-BHL101516-GBD10338_9818-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTTGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATGGCATTCCCACGAATAAATAACATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612569 Oligochaeta sp. water mite diet isolate 11529-BHL101516-GBD9310_6164-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGTACTAGACTACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCAGGAGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612570 Oligochaeta sp. water mite diet isolate 11531-BHL101516-GBD12258_13652-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTACTTTAGGAGTTTGAACAGGAACAATTGGAACCGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTGCTACCACCATCTCTAACCTTACAAATATCTTCTGCAGCAGTAGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612571 Oligochaeta sp. water mite diet isolate 11532-BHL101516-GBD11296_26502-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCGCATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGCCTAAATAATCTAAGATTCTGACCACTACCCCCCTCGCTAATCTTACTAATATCTTCTGCAGCATTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612572 Oligochaeta sp. water mite diet isolate 11534-BHL101516-GBD19514_7235-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGACTAGAATACTAATTCGAATTGAATTATCACAACCCGGATCATTCTTAGGAAGATATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAAAAATTTAAGATTCTGACTACTACCACCATCGCGAATCTTACTACTTGCTTCTGCAGCAGGAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612573 Oligochaeta sp. water mite diet isolate 11539-BHL101516-GBD18113_11703-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGCACAGCGTCTAGAATACTAATTCGACTTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCACTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612574 Oligochaeta sp. water mite diet isolate 11540-BHL101516-GBD22269_20309-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTGGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGCCTAAAAAAATTAAGATACTGACTACTACCACCATCTCTAAACTTACAAATTGCCTCTGCAGCAGTAGAAAATGGCGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612575 Oligochaeta sp. water mite diet isolate 11541-BHL101516-GBD21017_10932-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCACTAAAATTACTAAGATCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612576 Oligochaeta sp. water mite diet isolate 11545-BHL101516-GBD9113_16818-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTTTTATAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCACCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612577 Oligochaeta sp. water mite diet isolate 11547-BHL101516-GBD9160_3197-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGATCTGGAATAGTTGGAACAAGTCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTTGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAAATGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGTTTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612578 Oligochaeta sp. water mite diet isolate 11548-BHL101516-GBD18819_10721-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTTATTCGAGTTGAATTATCACAACCAGGAACATTCTTAGGTAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTTTTATTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612579 Oligochaeta sp. water mite diet isolate 11549-BHL101516-GBD16320_12784-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGATCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGCTCATTCTTAGGAAAAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTACTGCAGCAGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.9% identical to accession ID KT716826, identified in GenBank as Amynthas morrisi. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612580 Oligochaeta sp. water mite diet isolate 11552-BHL101516-GBD25857_15938-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTACGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACACTAGTTACTGCACATGCATTTTTAATAATTTTCTTTCTTGTAATACCAGTTTTTATTGGAGGATTTGGAAACTGATTAGTTCCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCCTACTAATTTCTTCTGCATCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612581 Oligochaeta sp. water mite diet isolate 11553-BHL101516-GBD5413_16101-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTCTATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAACATAAGATTCTGACTACTACTACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612582 Oligochaeta sp. water mite diet isolate 11557-BHL101516-GBD13624_4664-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATAGGAACAGGGACTAGAATACTAATTCGAATTGAATTAGCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTTTTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTACCGATATGGCTTTCCCGCGACTAAATAATTTAAGATTCTGACTACTACCCCCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGCGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612583 Oligochaeta sp. water mite diet isolate 11558-BHL101516-GBD7801_11434-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGACTTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCAGACTCCTCCCACCATCTATAAACTTACTAATTTCTTCTGCAGCAGTACAAAATGGAGATAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612584 Oligochaeta sp. water mite diet isolate 11561-BHL101516-GBD14925_8705-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGATCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGAACATTCTTAGGAGGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCCCCATCTCTAACCTTACTAATTTCTGCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612585 Oligochaeta sp. water mite diet isolate 11562-BHL101516-GBD17473_7720-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAGGAGATCAACTATATAACACCCTAGTTACTGCTCATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCCTACTAATTTCTAGTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612586 Oligochaeta sp. water mite diet isolate 11563-BHL101516-GBD26639_11277-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTTTATAACACTCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTATAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612587 Oligochaeta sp. water mite diet isolate 11568-BHL101516-GBD2481_12990-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACATGGACTATAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTATTTCTTGTAATACCAGTATTAATTGGCGGGTTTGGAAACTGACTAGTTCCATTAATACTCGGAGACCCAGATATGGCATTCCCACGAATAAATAATATAAAATTCTGACTACTACCACCATCTCTAACCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 84.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612588 Oligochaeta sp. water mite diet isolate 11572-BHL101516-GBD26020_22307-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATACTTAATTTTAGGAGTACAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCTCATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGACTAGTTCCATTAATACTAGGAGCCCCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCCCCATCTCTAATCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612589 Oligochaeta sp. water mite diet isolate 11573-BHL101516-GBD13150_11153-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATGCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTTTTCCTTGTAATACCAGTATTCATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTTCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAAACTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612590 Oligochaeta sp. water mite diet isolate 11575-BHL101516-GBD8939_11588-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTAGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTGACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGAATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACGAAATAAAATAAGATTCTGACTACTACCACCATCTCCAAACTTACAAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612591 Oligochaeta sp. water mite diet isolate 11576-BHL101516-GBD25932_13841-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGACTAGAATACTAATTCGAATTGAATTATCACAACCATGATCATTCTTAGGAAGAGATCAACTATATAACATCCTAGTTACTGCACATGCATTCTTTATAATTTTTTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612592 Oligochaeta sp. water mite diet isolate 11577-BHL101516-GBD22361_13318-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTCATTTTAGGAGTATGAGCAGGAATAATTGGAACTGCGACTAGAATACTAATTCGAATTGAACTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAAACTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612593 Oligochaeta sp. water mite diet isolate 11578-BHL101516-GBD24464_24189-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTCGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAGTTATCACAACCAGGAACATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCATTATTTATTGGGGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612594 Oligochaeta sp. water mite diet isolate 11579-BHL101516-GBD17370_14681-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTATTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATATTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTACTTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612595 Oligochaeta sp. water mite diet isolate 11583-BHL101516-GBD28576_16798-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCTCATGCATTCTTAAAAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGAATTGGAAACGGATTAGTACAACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTGCCACCATCTATAATATTACTAAATTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612596 Oligochaeta sp. water mite diet isolate 11587-BHL101516-GBD26962_15006-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACTATAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCTGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCCCCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.0% identical to accession ID KU728850, identified in GenBank as Enchytraeus albidus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612597 Oligochaeta sp. water mite diet isolate 11588-BHL101516-GBD4356_21697-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTGGGAGTATGATCAGGAATAATTGGAACAGGTACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAAAGATCAACTATATAACACCATAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612598 Oligochaeta sp. water mite diet isolate 11590-BHL101516-GBD28093_15384-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAAATATATAACACAATAGTTACTGCACATGCATTCTTAATAATTTTCTTTATAGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCCCCATCTCTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612599 Oligochaeta sp. water mite diet isolate 11593-BHL101516-GBD8682_9545-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGTATATTAATTCGCATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTGTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCGCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAAGTTCTGCTGCAGCAGTAGAAAAGGGAGCCGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612600 Oligochaeta sp. water mite diet isolate 11594-BHL101516-GBD20293_22708-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAATTTTTATTGGAGGATTTGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATATCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	#N/A
>MW612601 Oligochaeta sp. water mite diet isolate 11596-BHL101516-GBD14335_23815-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGTACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCGTAATAATTTTCTTTCTTGTAATACCAGTACTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCCCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612602 Oligochaeta sp. water mite diet isolate 11598-BHL101516-GBD14483_8014-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTCTGATCAGGAATAATTGGAACTGGGCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGTGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612603 Oligochaeta sp. water mite diet isolate 11599-BHL101516-GBD12799_2285-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATGAGCAGGAATAGTTGGAACATGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTATAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGACATGGCTTTCCCACGAATAAATAATATAAGATTCTGGCTACTACCACCATCTCTAACCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.0% identical to accession ID KY633404, identified in GenBank as Slavina sp. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612604 Oligochaeta sp. water mite diet isolate 11601-BHL101516-GBD20462_4175-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGAAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCTTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTAGTAATACCAGTATTTATTGGGGGATTTGGAAACTGATTAGGACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCATGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCTGACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LN810268, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612605 Oligochaeta sp. water mite diet isolate 11602-BHL101516-GBD25510_12704-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTTATTCGAATTGAATTATCACAACCCGGATCATTCTTAGGAAGAGATCAACTATATAACACTCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTAGTAATACCAATATTAATTGGAGGATTTGGAAACTGACTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCCCCATCTCTAATCTTACTAATTTCTTCTGCATCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612606 Oligochaeta sp. water mite diet isolate 11605-BHL101516-GBD11882_6873-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTTGGAGTATGATCAGGAATAGTTGGAACTTGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCTTTCTTAATAATTTTCTTTATTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612607 Oligochaeta sp. water mite diet isolate 11606-BHL101516-GBD20075_6588-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAACACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCTCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTCTGACTTCTACCACCATCTCTAACCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612608 Oligochaeta sp. water mite diet isolate 11609-BHL101516-GBD6412_16965-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGGGCATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTATTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCCCCATCTCTAACCTTACTAATTTCTTCAGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612609 Oligochaeta sp. water mite diet isolate 11610-BHL101516-GBD6351_9444-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGCATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACTCTAGTTACTGCACATGCTTTCTTAATAATTTTTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612610 Oligochaeta sp. water mite diet isolate 11613-BHL101516-GBD10553_19003-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAATTCTCACAACCAGGATCATTCTTAGGAAGAGATCAATTATATAACACCCTAGTAACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGTTATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.0% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612611 Oligochaeta sp. water mite diet isolate 11614-BHL101516-GBD24072_26032-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGTCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTATAGTAATACCAGTTTTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTACTGCAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612612 Oligochaeta sp. water mite diet isolate 11619-BHL101516-GBD9951_17688-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACTTTGTACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTTATAATTTTTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTACAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.4% identical to accession ID KT429020, identified in GenBank as Amynthas moniliatus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612613 Oligochaeta sp. water mite diet isolate 11620-BHL101516-GBD27312_14270-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTTCCCCCATCATTAACCTTACTAATATCTTCCGCAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612614 Oligochaeta sp. water mite diet isolate 11621-BHL101516-GBD24931_23396-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGTACTAGAATACTAATTCGAATTGAATTCTCACAACCAGGATCATTATTAGGAAGAGATCAACTATATAATACACTAGTTACTGCACATGCTTTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612615 Oligochaeta sp. water mite diet isolate 11622-BHL101516-GBD9794_13511-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATAGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTTGTTACTGCCCATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTCCCACCATCTCTAACCTTACTAATTTCTTCTGCAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612616 Oligochaeta sp. water mite diet isolate 11624-BHL101516-GBD24481_16075-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGATCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTCTGACTACTACCACCCTCTCTAACCTTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612617 Oligochaeta sp. water mite diet isolate 11625-BHL101516-GBD4548_13706-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACACCCAGGATCATTCTTAGGAAGAGATCAACTTTATAACATCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATACCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612618 Oligochaeta sp. water mite diet isolate 11626-BHL101516-GBD21042_9367-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTTCGTCTAGAATACTAGTTCGAATTGAATTATCACAACCAGGATCA-TTCTCAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGAATAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTATGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612619 Oligochaeta sp. water mite diet isolate 11627-BHL101516-GBD13815_25820-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGGACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAAATATGGCTTTCCCACGAATAAATAATATAGGATTCTGACTACTACCACCATCTCTAATCTTACTAACTACTTCTGCAGCAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612620 Oligochaeta sp. water mite diet isolate 11629-BHL101516-GBD7027_16745-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTTGGAGCATGATCAGGAATAATTGGAACATGGT-CTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612621 Oligochaeta sp. water mite diet isolate 11631-BHL101516-GBD26796_8743-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTTATTCGAATTGAATTATCACAACCAGGAACATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTTTTATAATTCTCTTTCTAGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612622 Oligochaeta sp. water mite diet isolate 11632-BHL101516-GBD15876_9046-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGATCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAAACAGGATCATTCTTAGGAAATGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAGTACTTGGAGCACCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCGTACTAATTTCTTGTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612623 Oligochaeta sp. water mite diet isolate 11633-BHL101516-GBD27787_21739-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCCGGATCATTCTTAGGAAGAGATCAAATATATAACACCATAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCATGTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612624 Oligochaeta sp. water mite diet isolate 11634-BHL101516-GBD16763_7919-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTCTGAGCAGGAATAATTGGAACAGGGACTAGAATATTAATTCGAATTGAATTATCACAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACACTAGTTACTGCACATGCATTCATAATAATTTTCTTTCTTGTTATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCCTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.0% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612625 Oligochaeta sp. water mite diet isolate 11635-BHL101516-GBD20901_7749-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGTATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTACAGATATGGCATTCCCACGACTAAAAAAAATAAGATACTGACTACGACCACAATCTCTAAACTTAAAAATGTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612626 Oligochaeta sp. water mite diet isolate 11636-BHL101516-GBD10505_27023-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGTACTAGAATACTAATTCGAATTGAATTATCACACCCAGGATCATTCTTAGGAAGCGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTTTTTCTAGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCATTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612627 Oligochaeta sp. water mite diet isolate 11639-BHL101516-GBD24671_16868-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCTCATGCATTCTTTATAATTTTCTTTCTTGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTGCCTCTAATACTAGGAGCTCCAGATATAGCTTTCCCTCGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612628 Oligochaeta sp. water mite diet isolate 11640-BHL101516-GBD28768_15178-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGAACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAATACTCTAGTTACTGCACATGCATTTATAATAATTTTCTTTCTAGTTATACCAGTTTTAAATGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612629 Oligochaeta sp. water mite diet isolate 11643-BHL101516-GBD3672_15565-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGATCAGGAATAATTGGAACATGTACTAGAATACTAATTCGAATTGAATTATCACAACCAGCATCATTCTTAGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCACTAACCTTACTAATATCTTCTGCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.0% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612630 Oligochaeta sp. water mite diet isolate 11644-BHL101516-GBD23882_5132-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTCTGAGCAGGAATAATTGGAACAGGGCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCATTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTTGTACCACTAATACTAGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612631 Oligochaeta sp. water mite diet isolate 11645-BHL101516-GBD2859_13965-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATCACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGAGTTGCAAACTGATTAGTACCACTAATACTTGGAGATCCAGATATCGCTTTCCCACGACTAAATAATTTAATATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGCAGCAGGAACA	Using NCBI BLASTN in June 2018, this sequence was 85.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612632 Oligochaeta sp. water mite diet isolate 11647-BHL101516-GBD15669_5264-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAACTATCACAACCATGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTATTTCTAGTAATACCAGTATTTATTGGAGAATTAGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGTCTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGCGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612633 Oligochaeta sp. water mite diet isolate 11649-BHL101516-GBD28235_20480-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGAACATTCTTAGGAAGAGATCAACTATATAATACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGACTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCTCGACTAAATAATATAAGATTCAGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTTCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612634 Oligochaeta sp. water mite diet isolate 11651-BHL101516-GBD20287_5776-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGGATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGTTTTCCCCCGCCTAAACAATTTAAGATTCTGTCTACGACCACCATCTCTAAACTTACCAATTTCTTCTGCAGCAGTAGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612635 Oligochaeta sp. water mite diet isolate 11653-BHL101516-GBD18929_6864-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGTTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGCTCACTCTTCGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCAATAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAATCTTACTAATATCATCAGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612636 Oligochaeta sp. water mite diet isolate 11654-BHL101516-GBD5744_16407-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATACTTAATTTTAGGAGTATGAGCAGGAATAGTTGGAACAGCGACTAGAATACTAATTCGAATTGAATTAGCACAACCAGGATCATTCTTAGGAAAAGATCAAATATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTTCCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCCCCATCTCTAACCTTACTAATTTCTTCTGCAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612637 Oligochaeta sp. water mite diet isolate 11655-BHL101516-GBD2697_15309-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTTTTAATAATTTTTTTTCTTGTAATACCAGTATTTATTGGAGGATCTGGAAACTGATTAGTACCACTAGTACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCAGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612638 Oligochaeta sp. water mite diet isolate 11658-BHL101516-GBD18593_22985-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGTACAGGGTTTAGAATTCTTATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTACTGCAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.8% identical to accession ID KT716826, identified in GenBank as Amynthas morrisi. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612639 Oligochaeta sp. water mite diet isolate 11661-BHL101516-GBD26981_16004-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTTGTACCATTAATACTTGGAGCTCCTGATATGGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCCTACTAATTGCTTCGGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612640 Oligochaeta sp. water mite diet isolate 11663-BHL101516-GBD13859_12984-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAGTTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTTATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCCTACTAATCTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612641 Oligochaeta sp. water mite diet isolate 11666-BHL101516-GBD25663_9029-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTGTACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCTTTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTACTTTCTACAGCAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612642 Oligochaeta sp. water mite diet isolate 11669-BHL101516-GBD8335_13796-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTTATACCAGTATTTATTGGAGGATTTGGAAACTGACTACTACCACTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCATCTCTAATCCTACTAATTTCCTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612643 Oligochaeta sp. water mite diet isolate 11670-BHL101516-GBD7266_12996-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATATTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAATACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAATTGATTAGTACCTCTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612644 Oligochaeta sp. water mite diet isolate 11671-BHL101516-GBD19140_24491-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTCTCACAACCAGGATCCTTCTTATGAAAAGATCAACTATATAACACCCTAATTACTGCACATGCATTCTTAACAATTTTCTTTCTTGTAATACCAATATTTATTGGAGGATTTAGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612645 Oligochaeta sp. water mite diet isolate 11672-BHL101516-GBD27090_15043-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACATGGTCTAGAATACTAATTCGAATTGAATTATCACACCCAGGATCATTCATAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATATTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCCGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612646 Oligochaeta sp. water mite diet isolate 11674-BHL101516-GBD25107_16982-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGACTTTCCCACGACTAAATAAAATAAGAAACGGACTACGACCGCCAGCTCTAAACTTACTAATTGCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612647 Oligochaeta sp. water mite diet isolate 11675-BHL101516-GBD21251_26119-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGATCAGGAATAATTGGAACAGGCACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAAAGATCAACTATATAACACACTTGTTACTGCACATGCATTTTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTGCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612648 Oligochaeta sp. water mite diet isolate 11677-BHL101516-GBD21235_10286-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAACTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCGACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAGTACCAGTATTTATTGGAGGATTTGGTAACTGATTAGTACCACTAATACTTGGAGCTCCGGATATGGCTTTCCCACGACAAAATAATATAAGATTCTGACTAATACCACCATCGCTAATCTTACTAATTTCGTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612649 Oligochaeta sp. water mite diet isolate 11678-BHL101516-GBD23978_20868-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTAGCACCATCTCTAATCTTACTAATTTCTCCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.7% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612650 Oligochaeta sp. water mite diet isolate 11679-BHL101516-GBD16205_2831-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTCACTGCACATGCATTCTTAATAATTTTATTTCTTGTAATACCAGTCTTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCCCCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTCGAAACTGGAGCTGG	Using NCBI BLASTN in June 2018, this sequence was 86.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612651 Oligochaeta sp. water mite diet isolate 11682-BHL101516-GBD11826_16001-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGACCTTCCCACGAAGAAAAAAAAAAAGATACTGACTACGACCGCCATCTCTAAACTTACAAATGTCTTCTGCAGCAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612652 Oligochaeta sp. water mite diet isolate 11685-BHL101516-GBD14507_14669-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGACTAATTGGAACAGGGACTAGAATGCTAATTCGAATTGAACTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACAACCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAAGTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATCCTGACTACTACCACCATCTCTAATCTTACGAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612653 Oligochaeta sp. water mite diet isolate 11689-BHL101516-GBD28745_19603-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAAGGGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTGTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACGACCACCATCTCTAATCTGACGAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612654 Oligochaeta sp. water mite diet isolate 11690-BHL101516-GBD24313_17839-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACATGGCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTTTATAACCCTCTAGTTACTGCACATGCATTTTTTATAATTTTCTTTCTTGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612655 Oligochaeta sp. water mite diet isolate 11695-BHL101516-GBD5694_12233-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGCCGTTCCCACGACTAAACAATTTAAGATTCTGACTCCTACCAACATCTCTAAACTGAAGAATTTCTTCGGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612656 Oligochaeta sp. water mite diet isolate 11696-BHL101516-GBD9295_17539-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTCGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTTATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATAGCTTTCCCACGTATAAATAATATAAGATTCTGACTACTACCCCCATCTCTAACCCTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612657 Oligochaeta sp. water mite diet isolate 11697-BHL101516-GBD17005_10032-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCCGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACTCTAGTTACTGCACATGCATTCTTTATAATTTTCTTTCTTGTTATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612658 Oligochaeta sp. water mite diet isolate 11698-BHL101516-GBD10673_26319-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTTTAGAATATTAATTCGAATAGAATTATCACAACCAGGATCATTCTTCGGAAGAGATCAACTATATAACACCCTAGTTACTGCTCATGCATTCTTAATAATTTTTTTTCTAGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612659 Oligochaeta sp. water mite diet isolate 11700-BHL101516-GBD10683_9225-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGCATCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCTTTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACCAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612660 Oligochaeta sp. water mite diet isolate 11703-BHL101516-GBD24370_6954-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATGGAATTATCACAACCAGGCTCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCTTTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGCACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTATTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612661 Oligochaeta sp. water mite diet isolate 11706-BHL101516-GBD12374_15065-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTTGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACATAATAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTAGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612662 Oligochaeta sp. water mite diet isolate 11709-BHL101516-GBD25943_9431-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAATGATCAACTTTATAACACACTTGTTACTGCACATGCATTCATAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTTCCACCATCTCTAATCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612663 Oligochaeta sp. water mite diet isolate 11712-BHL101516-GBD4929_15279-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGACATCCGGAAAAGACCTTCCCACGGCTAAAAAAATTAAGATTCTTACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.1% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612664 Oligochaeta sp. water mite diet isolate 11717-BHL101516-GBD5120_18080-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAATTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTGCCACCATCTCTAACCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612665 Oligochaeta sp. water mite diet isolate 11718-BHL101516-GBD11761_4507-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGGATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAACTATCACAACCAGGATCATTCATAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTTTTAATAATTTTCTTTATTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCATTCCCACGAATAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612666 Oligochaeta sp. water mite diet isolate 11720-BHL101516-GBD14323_23523-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATAGGAACTGGTACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCATTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAAGATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612667 Oligochaeta sp. water mite diet isolate 11724-BHL101516-GBD24391_7545-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAAATGGCTATTTCCATTAATAATTGGAGCCCCAGATATGGCATTCCCACGACTAAATAATATAAAATTCTGACTACTACCACCATCTCTAACCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612668 Oligochaeta sp. water mite diet isolate 11726-BHL101516-GBD25355_15775-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTACCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGATTACTACCACCATCCCTAACCTTACTAACAACTTCAGCAGCAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612669 Oligochaeta sp. water mite diet isolate 11727-BHL101516-GBD24600_15904-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGACTACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGTATTTTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGAATAGTACCACTAATACTTGGTGCTCCAGATATAGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTGCATCGGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.4% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612670 Oligochaeta sp. water mite diet isolate 11729-BHL101516-GBD18791_22192-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTTGGAGTATGAGCAGGAATAATTGGAACTTGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCTTTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAGCTGATTAGTACCACTAATATTTGGAGCTCCAGATATGGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.8% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612671 Oligochaeta sp. water mite diet isolate 11731-BHL101516-GBD26481_13135-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTCATTTTAGGAGTATGAGCAGGAATAGTTGGAACTGGCCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGAATCTGACTACTACCACCAGCTCTAACCTTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612672 Oligochaeta sp. water mite diet isolate 11732-BHL101516-GBD2653_16716-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGCATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGTGATCAACTTTATAACACGCTAGTTACTGCACATGCATTTTTAATAATTTTCTTTCTAGTTATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTTCTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612673 Oligochaeta sp. water mite diet isolate 11734-BHL101516-GBD22390_20931-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGATTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACATACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAGTCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612674 Oligochaeta sp. water mite diet isolate 11751-BHL101516-GBD21817_4986-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACATGGTCTAGAATACTAATTCGAATTGAATTATCACAAACAGGATCATTCTTAGGAAGAGATCAACTATATAACACCATAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.9% identical to accession ID KT716826, identified in GenBank as Amynthas morrisi. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612675 Oligochaeta sp. water mite diet isolate 11768-BHL101516-GBD24991_21682-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGATTAGAATACTAATTCGAATTGAATTATCACAACCAGGAACATTCATAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTAGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACCTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTTCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612676 Oligochaeta sp. water mite diet isolate 11771-BHL101516-GBD4423_23269-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGCGTTTAGAATACTAATTCGAATTGAATTATCACAACCCGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCGTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612677 Oligochaeta sp. water mite diet isolate 11785-BHL101516-GBD18672_7164-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCACTAACCTTACTAATATCTAGCGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612678 Oligochaeta sp. water mite diet isolate 11793-BHL101516-GBD13422_2948-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGTATCATTCTTAGGAAGATATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTTGAGACTGATTAGTACCACTAATACTTGGAGCTCCCGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTCGAAAATGGCGCTGGCACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612679 Oligochaeta sp. water mite diet isolate 11798-BHL101516-GBD7635_11301-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGACTAGAATATTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTTCTACCACCATCTCTAACCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612680 Oligochaeta sp. water mite diet isolate 11808-BHL101516-GBD28386_20288-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAAGTATCATCACCAGGATCATTCATAGGAAGAGATCAACTATTTAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGTATTTGGAACCTGATTAGTACCACTAATACTTAGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAATATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAAGGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 85.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612681 Oligochaeta sp. water mite diet isolate 11810-BHL101516-GBD7369_14023-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGCATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACACCCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTTTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTGATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612682 Oligochaeta sp. water mite diet isolate 11813-BHL101516-GBD16288_3398-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGTATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCGTTCTTAATAATTTTCTTTCTTGTCATACCAGTATTTATAGGAGGATTTGGAAACTGATTAGTAACACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACTATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGCGCTGGACCA	Using NCBI BLASTN in June 2018, this sequence was 85.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612683 Oligochaeta sp. water mite diet isolate 11826-BHL101516-GBD24773_12516-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGACTACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTTATAATTTTCTTTCCTGTAATAACAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCCTTCCCACGACTAAATAAATTAAGATTCTGACTACCACCACCATCTCTAAACTTACTAAATTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612684 Oligochaeta sp. water mite diet isolate 11829-BHL101516-GBD9358_13069-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGTTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTTTTTATTGTAATACTAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.0% identical to accession ID KT429020, identified in GenBank as Amynthas moniliatus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612685 Oligochaeta sp. water mite diet isolate 11836-BHL101516-GBD21250_18902-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTATTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCCCCATCACTAACCTTACTAATATCTTCTGCAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612686 Oligochaeta sp. water mite diet isolate 11840-BHL101516-GBD15853_21673-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACTTGCATTTCTGATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612687 Oligochaeta sp. water mite diet isolate 11842-BHL101516-GBD28858_17340-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGACTTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACACTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGACTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGGTATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCAGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612688 Oligochaeta sp. water mite diet isolate 11845-BHL101516-GBD18801_10913-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGCGTCTAGAATACTAATTCGAATTGAATTATCACACCCAGGATCCTTCTTAGGAAAAGATCAACTATATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTGGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCCGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612689 Oligochaeta sp. water mite diet isolate 11851-BHL101516-GBD7179_21516-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGACTAGAATACTAATTCGAACTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCTCGACTAAATAACATAAGATTCTGACTACTACCCCCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612690 Oligochaeta sp. water mite diet isolate 11852-BHL101516-GBD20887_25362-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTATATAACAACAC-AGTTACTGCACATGCATTTTTAATAATTTTCTTTATAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612691 Oligochaeta sp. water mite diet isolate 11853-BHL101516-GBD17307_18791-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATACAACACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGATTACTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGGCTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTGGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612692 Oligochaeta sp. water mite diet isolate 11859-BHL101516-GBD9842_9131-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCCGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAGTTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCACCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612693 Oligochaeta sp. water mite diet isolate 11869-BHL101516-GBD11746_23253-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGAAAAGGCTTTCCCACCACCAAAAAAATTAAGAATCTGGCCACCACCACCATCTCTAATCTTACTAGTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.8% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612694 Oligochaeta sp. water mite diet isolate 11872-BHL101516-GBD10787_4709-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATATTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCGTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCGCGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAACCTTACTAATATCTTGTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.4% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612695 Oligochaeta sp. water mite diet isolate 11877-BHL101516-GBD21186_13690-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTTGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTTATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCTTTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAAAACTTGGAGCTCCAGATATGACCTTCCCACGGCTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.4% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612696 Oligochaeta sp. water mite diet isolate 11879-BHL101516-GBD24646_6028-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACATTGACTAGAATACTAATTCGAATTGAATTATCACAACCAGAATCATTCTTAGGAAGATATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTGTCTAGTAATACCAATATTTATTGGAGGATTTGGAAAATGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAAGCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612697 Oligochaeta sp. water mite diet isolate 11881-BHL101516-GBD13959_5372-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAATTGTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTGGTAATACCAGTATTTATTTGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGCCTAAATAATTTAAGATTCTGACTACTTCCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGCGCTGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633404, identified in GenBank as Slavina sp. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612698 Oligochaeta sp. water mite diet isolate 11882-BHL101516-GBD25914_9539-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACATGTACTAGAATACTAATTCGAATTGAATTATCACAAACAGGATCATTCTTAGGAAGAGATCAACTTTATAACACACTTGTTACTGCACATGCTTTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCATTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612699 Oligochaeta sp. water mite diet isolate 11889-BHL101516-GBD24867_13674-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTAAATTATCACAACCAGGGTCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTTTTAATAATTTTTTTTCTTGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTCTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612700 Oligochaeta sp. water mite diet isolate 11897-BHL101516-GBD22123_19498-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGTTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCTTTCTTAGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCCCCAGATATGGCTTTCCCACGAATAAATAATTTAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612701 Oligochaeta sp. water mite diet isolate 11899-BHL101516-GBD10256_16042-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGTATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612702 Oligochaeta sp. water mite diet isolate 11901-BHL101516-GBD8453_15667-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCGTAATAATTTTTTTTATTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612703 Oligochaeta sp. water mite diet isolate 11912-BHL101516-GBD20233_14550-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACATCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATATTTGGAGCTCATGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGGAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612704 Oligochaeta sp. water mite diet isolate 11913-BHL101516-GBD25076_9679-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGACTTCTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTACTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.8% identical to accession ID LN810268, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612705 Oligochaeta sp. water mite diet isolate 11915-BHL101516-GBD16204_7971-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACATGGT-TTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAGGTGATCAACTATATAATACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGACTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAAACTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612706 Oligochaeta sp. water mite diet isolate 11916-BHL101516-GBD13567_24055-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTTGTACCTCTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCTCTAATCCTACTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612707 Oligochaeta sp. water mite diet isolate 11926-BHL101516-GBD10193_25213-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGAATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTTTTCTTGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACATTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612708 Oligochaeta sp. water mite diet isolate 11929-BHL101516-GBD22235_17124-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATATTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAATACCCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTACTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCATCACTAATCTTATTAGTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.5% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612709 Oligochaeta sp. water mite diet isolate 11931-BHL101516-GBD4975_8942-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAATACCCTTGTTACTGCACATGCATTTTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTTCTACCACCATCTCTGACCTTACTAATTTCTTCTGCAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612710 Oligochaeta sp. water mite diet isolate 11933-BHL101516-GBD13958_11820-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGTACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCATA-TAAAACCAGTATTTATTGGAGGATTTGGAAACTGATTCGTACCACTAATACTTGGAGCTCCAGATATAGCTTACCCACGACTAAATAATATAAGATTCTGACTTCTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612711 Oligochaeta sp. water mite diet isolate 11934-BHL101516-GBD4158_18475-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTTGGAAAAGATCAAATATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTGATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCACTAATCTTACTAATATCTTCTGCAGCAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612712 Oligochaeta sp. water mite diet isolate 11936-BHL101516-GBD17026_10063-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTCGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCCTTCCCACGTATAAATAACATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612713 Oligochaeta sp. water mite diet isolate 11944-BHL101516-GBD8295_10510-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTTTGAGCAGGAATAATTGGAACAGGGACTAGAATATTAATTCGGATTGAATTATCACAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCTTCACTAACCTTACTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612714 Oligochaeta sp. water mite diet isolate 11945-BHL101516-GBD23325_12648-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTTTTAATAATTTTTTTTATAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCCCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCCCCATCACTAACCCTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612715 Oligochaeta sp. water mite diet isolate 11947-BHL101516-GBD15190_25539-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTTTGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCTCAACCAGGATCATTCTTAGGAAGAGATCAACTATATAATACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTCGTAATACCAGTATTTATTGGAGGATTTGGAAATTGACTAGTACCTCTAATACTCGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCATCACTAATCCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612716 Oligochaeta sp. water mite diet isolate 11948-BHL101516-GBD22238_19003-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGCGATTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGACCAACTTTATAATACCATAGTTACTGCACATGCATTCTTAATAATTTTTTTCTTGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612717 Oligochaeta sp. water mite diet isolate 11959-BHL101516-GBD19099_25519-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGATCAGGAATAATTGGAACATGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGACTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCCTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTCACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612718 Oligochaeta sp. water mite diet isolate 11962-BHL101516-GBD25895_8128-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGATTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACATCCTAGTTACTGCACATGCATTTTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCACCAGATATAGCTTTCCCTCGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 87.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612719 Oligochaeta sp. water mite diet isolate 11963-BHL101516-GBD28183_15800-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCAGGAATAATTGGAACAGGGACTAGAATATTAATTCGGATTGAATTATCACAACCAGGATCATTCCTAGGAAGAGATCAACTATATAACACTCTAGTTACTGCACATGCATTCCTAATAATTTTCTTTCTTGTTATACCAGTATTTATTGGAGGATTTGGAAACTGACTACTACCTCTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCATCTCTAATCCTACTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612720 Oligochaeta sp. water mite diet isolate 11964-BHL101516-GBD17326_16584-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCGTTCTTAGGAAGAGACCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTCATTGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACCAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612721 Oligochaeta sp. water mite diet isolate 11965-BHL101516-GBD7605_5087-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGCACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGCGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTTTTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAAACTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 87.4% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612722 Oligochaeta sp. water mite diet isolate 11966-BHL101516-GBD20451_7782-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTAAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCCCCATCTCTAATCTTACTAATTTCTATTGCAGCAGTAGAAAATGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612723 Oligochaeta sp. water mite diet isolate 11968-BHL101516-GBD24090_16147-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTACTACCACCATCTTTAACCCTACTAATTTCAAGTGCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612724 Oligochaeta sp. water mite diet isolate 11978-BHL101516-GBD22663_25847-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTTTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTTGTTACTGCTCATGCATTCTTAATAATTTTTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTGGGAGCTCCAGATATGGCATTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAAACTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612725 Oligochaeta sp. water mite diet isolate 11979-BHL101516-GBD12230_21200-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGAACTAGACTACTAATTCGAATTGAATTATCCCAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTCCTTGTAACACCAGTATTTATTGGAGGATTTGGAAACTGAATACTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCCTACTAATTGCTTCGGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612726 Oligochaeta sp. water mite diet isolate 11980-BHL101516-GBD13124_15399-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCCGGATCATTCTTAGGAAGAGATCAACTTTATAACACCCTAGTTACTGCACATGCTTTCTTAATAATTTTCTTTATAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTAATAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612727 Oligochaeta sp. water mite diet isolate 11982-BHL101516-GBD7030_17693-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACATGGT-CTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAATATCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTAATAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612728 Oligochaeta sp. water mite diet isolate 11983-BHL101516-GBD19590_17706-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTCATTTTAGGAGCATGAGCAGGAATAATTGGAACTGGTACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTTTTAGGAAGAGATCAACTATACAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612729 Oligochaeta sp. water mite diet isolate 11984-BHL101516-GBD24859_23705-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTCATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAGACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTTCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTGACTAATTTCTACTACAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612730 Oligochaeta sp. water mite diet isolate 11985-BHL101516-GBD20919_14966-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGACTTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACCTCCTAGTTACTGCACATGCTTTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCCCCATCACTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.0% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612731 Oligochaeta sp. water mite diet isolate 11986-BHL101516-GBD16496_20403-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGCGCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCTTTCATAGGAAAAGATCAACTATATAACACCCTTGTTACTGCTCATGCATTCTTAATAATTTTTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATCCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612732 Oligochaeta sp. water mite diet isolate 11988-BHL101516-GBD3769_15205-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGCATGAGCAGGAATAATTGGAACAGGTTCTAGAATACTAACTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAATTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAAAAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612733 Oligochaeta sp. water mite diet isolate 11990-BHL101516-GBD25932_23138-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAACTGAATTATCACAAACAGGATCATTCTTAGGAAGAGATCAACTATATAATACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTCTAGTAATACCAGTTTTAATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATATCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612734 Oligochaeta sp. water mite diet isolate 11993-BHL101516-GBD8954_23262-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAACTATCACAACCAGGATCATTCTTAGGAAGTGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAAGAATTTTCTTTCTTGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAAACTTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612735 Oligochaeta sp. water mite diet isolate 12000-BHL101516-GBD16986_28349-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGCATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACGCCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAATTTTTATTGGAGGATTTGGAAACTGATTATTACCTCTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612736 Oligochaeta sp. water mite diet isolate 12003-BHL101516-GBD10735_4909-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGATTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACTCTAGTTACTGCACATGCATTATTAATAATTTTCTTTCTTGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAAACTTACTAATTTCTACTGCAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KY633404, identified in GenBank as Slavina sp. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612737 Oligochaeta sp. water mite diet isolate 12005-BHL101516-GBD11098_24198-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCTGGAATAATTGGAACAGGGACTAGAATATTAATTCGAATTAAATTATCACAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTTACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTCGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACGACCACCATCACTAATCCTATTAATTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612738 Oligochaeta sp. water mite diet isolate 12008-BHL101516-GBD24356_18550-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATCGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTCTCTTTCTAGTAATACCAATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTAGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCACTAATCTTACTAATATCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.9% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612739 Oligochaeta sp. water mite diet isolate 12010-BHL101516-GBD28205_9454-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAGTTGCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612740 Oligochaeta sp. water mite diet isolate 12011-BHL101516-GBD12123_5955-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGTTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATCTTCTTTCTAGTTATACCAATATTAACTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTTCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCCTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612741 Oligochaeta sp. water mite diet isolate 12012-BHL101516-GBD26567_7170-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGACTTGAATTATCACAACCAGGCTCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCTGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATATCGACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612742 Oligochaeta sp. water mite diet isolate 12014-BHL101516-GBD23489_5903-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAAATATATAAAACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCCTACTAATATCTTCTGCATCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612743 Oligochaeta sp. water mite diet isolate 12016-BHL101516-GBD10016_6381-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACCTAATTTTAGGAGTATGCGCAGGAATAATTGGAACAGGGACTGGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACGAAATAAAAAAAGATACTGACTACTACCACCATCGCTAAACGGAAAAATGTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612744 Oligochaeta sp. water mite diet isolate 12020-BHL101516-GBD8912_17235-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGCGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAGCTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTAGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612745 Oligochaeta sp. water mite diet isolate 12021-BHL101516-GBD17266_27645-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACAAATCATAAAGATATTGGCACTCTATATTTAATTTTAGGAGCATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTTGTTACTGCACATGCATTTTTAATAATTTTCTTTCTTGTAATACCAATATTAACTGGAGGATTTGGAAATTGATTAGTACCTCTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.2% identical to accession ID KT716826, identified in GenBank as Amynthas morrisi. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612746 Oligochaeta sp. water mite diet isolate 12022-BHL101516-GBD22942_17021-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTTATTTTAGGAGCATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACAATAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTTCTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCCCCAGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612747 Oligochaeta sp. water mite diet isolate 12023-BHL101516-GBD11061_4331-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTCGGAGTATGAGCAGGAATAATTGGAACAGGTATTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACAGCACATGCATTCTTAATAATTTTCTTTATTGTAATACCAGTCTTTATTGGAGGATTTGGAAACTGACTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTGCTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612748 Oligochaeta sp. water mite diet isolate 12024-BHL101516-GBD24251_12337-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACAATAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCCGATATAGCTTTCCCACGACTAAATAACATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCAACAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612749 Oligochaeta sp. water mite diet isolate 12027-BHL101516-GBD13070_8810-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACCGGGTCTAGTATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTCTCCCACGACTAAATAATTTAAGATTCTGACCACGACCACCATCTCTAACCTTACTAAAATCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612750 Oligochaeta sp. water mite diet isolate 12031-BHL101516-GBD24525_25986-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAATACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAACTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTACGGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612751 Oligochaeta sp. water mite diet isolate 12032-BHL101516-GBD8698_21768-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGTTCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCATCACTAAACTTACTAATTTCAAGTGTAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612752 Oligochaeta sp. water mite diet isolate 12035-BHL101516-GBD12178_27552-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCATAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGACATAGCATTCCCTCGAATAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612753 Oligochaeta sp. water mite diet isolate 12045-BHL040517-GBD11952_9993-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTATTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTA--TCT-TTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.2% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612754 Oligochaeta sp. water mite diet isolate 12056-BHL040517-GBD16923_26155-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCCAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATGTGGCCTTCCCACGACTTAACAATTTAAGATTTTGACTTCTACCACCTTCACTAATCCTACTAGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612755 Oligochaeta sp. water mite diet isolate 12060-BHL040517-GBD20540_25164-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTCTACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAAAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTAGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTTCCACCTTCACTAATCCTATTAGTATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612756 Oligochaeta sp. water mite diet isolate 12064-BHL040517-GBD28894_16682-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAACTCATAAAGATATTGGCACTTTATACATTATTTTTGGAGCTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAGTTAACAATGTAAGATTCTGACTACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612757 Oligochaeta sp. water mite diet isolate 12069-BHL040517-GBD12928_2316-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTC-TTTATATTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.2% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612758 Oligochaeta sp. water mite diet isolate 12077-BHL040517-GBD26039_6135-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGATTGAGCTGGAATAATTGGAACAGGAACTAGAATATGAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAAATCAACTATATAATACTCTAGTAACTGCACATACATTCCTAATAATTTTCTTTCTGATTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAACTGGAA	Using NCBI BLASTN in June 2018, this sequence was 85.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612759 Oligochaeta sp. water mite diet isolate 12091-BHL040517-GBD19842_8454-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTCGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTCCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTGCTGTTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612760 Oligochaeta sp. water mite diet isolate 12095-BHL040517-GBD11634_16003-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGCTTGATCTGGAATAATTGGAACAGCATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTTGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATGCTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612761 Oligochaeta sp. water mite diet isolate 12106-BHL040517-GBD23140_8761-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACACTATACTTTATTTTTGGAGCTTGATCGGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.4% identical to accession ID KU728854, identified in GenBank as Mesenchytraeus antaeus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612762 Oligochaeta sp. water mite diet isolate 12108-BHL040517-GBD27103_11181-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGTACACTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTTGGAACAGGATCTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCTTTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612763 Oligochaeta sp. water mite diet isolate 12110-BHL040517-GBD23718_4471-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACCCTATACTTAATTTTAGGAGTTTGAGCCGGAATAATTGGAACCGGAACTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTCCTAGGGAGAGATCAGCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTTTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATGGCCTTCCCACGACTTAACAATTTAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612764 Oligochaeta sp. water mite diet isolate 12113-BHL040517-GBD25676_11088-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTTGGAGTTTGAGCTGGAATAATTGGAACATGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGTGATCAAATATATAATACTCTAGTAACTGCACATGCATTTATAATAATTTTTTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612765 Oligochaeta sp. water mite diet isolate 12118-BHL040517-GBD28441_14433-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAGTTTAAGTTTTTGACTTTTACCCCCTTC-TTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.2% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612766 Oligochaeta sp. water mite diet isolate 12119-BHL040517-GBD16339_14074-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAATTATATAATACTCTAGTAACTGCTCATGCATTCCTAATAATTTTCTTTCTGATGATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATATTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612767 Oligochaeta sp. water mite diet isolate 12123-BHL040517-GBD14447_9157-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCATTCCCACGACTTAACAATATAAGATTCTGACTACTACCACCGTCATTAACCCTATTAGTATCTTCCGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612768 Oligochaeta sp. water mite diet isolate 12125-BHL040517-GBD18596_4335-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATATCATAAAGATATTGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTATCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATCGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTTACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612769 Oligochaeta sp. water mite diet isolate 12126-BHL040517-GBD9924_12161-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTAGCAATGAATTATCTCAATCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGGTTTCCCACGACTTAACAATTTAATATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612770 Oligochaeta sp. water mite diet isolate 12130-BHL040517-GBD6873_17749-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTCATCTTAGGAGCTTGAGCTGGAATAATTGGAACAGGACCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTTTATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTTCAGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATAAACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612771 Oligochaeta sp. water mite diet isolate 12141-BHL040517-GBD28887_18364-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGACCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTCTATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGTTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAAATTAAGATTCTGACTACTACCACCTGCACTAATCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612772 Oligochaeta sp. water mite diet isolate 12142-BHL040517-GBD27134_14970-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGAAACTAGAATATTAATTCGGATTGAATTATCCCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACTAGTATTTATTGGTGGATTTGGAAACTGACTTCTACCTCTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAA	Using NCBI BLASTN in June 2018, this sequence was 86.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612773 Oligochaeta sp. water mite diet isolate 12144-BHL040517-GBD19827_12298-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGATTTAGTATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAAAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTTCTGGTTATACCAGTATTAATTGGAGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCTATTAGTATCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612774 Oligochaeta sp. water mite diet isolate 12146-BHL040517-GBD19741_21199-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTGTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTTCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCATTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTATGACTACGACCACCTTCACTAATCCTATTAGATTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612775 Oligochaeta sp. water mite diet isolate 12151-BHL040517-GBD16038_7532-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACCGGAACTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTCCTAGGGAGAGATCAGCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTATACCTCTAATACTTGGAGCACCAGATATGGCCTTCCCACGACTTAACAATTTAAGATTTTGACTTCTACCACCTTCACTAATCCTACTAGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.9% identical to accession ID KU728856, identified in GenBank as Mesenchytraeus hydrius. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612776 Oligochaeta sp. water mite diet isolate 12153-BHL040517-GBD5367_17994-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAACAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTCCTAATAATTTTCTTACTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.8% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612777 Oligochaeta sp. water mite diet isolate 12155-BHL040517-GBD16151_4126-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCTACTCTATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGGGCACCAGATATAGCTTTCCCATGCCTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612778 Oligochaeta sp. water mite diet isolate 12158-BHL040517-GBD27440_19537-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAACTCATAAAGATATTGGTACACTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAAGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTGATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTGCCCACGACTTAACAAGTTAAGATTCTGACTACTACCACCTTCACTAATCCGATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612779 Oligochaeta sp. water mite diet isolate 12161-BHL040517-GBD12624_11443-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCTGACGTAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTCTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612780 Oligochaeta sp. water mite diet isolate 12166-BHL040517-GBD23837_18309-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGCACTGGATTTAGAATATTAATTCGGCTTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTGGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612781 Oligochaeta sp. water mite diet isolate 12179-BHL040517-GBD17105_27331-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTATAACATCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612782 Oligochaeta sp. water mite diet isolate 12180-BHL040517-GBD25887_24230-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAAATAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATACATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCATCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612783 Oligochaeta sp. water mite diet isolate 12190-BHL040517-GBD23374_24485-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGATTTTGAGCTGGAATAATTGGAACAGGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTTACTGCACATGCATTCCTAATAATTTTTTTCTGGTTGTACCAGTATTTATTGGTGGATTTGGAAATTGACTACTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTATCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612784 Oligochaeta sp. water mite diet isolate 12196-BHL040517-GBD26146_12792-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACTGGATCTACAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCATAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGACCTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612785 Oligochaeta sp. water mite diet isolate 12204-BHL040517-GBD26542_21489-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTCGAATATTCATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCATGACTTAACAATTTAAGTTTCTGACGTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612786 Oligochaeta sp. water mite diet isolate 12208-BHL040517-GBD5495_14441-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAAGTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGCTATACCAGTATTAATTGGTGGATTTGGAAATGGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTATCTTCTGCTGCCGTAGAAAATGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612787 Oligochaeta sp. water mite diet isolate 12215-BHL040517-GBD8092_19951-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACTGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTTCTGGTTATACCAGTATTAATTGGAGGATTTGGAAACTGACTGCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCTCACGACTTAACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612788 Oligochaeta sp. water mite diet isolate 12218-BHL040517-GBD22506_6764-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCTTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATGGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCTTCATTAATCCTATTAGTGTCTGCTGCGGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612789 Oligochaeta sp. water mite diet isolate 12222-BHL040517-GBD11535_11578-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATTAACAATATAAGATTCTGATTCCTACCACCTTCACTAATCCTATTAGTTTCTTCGGCTGCCATAGAAACTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612790 Oligochaeta sp. water mite diet isolate 12225-BHL040517-GBD8200_23852-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTCGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCACAACCAGGATCATTCCTAGGAAGAGATCATCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTAATACCAGTATTTATTGGTGGATTTGGAAACTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCATCTCTAATCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612791 Oligochaeta sp. water mite diet isolate 12227-BHL040517-GBD22811_7892-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATTATAAAGATATTGGCACCCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTGGAATAATAATTCGGGTTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTACTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612792 Oligochaeta sp. water mite diet isolate 12229-BHL040517-GBD13281_20451-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTTTTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCATCAGATATAGCTTTCCCACGAATAAACAATATAAGATTCTGGCTAGTACCCCCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612793 Oligochaeta sp. water mite diet isolate 12231-BHL040517-GBD3766_11413-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAACAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTTCTTGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCATCACTAATCCTATTAGTTTCAACTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612794 Oligochaeta sp. water mite diet isolate 12232-BHL040517-GBD3696_13945-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGACCATTCCTAGTAAGAGATCAACTATATAATACCCTAGTAACTGCACATGCATTCCTAATATTTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCATCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCGTCTGCTGCCGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612795 Oligochaeta sp. water mite diet isolate 12234-BHL040517-GBD19483_17289-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGTATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGATGTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCAAATCAGTTTCTTCTGCGGCCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 86.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612796 Oligochaeta sp. water mite diet isolate 12240-BHL040517-GBD15707_8785-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.2% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612797 Oligochaeta sp. water mite diet isolate 12242-BHL040517-GBD27645_22557-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGTACACTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGGTTGAATTATGTCAACCAGGATCATTTCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTTCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCATCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612798 Oligochaeta sp. water mite diet isolate 12243-BHL040517-GBD15403_27730-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAGCTTTATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTTCTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCCGATATAGCTTTCCCACGGTTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612799 Oligochaeta sp. water mite diet isolate 12244-BHL040517-GBD24581_12357-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTATTTCTGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGC-TTCCCTACGACTTAACAATTGAAGATTCTGACTACTACCACCTACACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612800 Oligochaeta sp. water mite diet isolate 12245-BHL040517-GBD12675_3036-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAGTTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTACACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.5% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612801 Oligochaeta sp. water mite diet isolate 12246-BHL040517-GBD2149_15507-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTGGGAGTTTGAGCTGGAATAATTGGAACAGGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTTTATAATACTCTAGTAACTGCACATGCATTTCTAGTAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCCCCTTCTCTAACCCTATTAGTATCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612802 Oligochaeta sp. water mite diet isolate 12251-BHL040517-GBD15105_5518-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAAAATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612803 Oligochaeta sp. water mite diet isolate 12258-BHL040517-GBD22194_8239-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCTCTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCCCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTTCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGAAATAGCTTTCCCACGACTTAACAAATTAAGATTCTGACTACTACCACCTTCACTAAACCTATTAGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612804 Oligochaeta sp. water mite diet isolate 12262-BHL040517-GBD3586_18078-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTATCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTATCTCTAATACTTGGAGCACTAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACCACTACCACCTTCACCAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612805 Oligochaeta sp. water mite diet isolate 12265-BHL040517-GBD21609_22043-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGTACACTATACTTAATCTTAGGAGTTTGAGCCGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGACTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATTCTGACTACTATCACCTTCACTAATCCTATTAGTTTCTTCCGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612806 Oligochaeta sp. water mite diet isolate 12280-BHL040517-GBD18283_22705-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAGTCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAATTAGCATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTTGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCCACCTCTAATAGTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612807 Oligochaeta sp. water mite diet isolate 12282-BHL040517-GBD6168_14494-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGATCTGGAATAATTGGAACTGGCACTAGAATATTAATTCGGATTGAATTATCTCAACCTGGATCATTCCTAGGAAGTGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGAGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATATAAGATTCGGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612808 Oligochaeta sp. water mite diet isolate 12285-BHL040517-GBD15772_27980-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATCAAGATATTAGCACTCTATACTTAATCTTAGGAGATGGAGCTGGAATACTTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGTTCATTCCTAGGAAAAGATCAACTATATAGTACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACCTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATGAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612809 Oligochaeta sp. water mite diet isolate 12290-BHL040517-GBD10170_27433-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGGGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTTATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTTCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGACATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCATCACTAATCCTACTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.9% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612810 Oligochaeta sp. water mite diet isolate 12304-BHL040517-GBD28046_13410-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTGTACTTAATCTTAGGAGGTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATACAGCTTTCCCACGCCTTAACAATATAAGATTCTGACTACTCCCACCTTCACTAATCCAATCAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612811 Oligochaeta sp. water mite diet isolate 12316-BHL040517-GBD21323_8848-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGTACACTATACTTTATTTTTGGAGCTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTAAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAGCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACCTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTCCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612812 Oligochaeta sp. water mite diet isolate 12318-BHL040517-GBD23173_26869-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGTAACTAGAATATTAATTCGTATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAGTACTCTAGTTACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTTTTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATAATTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612813 Oligochaeta sp. water mite diet isolate 12332-BHL040517-GBD22236_23776-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGTATATTAATTCGGATTGAATTATCTCAACTAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTCCCCACGACATAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCAATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612814 Oligochaeta sp. water mite diet isolate 12337-BHL040517-GBD5728_10113-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCAACCAGGATCATTCCTAGGGAGAGAACAGCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTATAGTTATACTAGTATTTATTGGTGGATTTGGAAATTGACTTCTGCCTCTAATACTTGGAGCACCAGATATGGCCTTCCCATGACTTAACAATTTAAGATTTTGACTTCTACCCCCTTCACTAATCCTACTAGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.6% identical to accession ID KU728856, identified in GenBank as Mesenchytraeus hydrius. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612815 Oligochaeta sp. water mite diet isolate 12338-BHL040517-GBD26159_24107-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACATGTACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTTACTGCACATGCATTCCTAATAATTTTCTTTCTGGTGATACCAATATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCATTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTATCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612816 Oligochaeta sp. water mite diet isolate 12339-BHL040517-GBD27830_15967-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGATTTATCTCAACCAGGATCATTCATAGGAAGAGATCAACTTTATAATACTCTAGTAACTGCACATGCATTTCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCCCGACTTAACAATATAAGATTCTGACTACTACCACCTTCTCTAATCATATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612817 Oligochaeta sp. water mite diet isolate 12341-BHL040517-GBD25973_6406-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGCTTGATCTGGAATAATTGGAACATGAACTAGTATATTTATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAAATATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCGATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612818 Oligochaeta sp. water mite diet isolate 12348-BHL040517-GBD12707_14360-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGAAACAGGGACTAGAATATTAATTAGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATCGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAACATAAGATTCTGACTACTACCACCTTCTCTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612819 Oligochaeta sp. water mite diet isolate 12349-BHL040517-GBD15539_3197-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGAAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGGAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTCCCCCCTTCACTAATCCTATTATTTTCTTCAGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612820 Oligochaeta sp. water mite diet isolate 12360-BHL040517-GBD7167_19746-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATATTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAGCCAGGATCATTCCTAGGAAGGGATCAACTATATAATACTCCAGTAACTGCACATGCATTCCTATTAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTATCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612821 Oligochaeta sp. water mite diet isolate 12361-BHL040517-GBD19223_16682-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTCATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCCGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGTAAATTGACTTCTAACTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATTAACAATATAAGATTCTGACTACTACCACCTTCATTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612822 Oligochaeta sp. water mite diet isolate 12363-BHL040517-GBD21551_25282-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGTACACTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAATCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCATAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACTTCTACTACTAGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612823 Oligochaeta sp. water mite diet isolate 12367-BHL040517-GBD16288_16098-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTTTGAGCTGGAATAATTGGAACGGGGACTAGAATATTAATTCGGATTGAATTATCACAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTAATACCAGTATTTATTGGAGGATTTGGTAATTGACTACTACCTCTAATACTTGGAGTACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612824 Oligochaeta sp. water mite diet isolate 12372-BHL040517-GBD22728_18542-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTTGGTGTTTGATCTGGAATAATTGGAACTGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTTCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612825 Oligochaeta sp. water mite diet isolate 12375-BHL040517-GBD29404_17743-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAACCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTCCCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCATCACTAAGCCGAGGAGGGGCGGCGGCGGCCGGAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612826 Oligochaeta sp. water mite diet isolate 12380-BHL040517-GBD21015_20409-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGAATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGAATTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCATGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCGATTAGTATCTTCTGCTGCCGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612827 Oligochaeta sp. water mite diet isolate 12383-BHL040517-GBD4142_9881-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGTACACTATACTTTATTTTTGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAGTTCGGATTGAATTATATCAACCAGGATCATTCCTAGGAAGTGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATTCTGACTACTACCACCGTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612828 Oligochaeta sp. water mite diet isolate 12393-BHL040517-GBD13591_17105-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGCTTGAGCTGGCATAATTGGAACAGGATTTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACCGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGATCTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612829 Oligochaeta sp. water mite diet isolate 12396-BHL040517-GBD24813_11865-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTATAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACCCTAGTAACTGCACATACATTCCTAATAATTTTCTTTCTGATTATACCAGTATTTATTGGTGGATTTGGAAAATGACTTCTACCTCTAATACTTGGAGTACCAGATATAGCTTTCCCATGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612830 Oligochaeta sp. water mite diet isolate 12403-BHL040517-GBD21507_13108-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGTATATTGATTCGGATTGAATTATATCAACCAGGAGCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTTGTGGATGTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAAACCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612831 Oligochaeta sp. water mite diet isolate 12404-BHL040517-GBD26355_17759-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAAAGATCAACTATATAATACTATAGTAACTGCACATGCATTCCTTATAATTTTCTTTCTCGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTGTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612832 Oligochaeta sp. water mite diet isolate 12424-BHL040517-GBD5443_8657-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCTTTCCTAATAATTTTTTTCTAGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCTCTAACCCTATTAGTTCCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612833 Oligochaeta sp. water mite diet isolate 12425-BHL040517-GBD22095_23532-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTTTGAGCAGGAATAATTGGAACAGGAACTAGAATATTAATTCGAATTGAATTATCTCAACCAGGATCATTCATAGGAAGAGATCAACTATATAATACTCTAGTTACTGCACATGCATTCCTAATAATTTTCTTTCTGGTAATACCAGTATTTATTGGAGGATTTGGAAATTGACTTCTACCACTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATAAACAATTTAAGATTCTGACTACTACCACCATCACTAATCCTATTAGTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.6% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612834 Oligochaeta sp. water mite diet isolate 12429-BHL040517-GBD15616_8461-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATACTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGAGGATTTGGAAACTGACTAGTACCTCTAATACTTGGAACTCCAGATATGGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAGTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612835 Oligochaeta sp. water mite diet isolate 12441-BHL040517-GBD3657_20837-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGATATCAACTTTATAATACTCTTGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACGAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTATCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612836 Oligochaeta sp. water mite diet isolate 12445-BHL040517-GBD27830_21839-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACACTATACTCTATTTTTGGAGCTTGTTCAGGAATACTAGGAACTTCTTTAAGTATATTAATTCGGATTAAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAGTACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.6% identical to accession ID KU728854, identified in GenBank as Mesenchytraeus antaeus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612837 Oligochaeta sp. water mite diet isolate 12452-BHL040517-GBD12786_10543-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCAATCTATACTTAATCTTAGGAGTTTGATCTGTAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAATGATCAACTATATAATACTTTAGTTACTGCACATGCATTCCTAATAATTTCCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACTAGATATAGCTTTTCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612838 Oligochaeta sp. water mite diet isolate 12455-BHL040517-GBD7510_13066-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGGGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCACCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.1% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612839 Oligochaeta sp. water mite diet isolate 12456-BHL040517-GBD7593_14146-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAGCAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATATCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACGACCCCCTTCACTAACCCTACTAGTATCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612840 Oligochaeta sp. water mite diet isolate 12458-BHL040517-GBD15833_26258-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATCTTCGGAGCTTGAGCTGGAATAATTGGAACAGGCACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTACTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATAAACAACATAAGATTCTGACTACTACCACCATCACTAACCCTATTAGTATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612841 Oligochaeta sp. water mite diet isolate 12459-BHL040517-GBD22773_5766-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACATGAACTAGAATATTTATTCGGAATGAATTATCTCAACCAGGATCATTCCTAGGAAAAGATCAACTTTATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGTATCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612842 Oligochaeta sp. water mite diet isolate 12468-BHL040517-GBD2985_14626-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTTTATACTTTATCTTTGGAGTTTGAGCTGGAATAATTGGAACTGGATCTAGAATATTAATTCGGATTAAATTATCTCAATCAGGATCATTCCTAGGAAGAGATCAACTTTATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612843 Oligochaeta sp. water mite diet isolate 12544-BHL040517-GBD24821_7815-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTTTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGATGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612844 Oligochaeta sp. water mite diet isolate 12924-BHL040517-GBD17640_28773-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTAGGTTTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAACTGACTAGTTCTTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTA-TTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.1% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612845 Oligochaeta sp. water mite diet isolate 12931-BHL040517-GBD13823_5848-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATGCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LN810268, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612846 Oligochaeta sp. water mite diet isolate 13007-BHL040517-GBD5531_10094-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGAACACTTTAT--TTTATTTTCGGAGCTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTCATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612847 Oligochaeta sp. water mite diet isolate 13053-BHL040517-GBD26085_9340-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCAGATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACGTCTACCTCTAACACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGTCGTAGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612848 Oligochaeta sp. water mite diet isolate 13054-BHL040517-GBD4702_10627-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATATTTATCTTTGGAGCTTGAGCTGGAATAATTGGAACAGGATTTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCGACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTATCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612849 Oligochaeta sp. water mite diet isolate 13086-BHL040517-GBD10082_2632-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGCTTGAGCTGGAATAATTGGAACTGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCACCTATATAATCCTCTAGTTACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGAGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612850 Oligochaeta sp. water mite diet isolate 13098-BHL040517-GBD21497_16399-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACTGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTCATGGTTATACCAGTTTTAATTGGTGGATTTGGAAACTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCTCTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612851 Oligochaeta sp. water mite diet isolate 13113-BHL040517-GBD20928_16917-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGATCTGGAATAATTGGAACTGGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGTGATCAACTTTATAATACTCTAGTAACTGCCCATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATAAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612852 Oligochaeta sp. water mite diet isolate 13143-BHL040517-GBD19913_6250-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTCATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGCTCTAGAATATTAATTCGGCTTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGAGGATTTGGAAATTGACTTCTCCCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612853 Oligochaeta sp. water mite diet isolate 13152-BHL040517-GBD25911_21745-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTTGGAGTTTGAGCTGGAATAATTGGAACAGCATCTAGTATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTTCTAATAATTTTTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCATTCCCACGACTTAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612854 Oligochaeta sp. water mite diet isolate 13154-BHL040517-GBD26938_14534-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGCTTGAATTAGCTCAACCAGGATCATTCATAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTATGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCCCCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612855 Oligochaeta sp. water mite diet isolate 14597-BHL040517-GBD18504_28450-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTAATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTATTACCACCATCACTAATCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.9% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>MW612856 Oligochaeta sp. water mite diet isolate 14902-BHL040517-GBD20425_14723-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGTACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTACTAGGAAGAGATCAACTATATAACACTCTAGTAACTGCACATGCATTTCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTATCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW612857 Ophyra sp. water mite diet isolate 15062-BHL040517-GBD3739_17623-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTACTTCCTCCTTCACTTACACTATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID JX861461, identified in GenBank as Ophyra nigra. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612858 Orthocladiinae sp. water mite diet isolate 1162-BHL110116-GBD22962_9345-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTGTCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612859 Orthocladiinae sp. water mite diet isolate 4104-BHL032417-GBD14786_4222-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGATCAAATTTATAAGGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTACTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612860 Orthocladiinae sp. water mite diet isolate 4144-BHL032417-GBD21338_5944-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGCACTTCTTTAAGAATTCTAATTCGAGTAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCATTTAATATTAGGAGCACCTGATATAGCTTTCCCACGAATAAATAATATAAGATTTTGATTATTGCCCCCATCATTAACCTTATTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612861 Orthocladiinae sp. water mite diet isolate 4187-BHL032417-GBD14294_19658-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAGTGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612862 Orthocladiinae sp. water mite diet isolate 4231-BHL032417-GBD17523_27414-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTGGGACATGCTGGATCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTCTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612863 Orthocladiinae sp. water mite diet isolate 4263-BHL032417-GBD9235_4679-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTCGGGGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCAGGCACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATATTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612864 Orthocladiinae sp. water mite diet isolate 4282-BHL032417-GBD21396_3966-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGTACTTCTTTAAGTATTCTAATTCGAGCAGAATTAGGACATCCAGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGACTGTTGCCACCATCATTAACTTTACTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612865 Orthocladiinae sp. water mite diet isolate 4290-BHL032417-GBD20227_2216-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGTCATGCTGGCTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCACCTGATATAGCATTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCGTCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW612866 Orthocladiinae sp. water mite diet isolate 4296-BHL032417-GBD27182_15315-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCCTTAAGAATTTTAATTCGAGCTGAATTAGGACATGCAGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGACTGTTGCCCCCATCATTAACTTTATTATTATCAAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612867 Orthocladiinae sp. water mite diet isolate 4311-BHL032417-GBD18966_26985-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATGCTGGCTCGTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612868 Orthocladiinae sp. water mite diet isolate 4326-BHL032417-GBD16794_6979-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCAGGTTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCAGATATGGCATTCCCACGAATAAATAATATAAGATTTTGATTATTGCCCCCATCATTAACATTATTATTATCAAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612869 Orthocladiinae sp. water mite diet isolate 4332-BHL032417-GBD10261_22730-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCTTTGAGAATCCTAATTCGAGCAGAATTAGGACATGCCGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTATTGCCCCCATCATTAACCTTATTATTATCAAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612870 Orthocladiinae sp. water mite diet isolate 4353-BHL032417-GBD26238_9871-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATATTAATTCGAGCAGAATTAGGACATGCAGGCTCATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCACCAGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612871 Orthocladiinae sp. water mite diet isolate 4391-BHL032417-GBD16990_26243-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACATGCTGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGACCGTTGCCCCCCTCATTAACTTTATTACTATCAAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612872 Orthocladiinae sp. water mite diet isolate 4423-BHL032417-GBD9835_16098-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATATTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCCCCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGCTGCCCCCATCATTAACTTTATTACTATCTAGAACAATAGTGGAAAATGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612873 Orthocladiinae sp. water mite diet isolate 4435-BHL032417-GBD22172_19780-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGTCACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCCTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTTTTACTATCGAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID KR750073, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612874 Orthocladiinae sp. water mite diet isolate 4441-BHL032417-GBD16859_26048-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTGTTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCTGGCACATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATAATATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612875 Orthocladiinae sp. water mite diet isolate 4454-BHL032417-GBD26979_9357-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCTTGATCAGGGATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAAAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTATTGCCCCCGTCATTAACTTTATTATTATCTAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW612876 Orthocladiinae sp. water mite diet isolate 4459-BHL032417-GBD27874_11438-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATACAGGTTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTATTGACTGTTGCCCCCATCATTAACTTTATTATTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612877 Orthocladiinae sp. water mite diet isolate 4472-BHL032417-GBD8195_5508-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATCTTAATTGGAGGATTTGGAAACTGACTATTTCCTTTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTGCCCCCATCATTAACTTTATTATTATCTAAATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612878 Orthocladiinae sp. water mite diet isolate 4478-BHL032417-GBD10920_11718-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGGATTAGGACATGCAGGCTCATTAATAGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGGTTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612879 Orthocladiinae sp. water mite diet isolate 4487-BHL032417-GBD26941_23268-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATTAGGACATGCAGACTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATAATAGGAGCTCCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTACTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612880 Orthocladiinae sp. water mite diet isolate 4491-BHL032417-GBD6368_8270-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGTAGGATTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCACACGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACCTTATTATTATCTAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612881 Orthocladiinae sp. water mite diet isolate 5170-BHL032417-GBD17543_22590-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATTAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCATTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR513498, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612882 Orthocladiinae sp. water mite diet isolate 5256-BHL032417-GBD24147_20380-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTGCTGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTAGGAAACTGATTAGTTCCTTTAATATTAGAAGCATCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612883 Orthocladiinae sp. water mite diet isolate 5378-BHL032417-GBD7651_25353-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTATTTCCCCCCTCTTTAACTCTTCTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID KR725429, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612884 Orthocladiinae sp. water mite diet isolate 5488-BHL032417-GBD17634_8486-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGGGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCAGGCTCTTTAATTGGAGAAGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCATCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612885 Orthocladiinae sp. water mite diet isolate 5531-BHL032417-GBD24126_10902-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTTTTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGACACGCTGGGTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW612886 Orthocladiinae sp. water mite diet isolate 5614-BHL032417-GBD23004_24120-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTCTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCCTTAATATTAGGAGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCTTTAACTCTTCTTTTATCAAGCTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR729683, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612887 Orthocladiinae sp. water mite diet isolate 5619-BHL032417-GBD14882_21105-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGGGCCTGATCTGGGATAGTTGGAACTTCTTTAAGAATTCTTATTCGTGCAGAATTAGGACATGCTGGTTCCTTAATTGGAGACGACCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGACTAGTTCCCTTAATATTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR693741, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612888 Orthocladiinae sp. water mite diet isolate 5620-BHL032417-GBD4563_12971-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGATCAAATCTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGACTAGTTCCCTTAATATTAGGAGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCTTTAACTCTTCTTTTATCAAGCTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR694831, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612889 Orthocladiinae sp. water mite diet isolate 5649-BHL032417-GBD23315_4329-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGGGCCTGATCTGGGATAGTTGGAACTTCTTTAAGAATTCTTATTCGTGCAGAATTAGGACATGCTGGTTCCTTAATTGGAGACGACCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGACTAGTTCCCTTAATATTAGGAGCACCAGATATGGCCTTCCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTCTAACTCTACTATTATCAAGCGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR693741, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612890 Orthocladiinae sp. water mite diet isolate 5659-BHL032417-GBD25673_6414-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGGGCCTGATCTGGGATAGTTGGAACTTCTTTAAGAATTCTTATTCGAGCAGAATTAGGACATACTGGTTCCTTAATTGGAGACGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGACTAGTTCCCTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCCTCTTTAACTCTTCTATTATCAAGCACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR681805, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612891 Orthocladiinae sp. water mite diet isolate 5667-BHL032417-GBD8490_23017-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGGGCCTGATCTGGGATAGTGGGAACTTCTTTAAGAATTCTTATTCGTGCAGAATTAGGACATGCTGGGTCCTTAATTGGAGACGACCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAACTGACTAGTTCCCTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTCTGATTACTTCCCCCCTCTTTAACTCTTCTTCTTTCTTGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR681805, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612892 Orthocladiinae sp. water mite diet isolate 5679-BHL032417-GBD14035_23064-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGAATTCTTATTCGTGCAGAATTAGGACATGCTGGTTCCTTAATTGGAGACGACCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGACTAGTTCCCTTAATATTAGGGGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATCACTTCCCCCCTCTTTAACTCTTCTTTTATCAAGCTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR694831, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612893 Orthocladiinae sp. water mite diet isolate 5724-BHL032417-GBD28946_17844-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGGGCATGATCTGGGATTGTTGGAACTTCTTTAAGAATTCTTATTCGTGTAGCATTAGGACATGCTGGTTCCTTAATTGGAGACGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGACTAGTTCCCTTAATATTAGGGGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCTTTAACTCATCTTTTATCAAGCACAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR693741, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612894 Orthocladiinae sp. water mite diet isolate 5960-BHL032417-GBD24666_6369-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AATCATAAAGATATTGGAACTTTATATTTATTTCTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATGTTTATTCGAGCAGAATTAGGACAAGCTGGTTCTTTCATCGGAGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTTGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.1% identical to accession ID KP697617, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612895 Orthocladiinae sp. water mite diet isolate 9661-BHL032417-GBD22175_23139-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCTGGGATAGTTGGAACTTCTTTAAGAATTCTTATTCGTGCAGAATTAGGACATGCTGGTTCCTTAATTGGAGACTACCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCCCCTGATATAGCCTTCCCTCGTCTAAATAATATAAGATTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KR678405, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW612896 Orthocladiinae sp. water mite diet isolate 10310-BHL040517-GBD25970_13470-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612897 Orthocladiinae sp. water mite diet isolate 11151-BHL110116-GBD8134_5086-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCATTAATATTAGGAGCTCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCATTAACCTTACTTCTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612898 Orthocladiinae sp. water mite diet isolate 11231-BHL110116-GBD19624_27838-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGTTCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAACACCTGATATAGCTTTCCCGCGAATAAATAATATAAGATTTTGATTATTGCCCCCATCATTAACTTTATTGTTATCAAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612899 Orthocladiinae sp. water mite diet isolate 12956-BHL040517-GBD18772_20590-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCCGGAACATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGCTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612900 Orthocladiinae sp. water mite diet isolate 12996-BHL040517-GBD18724_17594-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGATTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTCATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTATTGCCACCATCATTAACCTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612901 Orthocladiinae sp. water mite diet isolate 12997-BHL040517-GBD24112_20674-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCTGGCACATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCACCATCACTAACTTTATTATTATCTAGAACAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612902 Orthocladiinae sp. water mite diet isolate 13006-BHL040517-GBD8901_11323-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGGCTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612903 Orthocladiinae sp. water mite diet isolate 13010-BHL040517-GBD27452_21760-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCCTTAAGAATACTAATTCGAGCAGAATTAGGACATCCAGGATCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATATTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACCTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612904 Orthocladiinae sp. water mite diet isolate 13017-BHL040517-GBD27181_23024-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATTCTAATTCGAGCTGAATTAGGACATGCAGGCTCATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGAACAGTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612905 Orthocladiinae sp. water mite diet isolate 13018-BHL040517-GBD9599_6948-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATTCTAATTCGAGCAGAATTAGGACATCCTGGCTCATTTATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAACATAAGTTTTTGATTGTTGCCCCCATCATTAACCCTATTATTATCTAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR513498, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW612906 Orthocladiinae sp. water mite diet isolate 13022-BHL040517-GBD14829_8613-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATTTTTTTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGACATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612907 Orthocladiinae sp. water mite diet isolate 13025-BHL040517-GBD25352_18711-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCTTGCTCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTAGAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612908 Orthocladiinae sp. water mite diet isolate 13043-BHL040517-GBD18272_27116-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCGGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGTAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAGATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGCTTTGGAAACTGACTAGTACCTTTAATATTAGGAGCACCTGATATAGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACCTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612909 Orthocladiinae sp. water mite diet isolate 13048-BHL040517-GBD19309_17139-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTTATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGGCTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGAATGTTACCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612910 Orthocladiinae sp. water mite diet isolate 13050-BHL040517-GBD20640_14391-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATAAGGCTTTCCCACGAATAAAAAAAAAAAGTTTTTGATTGTTGCCCCCATCATTAACCTTATTAATATCTAGAACAATTGGGGAAAATGGAGGCGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612911 Orthocladiinae sp. water mite diet isolate 13057-BHL040517-GBD28361_13564-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATCCAGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTATTTCCCCCATCATTAACCTTATTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612912 Orthocladiinae sp. water mite diet isolate 13080-BHL040517-GBD24972_12912-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCTGGAATAGTTGGAACTTCTTTTAGTATTCTAATTCGAGCAGAATTTGGACATGCAGGCACATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTATGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612913 Orthocladiinae sp. water mite diet isolate 13092-BHL040517-GBD21685_24805-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATGCTGGATCATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612914 Orthocladiinae sp. water mite diet isolate 13102-BHL040517-GBD20121_20786-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGCACTTCTTTAAGAATTCTAATTCGACCAGAATTAGGACACCCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCAATTTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTATTGCCCCCATCATTAACCTTATTATTATCTAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612915 Orthocladiinae sp. water mite diet isolate 13128-BHL040517-GBD12848_13971-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAAGAATAGTAGGAACTTCCTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGAGGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTATTACCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW612916 Orthocladiinae sp. water mite diet isolate 13130-BHL040517-GBD27146_9004-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAGGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTGCAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATCGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612917 Orthocladiinae sp. water mite diet isolate 13140-BHL040517-GBD29236_12208-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTAGGAGCTTGATCAGGAATAGTGGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGAACATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTTGTTCCTTTAATATTATGAGCACCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGTTCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612918 Orthocladiinae sp. water mite diet isolate 13141-BHL040517-GBD20906_27570-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTTAGAATTCTAATTCGAGCAGAATTAGATCATGCAGGTTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCAGATATGGCTTTCCCACGAATAAATAACATAAGATTTTGATTGTTGCCACCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612919 Orthocladiinae sp. water mite diet isolate 13146-BHL040517-GBD10510_5445-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCCTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACATCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTACTTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCACCGTCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612920 Orthocladiinae sp. water mite diet isolate 13159-BHL040517-GBD21583_24869-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTTAGAATTTTAATTCGAGCTGAATTAGGACTTGCCGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGAGTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612921 Orthocladiinae sp. water mite diet isolate 13163-BHL040517-GBD18622_23766-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTCGGAGCTTGACCAGGAATAGTTGGGACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGACATGCCGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACCTTATTATTATCAAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612922 Orthocladiinae sp. water mite diet isolate 13164-BHL040517-GBD25379_19939-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTTATTGGAGACGATCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTGCTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612923 Orthocladiinae sp. water mite diet isolate 13725-BHL040517-GBD5687_16187-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTGTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612924 Orthocladiinae sp. water mite diet isolate 14156-BHL040517-GBD10908_14410-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTGATCGGAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612925 Orthocladiinae sp. water mite diet isolate 14177-BHL040517-GBD17223_27102-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTGATCGGAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATTTTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAAC---TCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW612926 Orthocladiinae sp. water mite diet isolate 14198-BHL040517-GBD13931_8669-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGCACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612927 Orthocladiinae sp. water mite diet isolate 14260-BHL040517-GBD17174_19840-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGAGCGGGAATAGTAGGAACTTCTCTTAGTATTTTAATTCGAGCAGAATTAGGACATCCAGGTGCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612928 Orthocladiinae sp. water mite diet isolate 14266-BHL040517-GBD14083_20413-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTGATCGGAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCCTTTCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTTACATTACTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612929 Orthocladiinae sp. water mite diet isolate 14288-BHL040517-GBD12594_9998-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTCAATTCGACTAGAATTAGGGCACCCAGGCTCATTGATCGGAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTACTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGTTTTTGATTACTACCTCCTTCTCTTACCTTACTTTTAGTAAGCAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612930 Orthocladiinae sp. water mite diet isolate 14306-BHL040517-GBD11937_19323-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGACTAGAATTAGGACACCCAGGCTCATTGATCGGAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612931 Orthocladiinae sp. water mite diet isolate 14358-BHL040517-GBD12701_5770-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTGATCGGAGACGTCCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTAATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACCTCCCCCATCACTTACATTACTCCTTTCAAATTCATTTGCAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612932 Orthocladiinae sp. water mite diet isolate 14396-BHL040517-GBD26419_20365-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGCACTTCTTTAAGAATTTTAATTCGACTTGAATTAGGACACCCAGGCTCATTGATCGGAGACGACCAAATTTATAATGTAATTGTTACTGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCTGTACCCCGAAAAAAAAAATAAGATTTTGATTATTACCCCCTGCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612933 Orthocladiinae sp. water mite diet isolate 14467-BHL040517-GBD19181_26243-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTGATCGGAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACTCTTCTTCTTTCTAGCTCAATTGTAGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612934 Orthocladiinae sp. water mite diet isolate 14481-BHL040517-GBD22028_5988-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTATTTCGACTAGAATTAGGACACCCAGGCTCATTGATCGGAGACGACCAAATTTATAATGTAATTGTTACATCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGCGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTTTTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612935 Orthocladiinae sp. water mite diet isolate 536-BHL040517-GBD10507_18269-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAACTAGGACACCCAGGCTCATTGATCGGAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAGCAGGAGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW612936 Orthocladiinae sp. water mite diet isolate 846-BHL100916-GBD9148_23619-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTGATCGGAGACGACCAAATTTATAATGTAATTGTTACCGCATATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAGATTGATTAGTACCCTTAATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATGATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612937 Orthocladiinae sp. water mite diet isolate 961-BHL100916-GBD2438_14611-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAATGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTGATCGGAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATGAACCTTACGTTTATCAAGAACAGTAGGAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612938 Orthocladiinae sp. water mite diet isolate 2236-BHL072216-GBD22568_10710-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCTGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTGATCGGAGACGACCAAATTTATAATGTAATTGTTATAGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAACCCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTACTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612939 Orthocladiinae sp. water mite diet isolate 4323-BHL032417-GBD4247_14191-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGGGCCTGATCTGGGATAGTTGGAACTTCTTTAAGAATTCTTATTCGTGCAGAATTAGGACATGCTGGTTCCTTAATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGACTAGTTCCCTTAATATTAGGAGCACCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACCGCCCCCCTCTTTAACTTTATTTTTATCAAGCTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR693741, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612940 Orthocladiinae sp. water mite diet isolate 5193-BHL032417-GBD20668_6420-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGGGCCTGATCTGGGATAGTTGGAACTTCTTTAAGAATTCTTATTCGTGCAGAATTAGGACATGCTGGTTCCTTAATTGGAGACGACCAAATTTATAATGTAATTGTTACTGCTCACACTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGACTAGTTCCCTTAATATTAGGAGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCTTTAACTCTTCTTTTATCAAGCTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR693741, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612941 Orthocladiinae sp. water mite diet isolate 5222-BHL032417-GBD24247_16065-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGACTGTTGCCCCCATCATTAACATTATTGTTATCAAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612942 Orthocladiinae sp. water mite diet isolate 5226-BHL032417-GBD26400_8357-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCTTTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCACTAACTTTACTGTTATCTAGATCAATCGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612943 Orthocladiinae sp. water mite diet isolate 5348-BHL032417-GBD14922_6932-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCGGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACATGCAGGCTCATTAATTGGTGATGTTCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGTGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612944 Orthocladiinae sp. water mite diet isolate 9932-BHL040517-GBD9622_25158-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGGGCCTGATCTGGAATAGTTGGAACTTCTTTAAGAATTCTTATTCGTGCAGAATTAGGACATGCGGGTTCCTTAATTGGAGACGACCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGACTAGTTCCCTTAATATTAGGAGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCTTTAACTCTTCTTTTATCAAGCTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR694831, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612945 Orthocladiinae sp. water mite diet isolate 11309-BHL110116-GBD24708_10716-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGAAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTCCCCCGAATAAATAACATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW612946 Orthocladiinae sp. water mite diet isolate 12880-BHL040517-GBD13121_2706-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGGGCCTGATCTGGGATAGTTGGAACTTCTTTAAGAATTCTTATTCGTGCAGAATTAGGACATGCTGGTTCCTTAATGGGAGACGAGCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGACTAGTTCCCTTAATATTAGTAGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCTTTAACTCTTCTATTATCAAGCTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR693741, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612947 Orthocladiinae sp. water mite diet isolate 12907-BHL040517-GBD19631_16983-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAACTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTATTTCGAGCAGAATTAGGACATGCATGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTATTGCCCCCATCATTAACTTTATGATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612948 Orthocladiinae sp. water mite diet isolate 12945-BHL040517-GBD16368_19273-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTTGAAACTGACTAGTTTCTTTAATATTAGGAGCACCTGAAATGGCTTTCCCACGAAAAAAAAAAATAAGGTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612949 Orthocladiinae sp. water mite diet isolate 13042-BHL040517-GBD22273_7586-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAAATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.8% identical to accession ID KR285606, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612950 Orthocladiinae sp. water mite diet isolate 13056-BHL040517-GBD27176_17606-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGACCTGAATTAGGACATCCAGGCTCATTAATTGGAGATTATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATATTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCAGGAATAAATAAAATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612951 Orthocladiinae sp. water mite diet isolate 13110-BHL040517-GBD10106_15273-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCAGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCATAATTGGAGGTTTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTATTGCCCCCATCATTAACTTTATTATTATCTAGACCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612952 Orthocladiinae sp. water mite diet isolate 13112-BHL040517-GBD13724_16077-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGAAGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTGTAATATTAGGAGCACCTGATATGGCTTTCCCCCGAATAAATAACATAAGTTTTTGATTGTTGCCCCCATCATTAACCTTACTATTATCTAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR513498, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612953 Orthocladiinae sp. water mite diet isolate 13117-BHL040517-GBD27331_14714-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATTCTAATTCGAGCAGAACTAGGACATGCAGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGGTTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTTCCCCCTTCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612954 Orthocladiinae sp. water mite diet isolate 13120-BHL040517-GBD22822_17814-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGAGGCACCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCTCCATCATTAACTTTATTATTATCTAAAACAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612955 Orthocladiinae sp. water mite diet isolate 13136-BHL040517-GBD20901_7214-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGCACTTCTTTAAGAATTTTAATTCGACCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGTCCCCATCATTAACTTTATTATTATCAAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW612956 Orthocladiinae sp. water mite diet isolate 13638-BHL040517-GBD25264_14439-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTGATCGGAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612957 Orthocladiinae sp. water mite diet isolate 14403-BHL040517-GBD19580_20010-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGTTACTTCTTTAAGAATTTTAATTCGACTTGAATTAGGACACCCAGGCTCATTGATTTGAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATGTTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACCTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612958 Orthocladiinae sp. water mite diet isolate 14438-BHL040517-GBD17149_3285-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAAGTTTAATTCGACTAGAATTAGGACACTCAGGCTCATTGATCGGAGACGACCAAATTTATAATGAAATTGTTACAGCACATGCATTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTTGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGTGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612959 Orthocladiinae sp. water mite diet isolate 14464-BHL040517-GBD21312_27484-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTGATTGGAGACGACCAAATTTATAATATAATTGTTACTGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTAATATTAGGAGCCCCTGATATAGCTCTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCATCATTAACCTTACTATTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612960 Orthocladiinae sp. water mite diet isolate 14500-BHL040517-GBD26063_17842-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGGGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTCGGACACCCAGGTTCATTGATCGGAGACGAGCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCTTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612961 Orthocladiinae sp. water mite diet isolate 14512-BHL040517-GBD27632_20543-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTTATCGGAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGACTACTTCCCCCGTCATTAACCTTACTATTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612962 Orthocladius sp. water mite diet isolate 3488-BHL032417-GBD8121_12323-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAATAGCTCATGCTTTTGTTATAATTTTTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612963 Orthocladius sp. water mite diet isolate 3549-BHL032417-GBD9952_15201-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAACTAGGACATGCTGGTTATTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTGTGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612964 Orthocladius sp. water mite diet isolate 3575-BHL032417-GBD5676_8589-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID KR758170, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612965 Orthocladius sp. water mite diet isolate 3576-BHL032417-GBD13354_23819-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAACTAGGACATACTGATTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATCGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTT-TCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR745863, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW612966 Orthocladius sp. water mite diet isolate 3601-BHL032417-GBD9600_26828-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTATTTGATTGGAGACGACCAAATTTATAACGTAATGGTTACAGCTCATGCCTTTGTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTACCACTAATATTAGGTGCACCAGATATAGCTTTCCCTCGAATAAATAATATATGCTTTTGATTATTACCCCCATCTTTAACATTACTATTAGCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR749204, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612967 Orthocladius sp. water mite diet isolate 3663-BHL032417-GBD2744_20138-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTACGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCATTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACATACATTACTCCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612968 Orthocladius sp. water mite diet isolate 3712-BHL032417-GBD17145_3345-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTGTATTCGGAGCCTGATCAGGTATAGTAGGTACTTCCCTTAGTAATCTAGTACGAGCTGAATTAGGACACCCCGGGGCATTAATTGGAGACGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTCTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCAAATGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR291764, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612969 Orthocladius sp. water mite diet isolate 3739-BHL032417-GBD25208_18221-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGATCATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATATATAATATAAGTTTTTGAGTTCTCCCCCCATCTTTAACTCTTCTTCTT-TCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR745842, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612970 Orthocladius sp. water mite diet isolate 3751-BHL032417-GBD5413_14327-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGGATTAGGACATGCTGGTTATTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAAGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCTCTTACATTACTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612971 Orthocladius sp. water mite diet isolate 3790-BHL032417-GBD19848_5604-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATATTTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGATATTGATTAGTACCTTTAATGTTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612972 Orthocladius sp. water mite diet isolate 3815-BHL032417-GBD20784_2342-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATCTTCGGAGCATGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATCCGGGCCGAATTAGTACATGCCGGATCATTAATTAGTGACAATCAAATTTATAATGTTACTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCTTTCATTAACTTTATTATTGTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR291764, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612973 Orthocladius sp. water mite diet isolate 3816-BHL032417-GBD16965_27371-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAATAGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTCTCCCTCGAATAAATAATGTAAATTCTTGGCTTCTCCCTCCTTCTTTAACTCTTCTTCTT-TCTAGTTCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612974 Orthocladius sp. water mite diet isolate 3819-BHL032417-GBD7805_13650-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAACTGAATTAGGACATGCTGGTTATTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACTACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612975 Orthocladius sp. water mite diet isolate 3884-BHL032417-GBD18672_14197-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATCTTCGGAGCATGATCAGGATTAGTAGGAACATCTCTAAAAATTTTAATCCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACATCACATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGTCCCAGATATAGCTATCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR291764, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW612976 Orthocladius sp. water mite diet isolate 3900-BHL032417-GBD8790_22263-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAACTGAATTAGGACATGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAATTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR614960, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612977 Orthocladius sp. water mite diet isolate 3936-BHL032417-GBD25585_11532-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTATTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTGTTACCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR758170, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612978 Orthocladius sp. water mite diet isolate 3998-BHL032417-GBD10567_10786-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATCTTCGGAGCATGATCAGGAACATTAGGAACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACAGCACATGTTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATAAAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATGGTCTAGTTCGATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR291764, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612979 Orthocladius sp. water mite diet isolate 3999-BHL032417-GBD7552_20357-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTCTTTGTTTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTTTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTT-TCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR745863, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612980 Orthocladius sp. water mite diet isolate 4001-BHL032417-GBD2330_17828-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGTGACTTCTTTAAGAATATTGATCCGAACTGAATTAGGACATGCTGGTTCTTTGTTTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612981 Orthocladius sp. water mite diet isolate 5524-BHL032417-GBD17229_2070-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTATTTGATTGGAGACGACCAAATTTATAATGTTATTATAACAGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612982 Orthocladius sp. water mite diet isolate 3479-BHL032417-GBD4427_7765-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTCTAATTCGAGCTGAATTAGGACATGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612983 Orthocladius sp. water mite diet isolate 3788-BHL032417-GBD10890_24758-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCTTTAAGTATTTTATTTCGAGCTGAATTAGGACATGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACTCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.1% identical to accession ID KR758170, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612984 Orthocladius sp. water mite diet isolate 3854-BHL032417-GBD7009_13669-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTAAATTAGGACATGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAACTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCACTAACTTTATTATTGTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR284549, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612985 Orthocladius sp. water mite diet isolate 3912-BHL032417-GBD5438_20879-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGGGCTTGATCAGGAATAGTAGGAACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATCCTGGTTCTTTGATTGGAGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCCTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR749204, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW612986 Orthocladius sp. water mite diet isolate 4013-BHL032417-GBD19737_7000-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTCTATTTTATTTTTGGTGCTTGATCAGGAATAGTAGGTACTTCCTTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTCTTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCCCCGGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR741173, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612987 Orthocladius sp. water mite diet isolate 4029-BHL032417-GBD6560_17371-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGAGCTTGACCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGACTTGAATTAGGACATGCTGGTTCTTTGATTGGAGACGAACAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTATTATTGTCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612988 Orthocladius sp. water mite diet isolate 4827-BHL032417-GBD26756_11424-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTACTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTATTGTTATAATTTTTTTTATGGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612989 Orthocladius sp. water mite diet isolate 5790-BHL032417-GBD17114_17075-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.7% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612990 Orthocladius sp. water mite diet isolate 8146-BHL040517-GBD24212_24739-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTCTTTGATTGGAGATGACCAAATTTATAATGTTATTGTAACAGCTCATGCCTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612991 Orthocladius sp. water mite diet isolate 8470-BHL101416-GBD25119_22666-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTATTTGATTGGAGACGACCAAATTTATAATGTTATCGTAACAGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612992 Orthocladius sp. water mite diet isolate 12109-BHL040517-GBD25119_22666-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTATTTGATTGGAGACGACCAAATTTATAATGTTATCGTAACAGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612993 Orthocladius sp. water mite diet isolate 12586-BHL040517-GBD13906_4002-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATTCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAGCAGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612995 Palloptera sp. water mite diet isolate 14757-BHL040517-GBD3350_9980-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACACTATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID KR262652, identified in GenBank as Palloptera ambusta. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612996 Palloptera sp. water mite diet isolate 14939-BHL040517-GBD24784_13717-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACACTATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID KR262653, identified in GenBank as Palloptera ustulata. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW612997 Parachironomus sp. water mite diet isolate 1999-BHL022317-GBD27879_14542-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGGGCAAAACTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCACACGCATTTATTATAATTTTTTTCATAGTTATGCCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTAATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCACTAACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KC750459, identified in GenBank as Parachironomus delinificus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612998 Parachironomus sp. water mite diet isolate 2380-BHL072216-GBD25900_20195-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGAACTGGAACCTTTATTGGAGATGATCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATCATAATTTTTTTCATAGTTATGCCTATTTTAATTGGGGGCTTTGGAAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTACTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KJ166526, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW612999 Parachironomus sp. water mite diet isolate 3555-BHL032417-GBD11087_10803-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACAACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTTTAACCCTTTTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR687306, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613000 Parachironomus sp. water mite diet isolate 3558-BHL032417-GBD14745_11604-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTAAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATTTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTAATTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613001 Parachironomus sp. water mite diet isolate 3589-BHL032417-GBD13164_11526-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATCTTATTTTTGGGGCTTGATCCGGAATAATGGGAACGTCTTTAAGTATGCTAATTCGAGCAGAAATAGGACGACCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTCTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTGTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613002 Parachironomus sp. water mite diet isolate 3603-BHL032417-GBD7410_5812-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTTATATTAGGTGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613003 Parachironomus sp. water mite diet isolate 3609-BHL032417-GBD16094_21357-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTATTTTCGGAGCATGATCAGGAATAGTAGGGACTTCGTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGATGATGATCAAATTTACAATGTCATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCTAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCTCTTACATTACTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613004 Parachironomus sp. water mite diet isolate 3610-BHL032417-GBD20040_17963-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCATCTCCGACTCTATTACATTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613005 Parachironomus sp. water mite diet isolate 3614-BHL032417-GBD28399_9682-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTTAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCGGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACGTCTTCCCTCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613006 Parachironomus sp. water mite diet isolate 3619-BHL032417-GBD18367_21029-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATATTTATTCGAGCTGAATTAGGTCGACCTGGTACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613007 Parachironomus sp. water mite diet isolate 3620-BHL032417-GBD23125_20979-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTAAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGTACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACATACATTACTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613008 Parachironomus sp. water mite diet isolate 3651-BHL032417-GBD29636_16641-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTTTTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTGGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCGGTGACGCGGGGACGGGCGAGGGCAAGGGGAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613009 Parachironomus sp. water mite diet isolate 3652-BHL032417-GBD24224_5951-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTGTATTCGGAGCCTGATCAGGTATAGTAGGTACTTCCCTTAGTAATCTAGTACGAGCTGAATTAGGACACCCCGGGGCATTAATTGGTAATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGGCATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613010 Parachironomus sp. water mite diet isolate 3660-BHL032417-GBD22039_4489-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACATCCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTTATATTAGGTGCTCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613011 Parachironomus sp. water mite diet isolate 3670-BHL032417-GBD24907_9428-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACCTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGACTTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.4% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613012 Parachironomus sp. water mite diet isolate 3676-BHL032417-GBD9334_8313-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCGAATTTACAATGTAATTGTAACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAGTATATAATATAAGTTTTTGAGTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613013 Parachironomus sp. water mite diet isolate 3681-BHL032417-GBD24112_6146-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTCCCTCTAATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCACCTTCTCTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613014 Parachironomus sp. water mite diet isolate 3684-BHL032417-GBD12294_9200-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGTACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGTACTTTTATTGGTGACGGTCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613015 Parachironomus sp. water mite diet isolate 3691-BHL032417-GBD20507_12602-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAACATAAGTTTTTGACTTCTTCCCCCTTCTTTGACCCTTTTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613016 Parachironomus sp. water mite diet isolate 3696-BHL032417-GBD23916_22763-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTTAGAATACTTATTCGAGCTGAATTAGGACGTCCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAGATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACGACTTCCCCCTTCTTTGACACTATTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613017 Parachironomus sp. water mite diet isolate 3699-BHL032417-GBD28027_13607-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTTAGAATATTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGTGATGATCAAATTTATAATATAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTTGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTAACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613018 Parachironomus sp. water mite diet isolate 3701-BHL032417-GBD21094_14845-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTCTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATATTTATTCGAGCTGAATTAGGACGACCCGGATCTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACGGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCTTTGACTCTATTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613019 Parachironomus sp. water mite diet isolate 3703-BHL032417-GBD8515_13775-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAATAGGGACTTCCTTAAGAATACTTATTCGAGCTGAATTAGGACAACCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGTGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACCCTTTTACTATCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613020 Parachironomus sp. water mite diet isolate 3705-BHL032417-GBD25479_9774-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613021 Parachironomus sp. water mite diet isolate 3713-BHL032417-GBD17814_18192-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613022 Parachironomus sp. water mite diet isolate 3718-BHL032417-GBD7377_14713-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGATCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGTTCCAGACAAGGCCTTCCCTCGAATAAAAAAAAAAAGGTTTTGGCTTCCTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613023 Parachironomus sp. water mite diet isolate 3721-BHL032417-GBD8114_22889-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATATCTATTCGAGCTGAATTAGGACGACCCGGAACCTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613024 Parachironomus sp. water mite diet isolate 3724-BHL032417-GBD7849_8179-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATATTTATTCGAGTTGAATTAGGACGACCAGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTAATTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCTTTGACTCTTTTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613025 Parachironomus sp. water mite diet isolate 3728-BHL032417-GBD27906_20244-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATATTTATTCGAGCTGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCAGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTAACTCTTTTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR687306, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613026 Parachironomus sp. water mite diet isolate 3738-BHL032417-GBD12618_7205-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGTATACTTATTCGAGCTGAATTAGGACAACCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTTTGACCCTTTTACTATCTAGTACAATTGTAGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613027 Parachironomus sp. water mite diet isolate 3741-BHL032417-GBD20291_3530-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTAGTTGTAACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTTCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613028 Parachironomus sp. water mite diet isolate 3743-BHL032417-GBD22886_22778-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCAGGAACATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTGATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCTTTGACCCTTTTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613029 Parachironomus sp. water mite diet isolate 3745-BHL032417-GBD25849_6668-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGAGATGATCAAATTTATGATGTAATTGTTACGGCTCATGCTTTTATAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCAGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCTTTAACTCTTTTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613030 Parachironomus sp. water mite diet isolate 3747-BHL032417-GBD9777_25658-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGTCGACCAGGAACTTTTATTGAAGATGATCAAATTTACAATGTAATTGTAACGGCACATGCCTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTTTGACTCTATTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613031 Parachironomus sp. water mite diet isolate 3753-BHL032417-GBD14426_27487-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGATTGCTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTTTTGGTGATGATCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTAACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613032 Parachironomus sp. water mite diet isolate 3755-BHL032417-GBD27202_7383-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTTATATTAGGAGCTCCAGACATGGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613033 Parachironomus sp. water mite diet isolate 3766-BHL032417-GBD21388_3123-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCTGGAACTTTTATCGGTGATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTCGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCATTGACTCTATTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613034 Parachironomus sp. water mite diet isolate 3774-BHL032417-GBD19126_20860-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTACATTAGGGGCTCCAGACATGGCTTTCCATCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613035 Parachironomus sp. water mite diet isolate 3777-BHL032417-GBD16384_21440-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGTATACTTATTCGAGCTGAACTAGGACGACCCGGTACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATGCCTATTTCAATTGGAGGTTTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCGTCCCCCTTCATTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613036 Parachironomus sp. water mite diet isolate 3778-BHL032417-GBD8901_26481-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTATGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTTCCTCTTATATTAGGGGCTACAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGAATCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613037 Parachironomus sp. water mite diet isolate 3785-BHL032417-GBD22095_15672-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAACTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTGTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAATTCAATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613038 Parachironomus sp. water mite diet isolate 3787-BHL032417-GBD7386_21376-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCAAGCTAAATTAGGACATGCTGGTACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCGAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGAATCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613039 Parachironomus sp. water mite diet isolate 3793-BHL032417-GBD22926_21500-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTGGGGGCTCCTGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613040 Parachironomus sp. water mite diet isolate 3798-BHL032417-GBD28693_20218-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGATCAGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACGGCACATGGTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTGCTGCCCCCTTCATTGACTCTATTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613041 Parachironomus sp. water mite diet isolate 3799-BHL032417-GBD26303_18972-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGTTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTGATATTAGGGGCTCCAGACATGGCTTTCCCGCGAATAAACAATATAAGATTTTGACTACTTCCCCCTTCATTGACTCTTTTACTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613042 Parachironomus sp. water mite diet isolate 3804-BHL032417-GBD28168_15153-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCTTTAAGTATACTTATTCGAGCAGAACTAGGACGACCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCATATATTAGGAGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613043 Parachironomus sp. water mite diet isolate 3806-BHL032417-GBD16575_10100-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCTGGTACTTTTATAGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTCGACTCTATTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613044 Parachironomus sp. water mite diet isolate 3813-BHL032417-GBD23987_11399-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGTATACTTATTCGAGCTGAATTAGGACGCCCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGTGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCATCTTTAACGCTTTTACTATCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613045 Parachironomus sp. water mite diet isolate 3818-BHL032417-GBD26133_10608-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACAACCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTAATATTGGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCATCTTTAACTCTTTTACTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KJ166526, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613046 Parachironomus sp. water mite diet isolate 3822-BHL032417-GBD8526_10387-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGGGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTCTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTGGGGGCTCCTGACATGGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTCTTCCCCCCTCTCTGACTCTTTTACTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613047 Parachironomus sp. water mite diet isolate 3826-BHL032417-GBD25805_19008-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAACTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGTGCTCCTGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTATCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613048 Parachironomus sp. water mite diet isolate 3828-BHL032417-GBD16243_3026-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTCGGAGCTTGATCGGGAATAGTAGGGACTTCTTTGAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACCTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613049 Parachironomus sp. water mite diet isolate 3835-BHL032417-GBD21674_17166-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCTTTAAGAATACTTATTCGAGCTGAATTCGGACAACCAGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACGGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTGACTCTATTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613050 Parachironomus sp. water mite diet isolate 3839-BHL032417-GBD16924_11716-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGTCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCACCAGACATGGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTGACTCTTTTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613051 Parachironomus sp. water mite diet isolate 3840-BHL032417-GBD17499_22975-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGATATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACAGCACATGCCTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGACTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613052 Parachironomus sp. water mite diet isolate 3843-BHL032417-GBD23134_4215-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTATAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613053 Parachironomus sp. water mite diet isolate 3845-BHL032417-GBD9360_5988-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACTAACCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCACGAATAAATAATATAAGTTTTTGACTGTTGCCCCCATCATTGACTCTATTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613054 Parachironomus sp. water mite diet isolate 3851-BHL032417-GBD23769_6366-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCCGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGACATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTCTTCCCCCTTCTTTGACTCGTTGACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613055 Parachironomus sp. water mite diet isolate 3855-BHL032417-GBD25494_20172-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATATTTATTCGAGCTGAATTAGGACGACCAGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGAAAATTGATTAGTTCCTCTTATATTAGGTGCTCCAGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCTTTAACTCTTTTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613056 Parachironomus sp. water mite diet isolate 3856-BHL032417-GBD8041_16554-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGTGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATAATAGGGGCTCCAGACATGGCTTGCCCTCGAAGAAATAATATAAGTTTTTGACTTCGTCCCCCTTCTTTGACACGATTACTGTCTAGTGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613057 Parachironomus sp. water mite diet isolate 3862-BHL032417-GBD20652_11985-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTCCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCACAGTTATACCTATTTTAATCGGGGAATTTGGAAATTGATTAATCCCTCTTATGCTGGGAGCTCCTGATAAGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTATTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613058 Parachironomus sp. water mite diet isolate 3870-BHL032417-GBD23899_8992-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGGACTTTTATTGGTGATGATCAAATTTACAATGTAATTATAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAAGTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAAAATAAGTTTTTGACTTCTTCCCCCGTCTTTGAAACTATTACTTTCTAATGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613059 Parachironomus sp. water mite diet isolate 3871-BHL032417-GBD5955_19749-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACAACCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGATATGGCATTTCCTCGTATAAATAATATAAGATTCTGATTTCTTCCCCCTTCTTTGACTCTTCTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613060 Parachironomus sp. water mite diet isolate 3872-BHL032417-GBD24405_4527-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGGGCTTGATCAGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGTCATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613061 Parachironomus sp. water mite diet isolate 3873-BHL032417-GBD28172_18710-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCATGATCAGGAATAATAGGAACTTCTTTAAGTATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATCTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTTTGACCCTTTTACTATCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613062 Parachironomus sp. water mite diet isolate 3877-BHL032417-GBD19914_16596-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTGGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAGCGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGACTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATAGCTTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613063 Parachironomus sp. water mite diet isolate 3878-BHL032417-GBD24732_22639-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCAGACATAGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCTTTGACTCTATTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613064 Parachironomus sp. water mite diet isolate 3879-BHL032417-GBD24305_13836-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGTCAAACCGGTACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACGGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCTTTAACTCTATTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613065 Parachironomus sp. water mite diet isolate 3883-BHL032417-GBD29208_16147-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGGTCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613066 Parachironomus sp. water mite diet isolate 3885-BHL032417-GBD8353_11046-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCGGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACGGCATATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613067 Parachironomus sp. water mite diet isolate 3889-BHL032417-GBD27984_18137-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTTTTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613068 Parachironomus sp. water mite diet isolate 3893-BHL032417-GBD12044_24174-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGAAAGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGCAGGATTTGGAAATTGACTTGTCCCCCTAATACTTGGAGCACCTGACAAAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613069 Parachironomus sp. water mite diet isolate 3894-BHL032417-GBD23304_10359-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAGGAATACTTATTCGAGCTGAATTAGGACATCCCGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCACCAGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCTTTAACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613070 Parachironomus sp. water mite diet isolate 3898-BHL032417-GBD21158_27753-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGTCGACCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTCCCCCCTTCTCTGACTCTTTTACTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR687306, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613071 Parachironomus sp. water mite diet isolate 3902-BHL032417-GBD12731_6636-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATATTAATTCGAGCTGAATTAGGACAACCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCGCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCATTGACCCATTTACTATCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613072 Parachironomus sp. water mite diet isolate 3920-BHL032417-GBD27504_11627-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATATTTATTCGAGCTGAACTAGGACGCCCCGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTAACTCTTTTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613073 Parachironomus sp. water mite diet isolate 3921-BHL032417-GBD15748_21130-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACAACCCGGAACATTTATTGGTGATGATCAAATTTACAATGTAATTGTTACAGCACATGCTTTTATAATAATTTTTTTCATAGTTATAACAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTGCTGCCCCCTTCTTTGACTCTATTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613074 Parachironomus sp. water mite diet isolate 3923-BHL032417-GBD27922_16482-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACATCCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTTTAACTCTTTTACTTTCTAGTTGAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR687306, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613075 Parachironomus sp. water mite diet isolate 3926-BHL032417-GBD25106_21508-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTAACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTACTTCCTCTAATATTAGGAGCTCCCGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTAACTCTTTTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613076 Parachironomus sp. water mite diet isolate 3930-BHL032417-GBD18781_10385-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATATTTTATTTTCGGAGCTTGATCAGGAATAGTGGGGACTTCTTTAAGAATGCTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAGTTGTAACGGCACATGCTTTTATTATAATTTTTTTCGTAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCCCTTATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTCTACCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613077 Parachironomus sp. water mite diet isolate 3939-BHL032417-GBD26902_13719-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACAACCTGGAACATTTATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTATCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613078 Parachironomus sp. water mite diet isolate 3942-BHL032417-GBD9688_16920-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTCCATTAAGAATTTTTATTCGAGCTGAATTAGGACATGCTGGTTATTTGATTGGAGACGACCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTTGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613079 Parachironomus sp. water mite diet isolate 3947-BHL032417-GBD10656_17002-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTATGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCACCAGACATAGCTTTCCATCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACCCTATTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613080 Parachironomus sp. water mite diet isolate 3950-BHL032417-GBD10983_28495-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCTTTAAGAATATTTATTCGAGCAGAATTAGGACGCCCCGGATCTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCGTCTTTGACTCTTTTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613081 Parachironomus sp. water mite diet isolate 3951-BHL032417-GBD14091_1900-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTATGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTGACACAATTACGATCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613082 Parachironomus sp. water mite diet isolate 3955-BHL032417-GBD8193_4616-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTAATACTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTCACTTCTTCCCCCTTCTTTGACTCCTTTACTTTCTAATTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613083 Parachironomus sp. water mite diet isolate 3957-BHL032417-GBD9839_17955-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTCCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATATTTGTTCGAGCTGAATTAGGACGAGCAGGAACGTTTATTGGTGATGATCAAATTTACAATGTAATTGTATCGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613084 Parachironomus sp. water mite diet isolate 3958-BHL032417-GBD8458_21828-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTAGGAGCTTGATCAGGAATAGTAGGGACTTTTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAACCTGACTTGTCCCCCTAATACTTGGAGCGCCTGACATAGTTTTTCCTAGAAAAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613085 Parachironomus sp. water mite diet isolate 3959-BHL032417-GBD8224_17370-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTTTAACTCTCTTACCATCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613086 Parachironomus sp. water mite diet isolate 3965-BHL032417-GBD25053_14965-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATTCTTATTCGAGCAGAATTAGGACGACCCGGAACATTAATTGGTGATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTGACTCTATTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613087 Parachironomus sp. water mite diet isolate 3973-BHL032417-GBD21693_19570-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTAAGTATATTTATTCGAGCTGAATTAGGACAACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTTATATTACGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613088 Parachironomus sp. water mite diet isolate 3974-BHL032417-GBD11115_27803-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGTATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATCTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTTTGACCCTTTTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613089 Parachironomus sp. water mite diet isolate 3975-BHL032417-GBD21977_25430-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTGACTCTTCTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ166526, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613090 Parachironomus sp. water mite diet isolate 3980-BHL032417-GBD23686_20933-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATACTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGAACCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCATTCCCTCGAATAAATAACATAAGATTTTGACTACTTCCCCCTTCTTTGACACTATTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613091 Parachironomus sp. water mite diet isolate 3983-BHL032417-GBD21506_3416-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGTCCCGGAACTTTTACTGGTGATGATCAAATTTATAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACGTCTTCCCCCATCTTTGACTCTTTTACTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613092 Parachironomus sp. water mite diet isolate 3986-BHL032417-GBD28489_17664-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATTCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTAACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTGGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTATTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613093 Parachironomus sp. water mite diet isolate 3988-BHL032417-GBD19152_3506-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTAAGAATACTAATTCGAGCTGAATTAGGACGACCCGGAACATTTATTGGAGATGATCAAATTTACAATGTAATTGTTACGGCCCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCATCTTTGACTCTTTTATTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613094 Parachironomus sp. water mite diet isolate 3989-BHL032417-GBD13055_26593-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTAGGAGCTTGATCAGGAATAGTAGGGACTTGTTTAAGAATACTTATTCGAGTTGAATTAGGACGACCAGGAACATTTATTGGAGATGATCAAATTTACAATGTAATTGTAACGGCATATGCTTTTATTATAATTTTTTTCGTAGTTATACCTATTTTAATCGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613095 Parachironomus sp. water mite diet isolate 3990-BHL032417-GBD25704_10696-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCCTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACAACCCGGAACATTTATTGGTGATGATCAAATTTACAATGTAATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCGTTGACTCTTTTACTTACTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613096 Parachironomus sp. water mite diet isolate 4003-BHL032417-GBD27974_21898-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTTATTCGAGCTGAACTAGGACGTTCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTAGAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613097 Parachironomus sp. water mite diet isolate 4008-BHL032417-GBD20280_26110-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATAATAGGGACTTCTTTAAGAATACTTATTCGAGTTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCTTTGACTCTATTACTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613098 Parachironomus sp. water mite diet isolate 4009-BHL032417-GBD12054_22282-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACAACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGTGCTCCTGACATACCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCTTTGACTCTATTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613099 Parachironomus sp. water mite diet isolate 4011-BHL032417-GBD6565_25460-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTCGGGACTTCTTTAAGTATACTTATTCGAGCTGAATTAGGACGCCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTTCTATCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613100 Parachironomus sp. water mite diet isolate 4012-BHL032417-GBD2432_17652-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTTGTTCCTCTAATATTTGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613101 Parachironomus sp. water mite diet isolate 4014-BHL032417-GBD27303_12251-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCTGGAACTTTTATTGGTGATGATCAAATTTATAATGCAATTGTAACGGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCCCCAGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCTAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KJ166526, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613102 Parachironomus sp. water mite diet isolate 4016-BHL032417-GBD6815_18772-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTGTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAATTCCTCTTATATTAGAGGCTCCAGACATAGCTTTCCCTCGAATAAATAATATAAGGTTTTGACTTCTTCCCCCTTCTGTGACTATGTTACTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613103 Parachironomus sp. water mite diet isolate 4018-BHL032417-GBD7339_17099-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATATTTATTCGAGCTGAATTAGGACGTCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCACGAATAAATAATACAAGATTTTGACTACTACCCCCTTCTTTGACTCTATTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613104 Parachironomus sp. water mite diet isolate 4028-BHL032417-GBD13432_10189-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCTTTAAGAATATTTATTCGAGCTGAATTAGGACGACCTGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACCGCACATGCTTTTATTATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGACATGGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTGACTCTATTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613105 Parachironomus sp. water mite diet isolate 4044-BHL032417-GBD14746_26198-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGTTGAATTAGGACAACCAGGAACTTTTATTGGTAATGATCAAATTTACAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATATTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCAGACATGGCTTTCCCACGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCTTTGACCCTTTTACTTTCTAGTGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613106 Parachironomus sp. water mite diet isolate 4049-BHL032417-GBD22138_7431-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTTATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTACCCCCCTCTCTGACTCTTTTACTTTCTACTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613107 Parachironomus sp. water mite diet isolate 4051-BHL032417-GBD17390_12315-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACAAACCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACGGCACATGCTTTTATAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGTGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTGTTTCCCCCTTCATTGACTTTATTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613108 Parachironomus sp. water mite diet isolate 4053-BHL032417-GBD18258_11410-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCATTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACCACGTCCCCCTTCTTTAACACTTTTACAAGCTAGTGCAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613109 Parachironomus sp. water mite diet isolate 4055-BHL032417-GBD28049_17083-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAACTAGGACGACCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTATTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613110 Parachironomus sp. water mite diet isolate 4056-BHL032417-GBD21082_4233-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATATTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTATATTGTAATTGTAACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTGTTTGACTCTTTTACTATCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613111 Parachironomus sp. water mite diet isolate 4059-BHL032417-GBD18597_26862-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACAACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTTTGACCCTATTACCATCTAGTACACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613112 Parachironomus sp. water mite diet isolate 4061-BHL032417-GBD17763_14746-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATACTTTATTTTCGGGGCTTGATCCGGAATAGTAGGGACTTCTTTAAGAATTCTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTAATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613113 Parachironomus sp. water mite diet isolate 4064-BHL032417-GBD21090_22024-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAAAAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAATGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAAGCATGGCTTTCCCTCCAAAAAAAAAAAAAGTTTTTGACTTCCTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613114 Parachironomus sp. water mite diet isolate 4075-BHL032417-GBD13956_23388-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGTGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATATTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGTGCTCCAGACATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTGACTCTTTTACCTTCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613115 Parachironomus sp. water mite diet isolate 4076-BHL032417-GBD6339_17417-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTTAGAATACTTATTCGAGTTGAATTAGGACGACCAGGAACATTTATTGGTAATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGACATGGCTTTCCCTCTAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTTTGACCCTATTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613116 Parachironomus sp. water mite diet isolate 2746-BHL032417-GBD24553_6497-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCCTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAATTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613117 Parachironomus sp. water mite diet isolate 3516-BHL032417-GBD15085_23766-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATTTTTATTTTCGGAGCTTGATCAGAATTAGTAGGGACTTCTTTAAGAATACTTTTTCGAGCTGAATTAGGACGACCCGGAACTTTTATCGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613118 Parachironomus sp. water mite diet isolate 3532-BHL032417-GBD26385_11506-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAACTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCATCCCCCTTCTTTGACTCTTTTATTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613119 Parachironomus sp. water mite diet isolate 3550-BHL032417-GBD25720_21664-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGTGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCATCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAACTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613120 Parachironomus sp. water mite diet isolate 3559-BHL032417-GBD13553_14465-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATAGATTAGTTCATCTTATATTAGGGGCTCCAGACGTGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCCTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613121 Parachironomus sp. water mite diet isolate 3564-BHL032417-GBD12499_13206-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATATTTATTCGAGCTGAATTAGGACGTCCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCTTTGACTTTATTACTTTCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613122 Parachironomus sp. water mite diet isolate 3569-BHL032417-GBD16442_14763-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTTGAGCGGAATTAGGACGACCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCTTTGACTCTATTACTTTCTAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613123 Parachironomus sp. water mite diet isolate 3571-BHL032417-GBD27968_18119-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATACTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTGTGACTTCTTCCCCCTTCTGTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613124 Parachironomus sp. water mite diet isolate 3578-BHL032417-GBD25550_11211-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATATTTATTCGAGTTGAATTAGGACGACCCGGAACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTAATGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCGCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTTTGACCCTATTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613125 Parachironomus sp. water mite diet isolate 3582-BHL032417-GBD21705_3021-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGAACAGGAATAGTAGGGACTTCTTTAAGAATATTTATTCGAGATGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613126 Parachironomus sp. water mite diet isolate 3592-BHL032417-GBD6806_16903-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATAAAAGATTTTGACATCTTCCCCCTGCTTTGACACTATTACTGTCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613127 Parachironomus sp. water mite diet isolate 3593-BHL032417-GBD14293_2942-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGTAACATTTATTGGAGATGATCAAATTTACAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACATTCTAGTTCAATTGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613128 Parachironomus sp. water mite diet isolate 3599-BHL032417-GBD15961_27191-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGATCTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTAAACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGACTCCAGACATGGCTTTCCCTCGAATAAAAAAAATAAGTTTTTGAATTCTTCCCCCTTCTTTGACTGTTTTACTTTTTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613129 Parachironomus sp. water mite diet isolate 3600-BHL032417-GBD16884_5982-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGCCGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGCTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613130 Parachironomus sp. water mite diet isolate 3612-BHL032417-GBD17738_2213-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATGTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTAACGGCTCATGCTTTTATTATAATTTTTCTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGCCTCTTTTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613131 Parachironomus sp. water mite diet isolate 3613-BHL032417-GBD28513_13556-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTAACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTTTGACACTTTTACTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613132 Parachironomus sp. water mite diet isolate 3616-BHL032417-GBD17858_5703-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACGGATGCGAGCTGAATTAGGACCACCCTTAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATCCCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTGATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613133 Parachironomus sp. water mite diet isolate 3621-BHL032417-GBD15802_15721-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCAGTAATAGTAGGTACTTCTTTATGAATACTTATTCGAGTTGAATTAGGATGACCCGTAACTTTTATTTGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613134 Parachironomus sp. water mite diet isolate 3627-BHL032417-GBD21097_4956-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGAACAGGAATAGTAGGTACTTCTTTAAGAATTCTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTATTACTATCTAGTCCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613135 Parachironomus sp. water mite diet isolate 3631-BHL032417-GBD26670_16466-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGATTAGTAGGGACTTCTTTAAGAATACTTATTCGAACTGAATTAGGACGACCCGTAACTTTTTTTGGTTATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGACTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613136 Parachironomus sp. water mite diet isolate 3633-BHL032417-GBD18698_28582-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACATTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCGCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTGACACTTTTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613137 Parachironomus sp. water mite diet isolate 3642-BHL032417-GBD3804_18375-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGCCCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATAATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGACATGGCAATCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613138 Parachironomus sp. water mite diet isolate 3645-BHL032417-GBD9140_19116-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATATTTTATTTTCGGAGCTTGATCCGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATACTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTCTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613139 Parachironomus sp. water mite diet isolate 3646-BHL032417-GBD15819_20089-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTATGACGACCAGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCACTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTTTGACTCTTTTACTTTCCAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613140 Parachironomus sp. water mite diet isolate 3647-BHL032417-GBD28654_12078-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGTATAGTAGGGTCTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGTGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCTTTGACTCCTTTACTATCTAGTTCAACTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613141 Parachironomus sp. water mite diet isolate 3648-BHL032417-GBD23430_17862-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTTATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGCCCCGGAACTTTTATTAGTGATGATCAAATTTACAATGTAACTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTATTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613142 Parachironomus sp. water mite diet isolate 3649-BHL032417-GBD26624_22295-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGTATATTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTACCCCCTTCTTTAACTCTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613143 Parachironomus sp. water mite diet isolate 3653-BHL032417-GBD28184_15142-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACCTTTATTGGTGATGATCAGATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCATATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAAAATAAGTTATTGACTTCTTCCCCCTTCTTCGACTCTATTACTTTCTAGTTCAATTGTAGAAAATGGCGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613144 Parachironomus sp. water mite diet isolate 3656-BHL032417-GBD27352_17308-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACATCCCGAAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGATATGGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613145 Parachironomus sp. water mite diet isolate 3658-BHL032417-GBD23991_11436-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTCGGAGCTTGATCCGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCACCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCCTCTCTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613146 Parachironomus sp. water mite diet isolate 3665-BHL032417-GBD21853_25620-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGTATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGACTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTGACTCTATTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613147 Parachironomus sp. water mite diet isolate 3666-BHL032417-GBD9775_12161-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTCTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTTATATTAGGGGCTACAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTGTATTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613148 Parachironomus sp. water mite diet isolate 3675-BHL032417-GBD17513_3289-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCTGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTTCTATCTAGTTCAATTGTAGAAAATGGAGCTGGACCAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613149 Parachironomus sp. water mite diet isolate 3679-BHL032417-GBD22096_22211-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTTGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCTCTAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613150 Parachironomus sp. water mite diet isolate 3682-BHL032417-GBD26418_23050-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATCCTTATTCGAGCTGAATTAGGACGTCCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTTACGGCACATGCTTTTATTATAATCTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTTTGACTCTATTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613151 Parachironomus sp. water mite diet isolate 3683-BHL032417-GBD16832_10818-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATACTTATTCGACCTGCATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGACTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCGATTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613152 Parachironomus sp. water mite diet isolate 3686-BHL032417-GBD19287_6168-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTACCCTCGAATAAATAATATAAGTTGTTGACTTCTTCCCCCTTCTTTGACTCTTTTAATATCTAGTGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613153 Parachironomus sp. water mite diet isolate 3688-BHL032417-GBD8522_20811-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGAAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCAGACATGGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTTACTCTTTTTCTTTCTATTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613154 Parachironomus sp. water mite diet isolate 3692-BHL032417-GBD20807_25270-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACAACCTGGATCTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTGATATTAGGTGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCACTTCTTTGACTCTTTTACTTTCTAATTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613155 Parachironomus sp. water mite diet isolate 3694-BHL032417-GBD28594_14161-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCTTTAAGTATACTTATTCGAGCTGAATTAGGTCGCCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATGTAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613156 Parachironomus sp. water mite diet isolate 3695-BHL032417-GBD9483_5013-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTAATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGAATTCTTCCCCCTTCTTTGACACTTTTACTTTCTAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613157 Parachironomus sp. water mite diet isolate 3697-BHL032417-GBD3604_18800-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCAGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTCATTAGTTCCTCTTATATTAGGGGCTCCAGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTATTACTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613158 Parachironomus sp. water mite diet isolate 3706-BHL032417-GBD23060_9457-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGGACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTAAACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTGCCACTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTTTGACACTATTACTTTCTAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613159 Parachironomus sp. water mite diet isolate 3714-BHL032417-GBD13961_7465-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTATGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCGGGTACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATTATATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCTTTGACTCTTTTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613160 Parachironomus sp. water mite diet isolate 3715-BHL032417-GBD27906_15737-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATTTTTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCTCATGCGTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGACATGGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTTTGACTCTTTTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613161 Parachironomus sp. water mite diet isolate 3717-BHL032417-GBD18847_3609-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCTGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613162 Parachironomus sp. water mite diet isolate 3720-BHL032417-GBD26910_7339-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACAACACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTTGAAATTGATTAGTTCCTCTTATATTAGGGACTCCAGACATGGCTTTCCCTCTAATAAATAAAAAAAGTTTTTGACTTCTTCTCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613163 Parachironomus sp. water mite diet isolate 3723-BHL032417-GBD13448_24320-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGTTCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAAGGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGTGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTGTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613164 Parachironomus sp. water mite diet isolate 3727-BHL032417-GBD9127_12022-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATCTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGTGCTCCAGACATGGTTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613165 Parachironomus sp. water mite diet isolate 3730-BHL032417-GBD16444_18324-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGAACCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTATTCCCCCTTCTGTGACTCAGTCACTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613166 Parachironomus sp. water mite diet isolate 3732-BHL032417-GBD17509_4870-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCTTAACTTTTATTGGTTATGATCAAATTTACAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATCCCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATGAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAATTCAATCGTAGAAAATGGAGCTGGACCAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613167 Parachironomus sp. water mite diet isolate 3733-BHL032417-GBD26483_9107-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATTCTTATTCGAGCTGAATTAGGACAACCCGGAACTTTTATTGGTGACGATCAAATTTATATTGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACACTATTACGTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613168 Parachironomus sp. water mite diet isolate 3740-BHL032417-GBD26010_7039-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATTCTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAACGTAATTGTAACGGCACATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGGATAAATAATATAAGTTTTTGACTTCTTCCCCCTGCTTTAACTCTTTTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR288271, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613169 Parachironomus sp. water mite diet isolate 3748-BHL032417-GBD27509_22760-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTCTAGGAATACTAATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGAAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACCCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613170 Parachironomus sp. water mite diet isolate 3749-BHL032417-GBD25411_6150-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATTAGGAACAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATAGCTTTCCCTCGAATAAACAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTATTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613171 Parachironomus sp. water mite diet isolate 3756-BHL032417-GBD24147_6284-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATACTTTATTTTCGGAGCTTGATCAGGAATAATAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTATTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613172 Parachironomus sp. water mite diet isolate 3758-BHL032417-GBD25517_15019-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTTTATTTAATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTAACTCTTTTATTTGCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613173 Parachironomus sp. water mite diet isolate 3759-BHL032417-GBD21502_2670-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATACTTATTCGAGCTAAATTAGGACGACCCAGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTGATATTAGGGGCTCCAGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTTTGACCCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613174 Parachironomus sp. water mite diet isolate 3762-BHL032417-GBD15240_6354-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCAGAGTTATACCAATTTTAATTGGAGGATTGGGAAATTGATTAGTTCCTCTAATATTAGGGGCGCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613175 Parachironomus sp. water mite diet isolate 3767-BHL032417-GBD7217_18517-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGTATAGTAGGGACTTCTTTAAGTATACTTATTCGAGCTGAATTTGGACGACCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTCACGGCACATCCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTGATATTAGGAGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613176 Parachironomus sp. water mite diet isolate 3772-BHL032417-GBD17367_8346-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATCTTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTGCCTCTTTAAGAATACTTATTCGAGCTAAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTGTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCATTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613177 Parachironomus sp. water mite diet isolate 3773-BHL032417-GBD29468_15962-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGTATACTTATTCGAGCTGAATTAGGACGACCAGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACGGCACATGCCTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCGTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613178 Parachironomus sp. water mite diet isolate 3775-BHL032417-GBD28144_11738-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTATTTTAGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCAGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCACATGCTTTTAGTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTCCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613179 Parachironomus sp. water mite diet isolate 3779-BHL032417-GBD23216_23570-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTATTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTCAGAATACTTATTCGAGCTGAATTAGGACGAACCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAAGTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGTGCTCCAGACATGGCTTTCCCTCGAATAAATAAAATAAGTTTTTGACGTCTTCCCCCTTCTTTGACTCCTTTACTCTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613180 Parachironomus sp. water mite diet isolate 3782-BHL032417-GBD28487_15563-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGATGACCCGGAACTTTTATTAGTGATGATCAAATTTACAATGTAATTGTAAATGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTAATATTAGGTGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613181 Parachironomus sp. water mite diet isolate 3783-BHL032417-GBD14693_7725-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGTATACTTATTCGAGCTGAATTAGGACGACCGGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGCGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCATCTTTGACTCTTTTACTTTCTAATTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613182 Parachironomus sp. water mite diet isolate 3784-BHL032417-GBD13427_22057-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCATTAAGAATATTTATTCGAGCTGAATTAGGACGACCAGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGACATAGCTTTCCCACGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613183 Parachironomus sp. water mite diet isolate 3794-BHL032417-GBD14107_2605-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCTGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCATTTATTATAATTTTTTTCATATTTATACCTATTTTAATTGGAGGATTTTGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAATTCAATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613184 Parachironomus sp. water mite diet isolate 3795-BHL032417-GBD29653_16440-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTGTATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTAATCGAGCTGAATTAGGACGACCAGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAATAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGTCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTATTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613185 Parachironomus sp. water mite diet isolate 3796-BHL032417-GBD19017_25999-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAAATGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGAGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCGTTGACTCAGTTACTTTCTAGTACAATTGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613186 Parachironomus sp. water mite diet isolate 3801-BHL032417-GBD10824_7293-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGTACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAACATAAGTTTTTGACTACTACCCCCTTCTTTGACACTTTTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613187 Parachironomus sp. water mite diet isolate 3802-BHL032417-GBD4133_16352-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATACTTTATTTTCGGAGCTTGATCAGGAATCGTAGGGACTTCATTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGTGATGATCAAATTTACAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613188 Parachironomus sp. water mite diet isolate 3810-BHL032417-GBD22168_3729-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGAAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTAAATTAGGACGACCCGGAACTTTTATTGGTGATGACCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCATCCCCCATCTTTGACTCTTTTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613189 Parachironomus sp. water mite diet isolate 3811-BHL032417-GBD22856_17079-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATTCTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTAATATTAGGTGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCGGCCCCCTTCTTTGACTCTATTACTATCTAGTTCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613190 Parachironomus sp. water mite diet isolate 3814-BHL032417-GBD14216_22086-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCAGGGATAGTTGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCAGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACGTCTTCCCCCTTCTTTGACTCTGTTACTGTCTAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613191 Parachironomus sp. water mite diet isolate 3820-BHL032417-GBD19116_12733-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGCATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAACGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTACTTTGACACTTTTACAAGCTAGTGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613192 Parachironomus sp. water mite diet isolate 3823-BHL032417-GBD15731_3265-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGAATTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGTAACTTTTATTGGTTATGATCAAATTTACAATGTAATTGTAACGGCACATGCATTTATTATATTTTTTTTCATAGTTATTCCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTGATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613193 Parachironomus sp. water mite diet isolate 3829-BHL032417-GBD8157_12859-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACAACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTACTTCCTTTTATATTAGGGGCTCCAGATATGGCTTTCCCTCGAATAAATAACATAAGTTTTTGACTTCTTCCCCCTTCTTTGACCCTTTTACTATCTAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613194 Parachironomus sp. water mite diet isolate 3830-BHL032417-GBD24504_18130-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTTGGAGCTTGATCAGCTATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTAATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTTTATTACCAACTAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613195 Parachironomus sp. water mite diet isolate 3834-BHL032417-GBD28396_13796-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGTCTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTGATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCGATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTAACTCTTTTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613196 Parachironomus sp. water mite diet isolate 3836-BHL032417-GBD17031_4384-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGGAGGGACTTCTTTAAGAATACTTATTCGAGCTGAAGTAGGACGACCCTGTACTTTTATTGGTTATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATGGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGATTAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613197 Parachironomus sp. water mite diet isolate 3844-BHL032417-GBD19479_18216-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTCGGAGCTTGATCCTGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATAATCAAATTTATAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCAGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTACCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613198 Parachironomus sp. water mite diet isolate 3846-BHL032417-GBD19353_13587-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGAGCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTAAATTAGGACGACCCAGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCTAATAAATAATATAAGTTTTTGGCTTCTTCCCCCTTCTTTGACACTTTTACAATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613199 Parachironomus sp. water mite diet isolate 3852-BHL032417-GBD7742_11983-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGTATACTTATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCAAGTTCAACTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613200 Parachironomus sp. water mite diet isolate 3864-BHL032417-GBD10765_18498-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGTTGAATTAGGACGTCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCATCTTTGACTCTTTTACTTTCTAATGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613201 Parachironomus sp. water mite diet isolate 3867-BHL032417-GBD20702_27006-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACAGTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTATTTAAGAATATTTATTCGAGATGAATTAGGACGACCCGAAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAATTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTAACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613202 Parachironomus sp. water mite diet isolate 3868-BHL032417-GBD17172_19686-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTCGGAGCTTGATCAGAAATAGTAGGAACTTCTTTAAGAATGCTTGTTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTGCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613203 Parachironomus sp. water mite diet isolate 3874-BHL032417-GBD25474_19054-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTGGGAACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACGGGACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGATATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613204 Parachironomus sp. water mite diet isolate 3886-BHL032417-GBD20871_20202-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGACTTCAATTAGGACGACCCGGAACTTTTATTGGTGATGTTCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTGATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTGACTCTTTTACTTTCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613205 Parachironomus sp. water mite diet isolate 3888-BHL032417-GBD15682_2414-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGACCTGAATTAGGACGACCCGTAACTTTTATTGTTTATGATCAAATTTACAATGTAATTGTATCGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAATTCAATTGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613206 Parachironomus sp. water mite diet isolate 3890-BHL032417-GBD11836_20232-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGTATACTTATTCGCGCTGAATTAGGACGACACGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATCAATAATATAAGGTTTTGACTTCTTCCCCCTTCTTTGACTCTGTTACTTTCTAGTAGAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613207 Parachironomus sp. water mite diet isolate 3892-BHL032417-GBD16510_5329-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTCTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTAATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTACTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACCCTTTTTCTTTCTAGTTCCATTGTAGAAAATGGCGCTGGAACCGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613208 Parachironomus sp. water mite diet isolate 3897-BHL032417-GBD21156_27771-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACTTCTTTTAGAATATTTATTCGAGCTGAATTTGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTTTAACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR687306, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613209 Parachironomus sp. water mite diet isolate 3904-BHL032417-GBD25519_11150-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATACTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGACTCCAAGCATGACCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613210 Parachironomus sp. water mite diet isolate 3905-BHL032417-GBD24832_19465-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTATGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTACCGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGTGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTTTTCCCCCTTCTTTGACGCTTTTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613211 Parachironomus sp. water mite diet isolate 3906-BHL032417-GBD25976_23005-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTCTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTCAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGAGTTCTTCCCCCTTCTCTGACTCTTTTACTTTCTAGTGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613212 Parachironomus sp. water mite diet isolate 3907-BHL032417-GBD7669_21626-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGGATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACAAACCGGGACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTTTGACTCTATTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613213 Parachironomus sp. water mite diet isolate 3909-BHL032417-GBD20104_11560-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAACTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATAATAATTTTTTTCATAGTTATACCTATTTTAATCGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCATCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTATTACTTTCTAGTTCAATTGTAGGAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613214 Parachironomus sp. water mite diet isolate 3911-BHL032417-GBD15206_9224-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGGACTTCTTTAAGAATACTCATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTATTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTTTGACTCTTTTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613215 Parachironomus sp. water mite diet isolate 3913-BHL032417-GBD11488_4621-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTTAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTAACGGCACATGCATTTATTATAATTTTTTTCATTGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGACTAAATAATATAAGATTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613216 Parachironomus sp. water mite diet isolate 3916-BHL032417-GBD5180_17279-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGCCTTCTTTAAGAATCTTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAAGGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTGTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613217 Parachironomus sp. water mite diet isolate 3918-BHL032417-GBD28567_20632-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTATTTTAGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTAGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGTCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTGTTTGACTTCTACCCCCTTCTTTGACTCAGTTACTTGCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613218 Parachironomus sp. water mite diet isolate 3919-BHL032417-GBD27792_17455-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTTTTCCCCATTCTGTGACACTATTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613219 Parachironomus sp. water mite diet isolate 3922-BHL032417-GBD22120_24518-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGGGATGATCAAATTTACAATGTAATTGTAACGGCACATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATCGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACCATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613220 Parachironomus sp. water mite diet isolate 3927-BHL032417-GBD6320_12944-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTAAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCCCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGGCTTCTTCCCCCTCCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613221 Parachironomus sp. water mite diet isolate 3928-BHL032417-GBD19674_27553-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATATTTATTCGAGCTGAATTAGGACAACCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGTAGTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613222 Parachironomus sp. water mite diet isolate 3931-BHL032417-GBD15644_3949-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATAGAAGGGACTTCTTTAAGAATACTAATTCGAGCTGAAGTAGGACGACCCTTAACTTTTATTGGTGATGATCAAATTTACAATGGAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGACATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613223 Parachironomus sp. water mite diet isolate 3934-BHL032417-GBD15006_2748-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTCTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCTTAACTTTTATTGGTGATGATCAAATTTACAATGTAATTTTAACGTCACATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCTTTGACTCTTTCACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613224 Parachironomus sp. water mite diet isolate 3935-BHL032417-GBD9040_17617-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCTTTAAGTATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACACTTTTACAATCTAGTGCAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613225 Parachironomus sp. water mite diet isolate 3941-BHL032417-GBD15110_6844-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTTATCTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTTAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGCAATTGTAACGGCATATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGTGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613226 Parachironomus sp. water mite diet isolate 3944-BHL032417-GBD6432_13531-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCATTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTTATATTTGGAGCTCCAGACATAGCTTCCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTAGTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613227 Parachironomus sp. water mite diet isolate 3946-BHL032417-GBD11480_7702-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATTTTTATTCGAGCTGAATTAGGACGACCCGGCACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGTGGTTTTGGAAATTGATTAGTTCCTCTTATATTAGGTGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACACTATTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613228 Parachironomus sp. water mite diet isolate 3961-BHL032417-GBD3120_11436-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACATCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGATATTGATTAGTTCCTTTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613229 Parachironomus sp. water mite diet isolate 3962-BHL032417-GBD27116_20434-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTATATTTATTTTCGGAGCTTGATCAGGAATAGTCGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACATTTATTGGTGATGATCAAATTTACAATGTAATTGTTACCGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTTCCTCTAATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613230 Parachironomus sp. water mite diet isolate 3968-BHL032417-GBD16676_15191-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCTTCTTATATTAGGTGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTTTAACACTTTTACATTCTATTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613231 Parachironomus sp. water mite diet isolate 3972-BHL032417-GBD24669_20577-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTATTTTCGGAGCTTGATCAGGAATAGTTGGGACTTCTTTAAGTATACTTATTCGAGCTGAACTAGGACGACCTGGAACTTTTATTGGTGATGATCAAATTTACAACGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613232 Parachironomus sp. water mite diet isolate 3976-BHL032417-GBD19868_14617-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTCGATCAGGAATAGTAGGGACTTCTGTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613233 Parachironomus sp. water mite diet isolate 3977-BHL032417-GBD21259_8255-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACACGGAACTTTTATTGGTGATGATCAAATTTACATTGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTATGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCTTTGACTCTTTTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613234 Parachironomus sp. water mite diet isolate 3981-BHL032417-GBD22991_7886-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTATTTTCGGAGCTTGATCAGGAATAATAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTCTTATATTAGGAGCTCCAGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTCTGACTCTTGTACTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613235 Parachironomus sp. water mite diet isolate 3984-BHL032417-GBD14970_4297-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCATTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGAGATGACCAATTTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCTGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613236 Parachironomus sp. water mite diet isolate 3985-BHL032417-GBD16863_19947-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACATTATTTTTGGGGCTTGATCCGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAATTTGATTAGTTCCTCTTGTATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCCTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613237 Parachironomus sp. water mite diet isolate 3997-BHL032417-GBD12397_23005-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTAAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAATTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGACTAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTGTTACTTTCTCGTTCAATAGTAGAAAATGGAGCTGAAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613238 Parachironomus sp. water mite diet isolate 4010-BHL032417-GBD23625_6033-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGACTAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTATGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCAGTGACTCTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613239 Parachironomus sp. water mite diet isolate 4020-BHL032417-GBD17189_4756-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGTAACTTTTATTGGTGATGATCAAATTTACAATGGAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGACATGGCTTTCCCTCGCATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTTCTTTCTAGTTCAATAGTCGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613240 Parachironomus sp. water mite diet isolate 4023-BHL032417-GBD25514_20008-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGTATATTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGTCGACCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACGGCACATGCTTTTATAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGTAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTGACTCTATTACTTTCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613241 Parachironomus sp. water mite diet isolate 4026-BHL032417-GBD14382_26380-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATTGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCCGACCTGGCCTTCCCTCCAATAAATAATATAAGTTTTTTACCTCTTCCCCCTTCTTTGACCCCTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613242 Parachironomus sp. water mite diet isolate 4032-BHL032417-GBD13268_5428-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGGATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGACTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613243 Parachironomus sp. water mite diet isolate 4033-BHL032417-GBD15570_2825-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATTATCAAATTTACAATATAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAACTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTCGAAACTG	Using NCBI BLASTN in June 2018, this sequence was 98.1% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613244 Parachironomus sp. water mite diet isolate 4035-BHL032417-GBD7417_17270-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTTAGAATATTTATTCGAGCTGAATTATGACGACCCGGAAAATTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613245 Parachironomus sp. water mite diet isolate 4037-BHL032417-GBD17621_22781-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACGTATTCGAGCTGAATTAGGACGACCCGGACCTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTTCCTCTGATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAGTATAAGTTTTTGACTACTTCCCCCTTCTTTGACCCTTTTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613246 Parachironomus sp. water mite diet isolate 4039-BHL032417-GBD6554_23617-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTTAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATATTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613247 Parachironomus sp. water mite diet isolate 4045-BHL032417-GBD8606_18882-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTGTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGCATAAATAGTATAAGGTTTTGTCTTCTTCCCCCTTCTTTGACTCTTTCACTTTCTAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613248 Parachironomus sp. water mite diet isolate 4046-BHL032417-GBD29035_12187-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATCTTTTATTTTCGGAGCTTGTTCAGGATTAGTAGGGACTTCTTTAAGCATACTTATTCGAGCTGACTTAGGACGACCCGGAACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613249 Parachironomus sp. water mite diet isolate 4047-BHL032417-GBD21075_14841-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTCTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTAAGAATACTTATTCGAGCTGAATTAGGACGGCCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCTTCTTTGACTCTTTTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613250 Parachironomus sp. water mite diet isolate 4048-BHL032417-GBD16421_2822-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACGATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCTTAACTTTTATTGGTGATGATCAAAGTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCAAGACATGGCTTTCCCTCGAATAAATAATATTAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGCGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613251 Parachironomus sp. water mite diet isolate 4058-BHL032417-GBD21765_10613-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACCTATTCGAGCTATATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGACTCCAGACATGACTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTATTACTTTCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613252 Parachironomus sp. water mite diet isolate 4063-BHL032417-GBD13653_5743-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTGAGAATACTTATTCGAACTGAATTAGGACGACCCTGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGCATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGCGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613253 Parachironomus sp. water mite diet isolate 4066-BHL032417-GBD24635_12009-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTAAATTAGGACGACCCGGAACTTTTATTGGTAATGATCAAATTTACAATGTAATTGTAAGGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGTGTCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCTTTGACTCTTTTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613254 Parachironomus sp. water mite diet isolate 4068-BHL032417-GBD10192_3084-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAAGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAAAAAAGGCTTTCCCTCGAAAAAATAAAAAAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAAATGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613255 Parachironomus sp. water mite diet isolate 4071-BHL032417-GBD2675_13463-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGTATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGATTTCCCTCGAGTAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTGACTCTTTTACTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613256 Parachironomus sp. water mite diet isolate 4072-BHL032417-GBD12239_17231-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCCGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGTGATGATCAAATTTATAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGTGCTCCAGACATGCCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTTTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613257 Parachironomus sp. water mite diet isolate 4096-BHL032417-GBD9804_2813-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGTGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613258 Parachironomus sp. water mite diet isolate 5573-BHL032417-GBD24416_5696-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613259 Parachironomus sp. water mite diet isolate 5787-BHL032417-GBD16942_12182-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTCACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTGTAACACTTTTACGATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613260 Parachironomus sp. water mite diet isolate 5791-BHL032417-GBD13141_24236-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGCACACTTATTTGAGCTGAATTAGGACTACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTCCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTATCTAGTTGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613261 Parachironomus sp. water mite diet isolate 5821-BHL032417-GBD13484_4371-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTAAATTAGGACGACCCGTAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCCCCTGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613262 Parachironomus sp. water mite diet isolate 5872-BHL032417-GBD7110_20913-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGTGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGAAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGACTCCAGACATGGCTTTCCCTCGAATAAATAATAAAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613263 Parachironomus sp. water mite diet isolate 6094-BHL032417-GBD14378_14592-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCCTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGAGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTGTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613264 Parachironomus sp. water mite diet isolate 6104-BHL032417-GBD21262_6348-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGATGACCTGGAACTTTTATTGGTGATGATCTAATTTACAATGTAATTGTAACGGCACATGCTTTTATCATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGTTCCAGACATGGCTTTCCCTAGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTATTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613265 Parachironomus sp. water mite diet isolate 6298-BHL032417-GBD8455_5932-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACAACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGATATAGCTTTGCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTTTGACTCTTTTATTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613266 Parachironomus sp. water mite diet isolate 8415-BHL101416-GBD10623_6632-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613267 Parachironomus sp. water mite diet isolate 12054-BHL040517-GBD10623_6632-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613268 Paracladopelma sp. water mite diet isolate 1950-BHL022317-GBD28408_20973-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACTTTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTTACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTCGGAAATTGATTAGTTCCTCTAATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTTCTTCCCCCATCCCTTACCCTTCTGCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID JF412134, identified in GenBank as Paracladopelma camptolabis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613269 Paracladopelma sp. water mite diet isolate 8283-BHL040517-GBD7086_25275-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATTTATAATGTACTTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTGTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTATCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR620938, identified in GenBank as Paracladopelma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613270 Paratanytarsus natvigi water mite diet isolate 13191-BHL040517-GBD27634_8921-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACTTCCTTAAGTATACTAATTCGAGCAGAACTAGGTCACCCTGGAACATTTATTGGAGATGATCAAATCTGTAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGAATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTACTATCAAGAAGATTAGTGGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KT100941, identified in GenBank as Paratanytarsus natvigi. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613271 Paratanytarsus natvigi water mite diet isolate 13389-BHL040517-GBD15420_14852-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATAATCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTGTTCCTTTAATATTAGGAGCTCCCGATACAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTACCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KT100941, identified in GenBank as Paratanytarsus natvigi. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613272 Paratanytarsus sp. water mite diet isolate 541-BHL040517-GBD25919_9070-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGAGCAGGAATAATCGGAACATCCTTAAGAATATTAATTCGAGCTAAATTATCACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGATTTTGATTACTTCCCCCATCTTTAACCCTTCTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613273 Paratanytarsus sp. water mite diet isolate 567-BHL040517-GBD15165_16178-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAGGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613274 Paratanytarsus sp. water mite diet isolate 1148-BHL110116-GBD23558_11346-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCCCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613275 Paratanytarsus sp. water mite diet isolate 1152-BHL110116-GBD17772_15423-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAGTATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613276 Paratanytarsus sp. water mite diet isolate 1210-BHL110116-GBD18571_15945-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACTTCCTTAAGTATATTAATTCGAGCCGAATTAGGGCACCCTGAAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGTAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGAATAAATAATATAAGTTTTTGATTACTTCCACCATCTCTAACCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613277 Paratanytarsus sp. water mite diet isolate 1812-BHL101516-GBD17262_13150-Ldc86 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGGTTTGGGAATTGATTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCATTCCCTCGAATAAATAACATAAGTTTTTGATTACTTCCCCCGTCTTTAACTTTACTATGATCTAGAACACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613278 Paratanytarsus sp. water mite diet isolate 2460-BHL072216-GBD9803_7326-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTATTGCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCACCATCTTTAACTTTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613279 Paratanytarsus sp. water mite diet isolate 2981-BHL032417-GBD24973_24017-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGAATGAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGCTCTCCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613280 Paratanytarsus sp. water mite diet isolate 2993-BHL032417-GBD12052_20125-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR743912, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613281 Paratanytarsus sp. water mite diet isolate 3167-BHL032417-GBD23256_22270-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTTTTTTGGAGCTTGATCAGGTGTAGTAGGAACTTCTTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTGATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCGTCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613282 Paratanytarsus sp. water mite diet isolate 3195-BHL032417-GBD6112_12134-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613283 Paratanytarsus sp. water mite diet isolate 4524-BHL032417-GBD3673_14600-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACATCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCGTTAACTTTATTATTATCTAGCCCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613284 Paratanytarsus sp. water mite diet isolate 4537-BHL032417-GBD21832_23477-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTTGGTGCCTGATCAGGATTAGTAGGAACTTCCCTATGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATTCCTATTTTACTTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATAAAAGATTTTGACTTCATCCCCCCTCTTTAACTCGTTTACATTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613285 Paratanytarsus sp. water mite diet isolate 4538-BHL032417-GBD9580_6618-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCATGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCTGAACTAGGACTTCCTGGAACTTTTATTGGAGATGACCAAATTTGTAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTAATGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTCGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613286 Paratanytarsus sp. water mite diet isolate 4542-BHL032417-GBD20230_2557-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGTGCCTGATCATGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613287 Paratanytarsus sp. water mite diet isolate 4545-BHL032417-GBD12262_9256-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATTTTAATTCGAGCTGAACTAGGACATCCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTATTTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTATAACTCTATTACTGTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613288 Paratanytarsus sp. water mite diet isolate 4549-BHL032417-GBD21878_4613-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGCACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTGCTGCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613289 Paratanytarsus sp. water mite diet isolate 4554-BHL032417-GBD10085_7218-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATTTTAATTCGAGTTGAATTAGGACATCCTGGAACTTTTATTGGAGATGTCCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGTGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613290 Paratanytarsus sp. water mite diet isolate 4568-BHL032417-GBD20655_4474-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTCATTTTTGGTGCTTGGTCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTACCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCCTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR294834, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613291 Paratanytarsus sp. water mite diet isolate 4570-BHL032417-GBD28336_9727-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGCACTTCTTTAAGAATATTATTTCAAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613292 Paratanytarsus sp. water mite diet isolate 4580-BHL032417-GBD24373_15821-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTTTACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCACTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGTAGCCCCAGATACAGCTTTTCCTCGAATAAATAATATAAGTTTTGGACTTCGCCCCCCATCTTTAACTCTTCTTCATTCTAGTTCATGTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613293 Paratanytarsus sp. water mite diet isolate 4581-BHL032417-GBD7966_7215-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACTCTTTTACTATCTAGCACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613294 Paratanytarsus sp. water mite diet isolate 4591-BHL032417-GBD21397_13674-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTAGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTATTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613295 Paratanytarsus sp. water mite diet isolate 4592-BHL032417-GBD9277_6040-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGACCCAGATATAGCTTTTCCTCGAATAAATAAGATAAGATTTTGACTTAATCCCACCTCTTTAACGCGTTGACGGTCAAGGAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613296 Paratanytarsus sp. water mite diet isolate 4597-BHL032417-GBD9011_5618-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCCTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCATTAACCCTACTACTATCAAGAATAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613297 Paratanytarsus sp. water mite diet isolate 4603-BHL032417-GBD4853_15715-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTTGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613298 Paratanytarsus sp. water mite diet isolate 4606-BHL032417-GBD26974_13014-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACATCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGTAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613299 Paratanytarsus sp. water mite diet isolate 4611-BHL032417-GBD20272_22770-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTACATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTCGGACATCCTGGTTCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGTCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613300 Paratanytarsus sp. water mite diet isolate 4628-BHL032417-GBD25745_20821-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCCGATAAAGCTTTTCCCCGAAAAAATAAAAAAAGATTTTGACTTATTCCCCCCTCTCTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613301 Paratanytarsus sp. water mite diet isolate 4629-BHL032417-GBD8732_17947-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCATTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTATTACCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613302 Paratanytarsus sp. water mite diet isolate 4640-BHL032417-GBD22334_9334-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATTACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTACTACCACCATCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613303 Paratanytarsus sp. water mite diet isolate 4642-BHL032417-GBD16212_20595-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613304 Paratanytarsus sp. water mite diet isolate 4644-BHL032417-GBD17588_16726-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTGTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCCCGAATAAATAACATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTTTTTCTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613305 Paratanytarsus sp. water mite diet isolate 4649-BHL032417-GBD10917_25849-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACAACCTGGATCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGACTATTTCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCTCTAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613306 Paratanytarsus sp. water mite diet isolate 4653-BHL032417-GBD15194_24405-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTTGGAACTTCCTTAAAAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCTTTAATATTAGGAGCCCCTGATATAGCCTTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCCTCTTTAACTCTTCTTCTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613307 Paratanytarsus sp. water mite diet isolate 4655-BHL032417-GBD10414_11658-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGTCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTTTTCCCCCCTCTTTAACCCTATTACCATCAAATAGAATAGCGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613308 Paratanytarsus sp. water mite diet isolate 4656-BHL032417-GBD13555_9360-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGATCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGTGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACCCTTTTAATTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613309 Paratanytarsus sp. water mite diet isolate 4657-BHL032417-GBD11930_15262-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGCACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCATTAACCCTTCTACTATCGAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613310 Paratanytarsus sp. water mite diet isolate 4668-BHL032417-GBD12842_7569-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTTATTTTCGGTGCTTGATCAGTAATAGTAGGAACTTCCTTAAGTATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGACTACTTCCCCCATCTTTAACCCTTTTACTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613311 Paratanytarsus sp. water mite diet isolate 4670-BHL032417-GBD24948_23482-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGACATCCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCCTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613312 Paratanytarsus sp. water mite diet isolate 4671-BHL032417-GBD10786_17623-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTACATTATACTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCAGAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613313 Paratanytarsus sp. water mite diet isolate 4672-BHL032417-GBD22380_15426-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGTTTGATCAGGAATAGTAGGAACTTCCCTACGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACGTCCCCCCTCTTTAACACATTTACATGCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613314 Paratanytarsus sp. water mite diet isolate 4673-BHL032417-GBD5078_9666-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGAAATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACGTCCCCCCTCTTTAACTCTTTTTCAATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613315 Paratanytarsus sp. water mite diet isolate 4675-BHL032417-GBD19005_21589-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTTATTTTTGGTGCCTGATCAGGAATAGTAGGTACTTCTTTAAGAATATTAATTCGAGCTGAACTAGGACACCCTGGAACTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613316 Paratanytarsus sp. water mite diet isolate 4676-BHL032417-GBD2217_12808-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCCTGGTCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAAAATTAGGGGCCCCAGATACAGCTTTTCCCCGAATAAATAACATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613317 Paratanytarsus sp. water mite diet isolate 4677-BHL032417-GBD24948_14592-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTGGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613318 Paratanytarsus sp. water mite diet isolate 4681-BHL032417-GBD21943_14308-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTTATTTTTGGTGTCTGATCAGGAATAGTTGGAACTTTCCTTAGAATATTAATTCGAGCTGAACTAGCACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACACTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613319 Paratanytarsus sp. water mite diet isolate 4683-BHL032417-GBD26516_14485-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATACTTCACTTTTGGTGCCTGATCAGGAATAGTAGGTACTTCCCTAAGAATATTAATTCGAGCTGAACTCGGACATCCTGGATCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCGTCATTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613320 Paratanytarsus sp. water mite diet isolate 4692-BHL032417-GBD22308_7733-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTCGGAACTTCCTTAAGTATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613321 Paratanytarsus sp. water mite diet isolate 4693-BHL032417-GBD10503_22645-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGCACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTATTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613322 Paratanytarsus sp. water mite diet isolate 4696-BHL032417-GBD14864_6893-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAACTCGGACATCCTGGATCTTTTATTGAAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACCCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613323 Paratanytarsus sp. water mite diet isolate 4697-BHL032417-GBD21498_22261-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGCTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGAGTTAGACTTCTTCCCCCCACTGTAACTCAGGTACTTGCAAGTAGAAGAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613324 Paratanytarsus sp. water mite diet isolate 4702-BHL032417-GBD25818_8070-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACACCCTGGAACTTTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTTTTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTTCTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613325 Paratanytarsus sp. water mite diet isolate 4705-BHL032417-GBD24700_5976-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATGGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGGCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACTCTATTACTATCAAGCAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613326 Paratanytarsus sp. water mite diet isolate 4706-BHL032417-GBD20035_6545-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGTGCCTGATCTGGAATAGTCGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTACTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTTTTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCATTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613327 Paratanytarsus sp. water mite diet isolate 4708-BHL032417-GBD3587_12208-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCCTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613328 Paratanytarsus sp. water mite diet isolate 4711-BHL032417-GBD20660_2444-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTACTACCCCCATCTTTAACTCGATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613329 Paratanytarsus sp. water mite diet isolate 4714-BHL032417-GBD27571_13610-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGTCATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTACCTCTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR294834, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613330 Paratanytarsus sp. water mite diet isolate 4715-BHL032417-GBD26604_17048-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCCCTAAGTATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTGTGACTACTTCCCCCCTCTTTAACTCTTGTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613331 Paratanytarsus sp. water mite diet isolate 4716-BHL032417-GBD15690_24459-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATACTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTCTACCCCCCTCTTTAACTCTTTTACTTTCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613332 Paratanytarsus sp. water mite diet isolate 4717-BHL032417-GBD7711_9028-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGTAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTGCCTCCCTCTTTAACTTTATTACTGTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR285045, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613333 Paratanytarsus sp. water mite diet isolate 4718-BHL032417-GBD20064_8555-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATACTTATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTTTAACTCTGTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613334 Paratanytarsus sp. water mite diet isolate 4719-BHL032417-GBD25530_11795-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTTATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTGCCTTTAATATTAGGAGTCCCAGACATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613335 Paratanytarsus sp. water mite diet isolate 4721-BHL032417-GBD11148_13689-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGCTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTCTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACACTTTTACTAGCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613336 Paratanytarsus sp. water mite diet isolate 4723-BHL032417-GBD5946_20496-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATTTTAATTCGAGCTGAACTAGGACATCCTGGATCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613337 Paratanytarsus sp. water mite diet isolate 4727-BHL032417-GBD9563_23196-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAGCATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATACATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCATCTTTAACCCTTTTACTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613338 Paratanytarsus sp. water mite diet isolate 4728-BHL032417-GBD21138_11141-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTCATTTTTGGTGCTTGATCAGGTATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTATTACTATCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613339 Paratanytarsus sp. water mite diet isolate 4731-BHL032417-GBD13070_26867-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTTGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACACTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613340 Paratanytarsus sp. water mite diet isolate 4732-BHL032417-GBD18703_5051-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTCAGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTTCTTTCAAGCACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613341 Paratanytarsus sp. water mite diet isolate 4733-BHL032417-GBD24455_9158-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTACCTTTAATATTAGGAGTCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613342 Paratanytarsus sp. water mite diet isolate 4743-BHL032417-GBD25833_8180-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTAAACTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTTCTAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR293963, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613343 Paratanytarsus sp. water mite diet isolate 4744-BHL032417-GBD13076_8748-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATACTTCATTTTTGGTGCCTGATCAGGAATAATAGGAACTTCTCTAAGAATATTAATTCGAGCTAAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCATTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613344 Paratanytarsus sp. water mite diet isolate 4748-BHL032417-GBD15747_10073-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGTGCTTGATCTGGTATAGTAGGAACTTCCTTAAGTATATTAATTCGAGCTGAACTTGGACATCCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCATTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613345 Paratanytarsus sp. water mite diet isolate 4749-BHL032417-GBD5944_20475-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGACTACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGGGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613346 Paratanytarsus sp. water mite diet isolate 4750-BHL032417-GBD12384_26542-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCCCCAATAAAAAATATAAGATTTTGACCTCCTCCCCCCTCTTTAACCCCTTTTCCTTCCAGTAGAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613347 Paratanytarsus sp. water mite diet isolate 4752-BHL032417-GBD8288_24019-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGTGCCTGATCAGGGATAGTAGGAACTTCCTTAAGTATATTAATTCGAGCTGAACTAGGACAACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTCTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCCGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613348 Paratanytarsus sp. water mite diet isolate 4753-BHL032417-GBD27914_21157-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGCGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTGCTTCCCCCCGCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR295226, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613349 Paratanytarsus sp. water mite diet isolate 4755-BHL032417-GBD24071_11980-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATTTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGTTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTCTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613350 Paratanytarsus sp. water mite diet isolate 4756-BHL032417-GBD28353_9605-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACACCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTACCTTTAATACTAGGAGCCCCAGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR294834, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613351 Paratanytarsus sp. water mite diet isolate 4757-BHL032417-GBD3773_16835-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTCATTTTTGGTGCCTGATCAGGAATAGTCGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGTTTTGGGAACTGACTTCTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTTTTACTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613352 Paratanytarsus sp. water mite diet isolate 4761-BHL032417-GBD3639_10940-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTCTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTTTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR293963, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613353 Paratanytarsus sp. water mite diet isolate 4768-BHL032417-GBD26557_12918-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGTATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCCTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCGTTGACGTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613354 Paratanytarsus sp. water mite diet isolate 4774-BHL032417-GBD7988_14469-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGTATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGGCCAAATTTATAATATAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGACTGTTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACTCTTTTACTGTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613355 Paratanytarsus sp. water mite diet isolate 4775-BHL032417-GBD8741_3484-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACTCTTTTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613356 Paratanytarsus sp. water mite diet isolate 4779-BHL032417-GBD15754_11501-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCCTCTTTAACTCTTTTTCTTTCAAATAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613357 Paratanytarsus sp. water mite diet isolate 4781-BHL032417-GBD22510_23878-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGGGCCTGATTAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGTCATCCTGGAATTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613358 Paratanytarsus sp. water mite diet isolate 4785-BHL032417-GBD6235_20731-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGTTCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTATTTAACTCTATTACTATCAGGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613359 Paratanytarsus sp. water mite diet isolate 4787-BHL032417-GBD23418_23952-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCAGAACTAGGACATCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGACTTTTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAACATAAGATTTTGACTACTTCCCCCATCTTTAACCCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613360 Paratanytarsus sp. water mite diet isolate 4790-BHL032417-GBD21429_17552-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTTATTCGAGCGGAACTAGGATATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613361 Paratanytarsus sp. water mite diet isolate 4791-BHL032417-GBD28538_16275-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGTTTTGGAAATTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTTTAACTCTTTTACTTTCAAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613362 Paratanytarsus sp. water mite diet isolate 4794-BHL032417-GBD4608_8729-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAACATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAAATGATTATTGACTTTAATATTAGGAGCCCCCGATATAGCTTTTCATCGAATAAAAAAAAAAAGATTTTGACCTCTACCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613363 Paratanytarsus sp. water mite diet isolate 4798-BHL032417-GBD23620_15367-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGCATAGTAGGCACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTAGAACCTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCCATTTTAATCGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613364 Paratanytarsus sp. water mite diet isolate 4804-BHL032417-GBD25768_15943-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAACTAGGACATCCTGGTACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613365 Paratanytarsus sp. water mite diet isolate 4805-BHL032417-GBD4077_15306-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCCTTATATTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGTTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGGACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACTCTTCTTCTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613366 Paratanytarsus sp. water mite diet isolate 4809-BHL032417-GBD4289_19193-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGTGCCTGATCGGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTGATATTAGGAGCTCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACCCTTTTACTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613367 Paratanytarsus sp. water mite diet isolate 4811-BHL032417-GBD16270_25385-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTTGGTGCCTGATCAGGAATAATAGGAATTTCCTTAAGATTATTATTTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGTTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613368 Paratanytarsus sp. water mite diet isolate 4812-BHL032417-GBD18754_10753-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATACTTTATTTTTGGTGTCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTATTGTCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTCTACCCCCCTCTCTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613369 Paratanytarsus sp. water mite diet isolate 4813-BHL032417-GBD16493_14746-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGTAAACTGATTATTGCCTTTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTCTACTTTCTAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR293963, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613370 Paratanytarsus sp. water mite diet isolate 4814-BHL032417-GBD20325_7083-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTATGACATCCTGGAACTTTTATTGGAGATTACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCAGCTTTAACTCTATTATTTTCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613371 Paratanytarsus sp. water mite diet isolate 4816-BHL032417-GBD28482_16549-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTTATTCGGGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATATAATTGTTACAGCTCATGCATTTACTATAATTTTCTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613372 Paratanytarsus sp. water mite diet isolate 4819-BHL032417-GBD21242_20318-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATTTTAATTCGAGCTGAACTCGGTCATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGATTTGGGAACTGATTAGTGCCTTTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCGTCATTAACTTTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613373 Paratanytarsus sp. water mite diet isolate 4821-BHL032417-GBD16066_8982-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTTACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR294834, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613374 Paratanytarsus sp. water mite diet isolate 4824-BHL032417-GBD9277_8212-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGCACTTCTCTAAGAATTTTAATTCGAGCAGAATTAGGACATCCTGGCACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613375 Paratanytarsus sp. water mite diet isolate 4828-BHL032417-GBD9341_20031-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGTACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCTTCTTTAACTCTTTTACTTTCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613376 Paratanytarsus sp. water mite diet isolate 4836-BHL032417-GBD19482_11574-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTGTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGTAATTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACATCATCCCCCCTCTTTAACACGGTTCCGTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613377 Paratanytarsus sp. water mite diet isolate 4840-BHL032417-GBD19956_11498-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGTGCCTGATCAGGTATAGTAGGAACTTCCTTAAGAATATTTATTCGAGCTGAACTAGGACATCCTGGATCTTTTGTTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCCTTAACCCTATTACCAACAAGTAGAATAGCGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613378 Paratanytarsus sp. water mite diet isolate 4843-BHL032417-GBD25535_19733-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATACTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTGCCTCGAATAAATAATATAAGATATTGACTTCGTCCCCCCTCTTTAACACGAATACTGTCAAGTACAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613379 Paratanytarsus sp. water mite diet isolate 4847-BHL032417-GBD26843_21046-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACCTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAAATGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAAAATAAGATTTTGACTTCTTCCCCCCGCTTTAACTCGATTACAATCAAGTAGAATAGTTGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613380 Paratanytarsus sp. water mite diet isolate 4848-BHL032417-GBD14881_17005-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTCCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGAAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACATCATCCAACCGCTTTAACACTTTGACGTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613381 Paratanytarsus sp. water mite diet isolate 4850-BHL032417-GBD9340_8669-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGTACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGTCATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTTCCTTTAATATTAGGAGCCCCAGAAACAGCTTTTCCTCGAATAAATGATATAAGATTTTGACTTCCTCCCCCCTCATTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613382 Paratanytarsus sp. water mite diet isolate 4855-BHL032417-GBD23616_13007-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTTGGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTGCCTCGAATAAATAATATAAGAAATTGACTTCTTCCCCCCGCGTTAACACGATTACTGGCAAGTAGAAGAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613383 Paratanytarsus sp. water mite diet isolate 4858-BHL032417-GBD23118_6384-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCTGAGCTAGGCCATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTACTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAAGAAATAATATAAGATTTTGACTTCTTCCCCCCGCTTTAACACGATTACTTGCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613384 Paratanytarsus sp. water mite diet isolate 4859-BHL032417-GBD27256_14557-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR294834, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613385 Paratanytarsus sp. water mite diet isolate 4861-BHL032417-GBD18761_23329-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTTTACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATTGTTATACCTATTTTAATTGGAGGATTTGTGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTGCTGCCCCCCTCATTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613386 Paratanytarsus sp. water mite diet isolate 4862-BHL032417-GBD16694_12100-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCTCAGATATATCTTTTCCTCTAATAAATAATATAAGATTTTGACTTCATCAACCCTCTTTAACACTGTTACGTACAAGTAGAATAGTGCAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613387 Paratanytarsus sp. water mite diet isolate 4863-BHL032417-GBD4710_22519-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTCGGACACCCTGGTACTTTTATCGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCATTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613388 Paratanytarsus sp. water mite diet isolate 4866-BHL032417-GBD21209_22280-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTTCATTATATTTCATTTTTGGTGCCTGCTCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTGTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR293963, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613389 Paratanytarsus sp. water mite diet isolate 4867-BHL032417-GBD17319_8263-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGTATTTGGCAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCACTCTGTAACACGGTTACTGACAAGTAGAATAGTGCAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613390 Paratanytarsus sp. water mite diet isolate 4869-BHL032417-GBD3270_14678-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTACATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATGCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCATTAACTCTATTACTTTCAAGTACACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613391 Paratanytarsus sp. water mite diet isolate 4872-BHL032417-GBD13939_16841-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCGCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTCTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTACTACCCCCATCTCTTACTTTATTACTTTCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR293963, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613392 Paratanytarsus sp. water mite diet isolate 4880-BHL032417-GBD24290_9268-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGCACTTCTTTAAGAATATTAATTCGAGTTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACCCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613393 Paratanytarsus sp. water mite diet isolate 4881-BHL032417-GBD27467_10753-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTTTATTTCATTTTTGGTGCCTGAGCAGGAATAGTAGGCACTTCCCTAAGAATGTTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCGCTTTAACCCTTTTACTATCAAGTAGAACAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613394 Paratanytarsus sp. water mite diet isolate 4882-BHL032417-GBD11102_6800-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCTCTAAGAATACTTATTCGAGCAGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTCTAACTCTTCTTCTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613395 Paratanytarsus sp. water mite diet isolate 4887-BHL032417-GBD26492_22155-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCTTTATACTTCATTTTTGGTGCCTGATCCGGAATAGTAAGAACTTCCCTAAGAATACTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTTTTGTTACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613396 Paratanytarsus sp. water mite diet isolate 4890-BHL032417-GBD28459_18351-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCA--TCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613397 Paratanytarsus sp. water mite diet isolate 4892-BHL032417-GBD14437_12744-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTAAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCACCATCTCTAACTATATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613398 Paratanytarsus sp. water mite diet isolate 4895-BHL032417-GBD28549_15364-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACAACCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTCTAACTCTTTTACTTTCAAGTACAACAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613399 Paratanytarsus sp. water mite diet isolate 4896-BHL032417-GBD6901_14920-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGGCATACTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTTCTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613400 Paratanytarsus sp. water mite diet isolate 4901-BHL032417-GBD18915_26834-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATACTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTATGACATCCTGGAACATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATAATAATTTTTTTAATAGTTATACCTATTTTAATTGGAGGATTTGGTAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCACCCTCTTTAACCCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613401 Paratanytarsus sp. water mite diet isolate 4913-BHL032417-GBD8128_16293-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTGCCCTAAGAATATTAATTCGAGTTGAATTAGGACATCCTGGAACTTTTATAGGAGATGACCAAATTTATAATATACTTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTGTTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613402 Paratanytarsus sp. water mite diet isolate 4915-BHL032417-GBD6801_16142-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGACCCAGAGATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTGCATCCAAAGTCTTTAACTCGTTTACGTACAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613403 Paratanytarsus sp. water mite diet isolate 4917-BHL032417-GBD13753_8343-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGATTATATTTCATTTTTGATGCTTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGTATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACCTCTTCCCCCCTCTTTAACACTTTTACAATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613404 Paratanytarsus sp. water mite diet isolate 4918-BHL032417-GBD28650_11800-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGAGCCTGATCAGGTATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGACATGCTGGATCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATACTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTTCCTTTAATATTAGGAGCCCCAGACATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613405 Paratanytarsus sp. water mite diet isolate 4921-BHL032417-GBD25713_24965-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTTTATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTAGGACATGCTGGCACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACTCTTTTACTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613406 Paratanytarsus sp. water mite diet isolate 4922-BHL032417-GBD25854_13637-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTAGGTCATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACCCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613407 Paratanytarsus sp. water mite diet isolate 4924-BHL032417-GBD7905_19310-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGTTCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTGCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACGCTATTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR285494, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613408 Paratanytarsus sp. water mite diet isolate 4927-BHL032417-GBD19981_17553-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGTACTTCTCTAAGTATGTTAATTCGAGCTGAACTAGGACATCCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATGCCTATTTTAATTGGAGGATTTGGAAACTGATTTTTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCATTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613409 Paratanytarsus sp. water mite diet isolate 4928-BHL032417-GBD23110_17815-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGAGCCTGGTCAGGAATAGTCGGAACTTCCTTAAGTATATTAATTCGAGCAGAACTAGGACAACCTGGAACTTTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTTTTGCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGAATAAATAACATAAGATTTTGACTACTTCCCCCATCTTTAACCCTTCTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613410 Paratanytarsus sp. water mite diet isolate 4929-BHL032417-GBD26226_19102-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATCCTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTATGTATATTAATTCGAGCTGAACTAGGACATCCTAGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGGACTGATTATTGCCTTTAATATTAGGTGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGAGTTTGACTTCTTCCCCCCTCGTTAACTCTGGTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613411 Paratanytarsus sp. water mite diet isolate 4932-BHL032417-GBD27468_17600-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCAGAACTAGGACAACCTGGCACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGGTTTGGGAACTGATTATTGCCTTTAATATTAGGCGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613412 Paratanytarsus sp. water mite diet isolate 4936-BHL032417-GBD17551_26437-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCAGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCACTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGCATTTGGGAATTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCATTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613413 Paratanytarsus sp. water mite diet isolate 4939-BHL032417-GBD13838_16894-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGTGCCTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCAGAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACTCTTTTACTATCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613414 Paratanytarsus sp. water mite diet isolate 4949-BHL032417-GBD19820_3447-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTCATTTTTGGTGCTTGATCAGGTATAGTAGGAACTTCCTTAAGAGTATTTATTCGAGCTGAGCTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCTTTTACTTTCAAGTGGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613415 Paratanytarsus sp. water mite diet isolate 5025-BHL032417-GBD4192_17631-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACATTGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR272133, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613416 Paratanytarsus sp. water mite diet isolate 5037-BHL032417-GBD5118_15759-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGACTTATACCCTCGTCATTAACTTTACTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613417 Paratanytarsus sp. water mite diet isolate 5068-BHL032417-GBD13511_19455-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTAGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613418 Paratanytarsus sp. water mite diet isolate 5070-BHL032417-GBD13405_10417-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATATTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGTAGATGACCAAATTTATAATGTAATTGTTACAGTTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR292109, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613419 Paratanytarsus sp. water mite diet isolate 5142-BHL032417-GBD26760_15138-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCCTTAACTCTTTTACTTTCAAGTAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR757714, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613420 Paratanytarsus sp. water mite diet isolate 5206-BHL032417-GBD11600_8365-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCACTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATTTAGCTTTTCCTCGAATAAATAATATAAGATTTTGACCTCTCCCCCCATCCTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR282105, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613421 Paratanytarsus sp. water mite diet isolate 5228-BHL032417-GBD18257_17941-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATACTTTATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACAACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTCCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTTTAACTCTTTTTCTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613422 Paratanytarsus sp. water mite diet isolate 5232-BHL032417-GBD11100_15859-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR664189, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613423 Paratanytarsus sp. water mite diet isolate 5263-BHL032417-GBD28000_12377-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATACTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCCTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613424 Paratanytarsus sp. water mite diet isolate 5288-BHL032417-GBD2161_12220-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACGGGTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCACTAATCCTATTGGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613425 Paratanytarsus sp. water mite diet isolate 5300-BHL032417-GBD4981_16790-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCGGAACTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCCTTTCCACGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613426 Paratanytarsus sp. water mite diet isolate 5316-BHL032417-GBD8653_14848-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGTACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613427 Paratanytarsus sp. water mite diet isolate 5322-BHL032417-GBD10891_26835-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGAGCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGACTTAACAATTTAAGATTTTGACTTCTACCACCTTCACTAATCCTACTGGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613428 Paratanytarsus sp. water mite diet isolate 5328-BHL032417-GBD12651_6835-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATCTTAGGAGTTTGAGCTGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCGCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613429 Paratanytarsus sp. water mite diet isolate 5335-BHL032417-GBD18980_19900-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTAGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAGTTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATCATATAAGTTTTTGGCATTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613430 Paratanytarsus sp. water mite diet isolate 5349-BHL032417-GBD25659_23472-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTTATTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGATCTTTTATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613431 Paratanytarsus sp. water mite diet isolate 5371-BHL032417-GBD19156_18511-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCGTTATACTTCATTTTCGGTGCCCGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCAGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGAAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR282105, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613432 Paratanytarsus sp. water mite diet isolate 5387-BHL032417-GBD12938_11165-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGCACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACACCCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTACCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACCCTGTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613433 Paratanytarsus sp. water mite diet isolate 5398-BHL032417-GBD18263_23342-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGATCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGCGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613434 Paratanytarsus sp. water mite diet isolate 5409-BHL032417-GBD5943_7514-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGAGCTCGATCAGGAATAGTGGGAACTTCCTTAAGAATACTAATTCGAGCTGAACTAGGACATCCCTGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGAAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613435 Paratanytarsus sp. water mite diet isolate 5421-BHL032417-GBD3902_9283-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAGCTTCCCTAAGAATATTAATTCGAGCTAAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTCTAATATTAGGAGCCCCAGATATAGCTTTTCCTTGAATAAATAATATAAGATTTTGACTTCTTCCCCCATCTTTAACTCTTCTTCTTTCTAGTACATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613436 Paratanytarsus sp. water mite diet isolate 5423-BHL032417-GBD6978_14988-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.1% identical to accession ID KR757714, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613437 Paratanytarsus sp. water mite diet isolate 5425-BHL032417-GBD6592_19874-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGTGCCTGATCAGGAGTAGTAGGAACTTCCCTAAGAATATTAATTCGAGGAGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCATTAACCCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613438 Paratanytarsus sp. water mite diet isolate 5450-BHL032417-GBD7831_9145-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCCGATCAGGAATAGTGGGAACTTCCCTAAGAATTTTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGAAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTTCTTCTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613439 Paratanytarsus sp. water mite diet isolate 5459-BHL032417-GBD24817_18843-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTATTTTTGGCGCCTGATCAGGAATAGTCGGAACTTCTCTAAGAATATTTATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGGCTTCTTCCCCCCTCTTTAACTCTTCTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613440 Paratanytarsus sp. water mite diet isolate 5474-BHL032417-GBD24476_22082-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATACTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTGTAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCATCTTTAACCCTTCTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613441 Paratanytarsus sp. water mite diet isolate 5482-BHL032417-GBD24789_18849-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCCTGATCTGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACTTTATTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613442 Paratanytarsus sp. water mite diet isolate 5521-BHL032417-GBD24298_20633-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATATTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGATATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGACATAGCTTTCCCCCGAATAAATAATATAAGCTTTTGGCTTTTACCCCCGTCATTAACTTTACTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613443 Paratanytarsus sp. water mite diet isolate 5522-BHL032417-GBD26233_12032-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCCTTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTCGGACATCCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGTTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCGTCATTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613444 Paratanytarsus sp. water mite diet isolate 5866-BHL032417-GBD18842_18539-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTATTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTCCCCCCGTCTTTAACTTTATTACTATCAAGCAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613445 Paratanytarsus sp. water mite diet isolate 5984-BHL032417-GBD12082_11340-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCACACTAGTGGAAAATGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613446 Paratanytarsus sp. water mite diet isolate 6362-BHL032417-GBD18838_4715-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATTTTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCCTCTTTAACTCTTCTTCTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR772535, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613447 Paratanytarsus sp. water mite diet isolate 6534-BHL032417-GBD20361_7108-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAACTGATTATTTCCTTTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACCTCCCCCTTCTTTAACTCTTCTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR293963, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613448 Paratanytarsus sp. water mite diet isolate 6550-BHL032417-GBD21518_19487-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCCTCTTTAACTCTTCTTCTGTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613449 Paratanytarsus sp. water mite diet isolate 6687-BHL032417-GBD18434_8472-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTTGGTACCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTATAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613450 Paratanytarsus sp. water mite diet isolate 6698-BHL032417-GBD12847_4463-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATCTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613451 Paratanytarsus sp. water mite diet isolate 6713-BHL032417-GBD7579_22841-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGATGCCTGATCAGGAATAGTCGGAACTTCCCTAAGTATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATGTTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTCTACTTTCAAGTAGAATAGTGGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613452 Paratanytarsus sp. water mite diet isolate 6716-BHL032417-GBD10886_10613-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGACAACCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCCCGAATAAAAAATAAAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACGTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613453 Paratanytarsus sp. water mite diet isolate 6722-BHL032417-GBD23307_27017-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATACTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTTATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613454 Paratanytarsus sp. water mite diet isolate 6727-BHL032417-GBD27804_10522-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAAATGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCATTTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATAAAAGATTTTGACGTCTTCCCCACTCTTGAACACGTTTACTTTCAAGTAGAATAGTGGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613455 Paratanytarsus sp. water mite diet isolate 6729-BHL032417-GBD21088_27589-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGTTGAACTAGGACATCCTGGCACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613456 Paratanytarsus sp. water mite diet isolate 6730-BHL032417-GBD23284_18627-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCAGAATTATGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAAGATTTGGGAACTGAATATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAAAAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613457 Paratanytarsus sp. water mite diet isolate 6737-BHL032417-GBD19701_11050-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGTGCCTGACCAGGAATAGTAGAACCTTCTTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGTTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613458 Paratanytarsus sp. water mite diet isolate 6739-BHL032417-GBD7986_23602-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613459 Paratanytarsus sp. water mite diet isolate 6742-BHL032417-GBD11487_8745-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCACCCTCTTTAACACTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613460 Paratanytarsus sp. water mite diet isolate 6747-BHL032417-GBD7525_7766-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATCAAGAATGCTTATTCGAGCAGAATTAGGACGACTCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACCTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.4% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613461 Paratanytarsus sp. water mite diet isolate 6750-BHL032417-GBD25227_18893-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATTTTAATTCGAGCTGAATTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTTCCTTTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613462 Paratanytarsus sp. water mite diet isolate 6753-BHL032417-GBD23964_22497-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGCACTTCCCTAAGAATATTAATTCGAGCTGAACTCGGACATCCTGGAACATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613463 Paratanytarsus sp. water mite diet isolate 6761-BHL032417-GBD21104_18404-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTTATTTTTGGTGCCTGATCCGGAATAATAGGAACTTCCTTAAGAATATTTATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTTTTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613464 Paratanytarsus sp. water mite diet isolate 6763-BHL032417-GBD16122_24434-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCTGAACTCGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACTCTTCTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613465 Paratanytarsus sp. water mite diet isolate 6770-BHL032417-GBD5682_21260-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCAGAACTAGGACATGCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613466 Paratanytarsus sp. water mite diet isolate 6771-BHL032417-GBD25858_17849-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCCTTAAGTATATTAATTCGAGCAGAACTAGGACACCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGTTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTTTTACTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613467 Paratanytarsus sp. water mite diet isolate 6772-BHL032417-GBD17192_21997-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGTCTGATCAGGAATAGTAGGTACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTGTGACCACGTCCCCCCACTTTAACACTTTTACAATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613468 Paratanytarsus sp. water mite diet isolate 6775-BHL032417-GBD29403_17173-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAGTTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCGGTAACGCAGGGACGGGCAAGGAGAAGAGGGGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613469 Paratanytarsus sp. water mite diet isolate 6776-BHL032417-GBD12112_20181-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATCTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTCTAACCCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613470 Paratanytarsus sp. water mite diet isolate 6782-BHL032417-GBD12212_8255-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTTGGTGCCTGACCAGGAATAGTAGGAACTTCCCTAAGAATATTATTTCGCGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGAAGCCCCAGATATAGCTTTTCCTCGAATAAATAAAATAAGATTTTGACTTCTGCCCCCCTCTTTAACGCTTTTACATTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613471 Paratanytarsus sp. water mite diet isolate 6786-BHL032417-GBD8389_6238-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAAGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAATTTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCATCCACCCTCTTGAACTCTTTTACTGGCAAGTAGAATAGTGGAAAATGGAGATGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613472 Paratanytarsus sp. water mite diet isolate 6788-BHL032417-GBD6667_25949-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTTATTTTCGGTGTCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTCTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAAAAAATAATATAAGATTTTGACTGCTTCCCCCCTCATTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613473 Paratanytarsus sp. water mite diet isolate 6792-BHL032417-GBD12420_3886-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCTTAAAAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTTCTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613474 Paratanytarsus sp. water mite diet isolate 6794-BHL032417-GBD20006_8060-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGTGACTGATCAGGAATAGTAGGAACTTCTCTAAGAATTTTAATTCGAGCTGAACTAGGACATCCTGGAACATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACTCCTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613475 Paratanytarsus sp. water mite diet isolate 6801-BHL032417-GBD18792_24304-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGGACTTCTTTAAGAATATTAATCCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTACTACCACCATCTTTAACTCTATTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613476 Paratanytarsus sp. water mite diet isolate 6803-BHL032417-GBD5264_12561-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCGTTATATTTTATTTTTGGGGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCTGAGCTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTCACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613477 Paratanytarsus sp. water mite diet isolate 6806-BHL032417-GBD16844_21154-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTATTTTTGGAGCCTGATCAGGAATAGTCGGAACTTCCTTAAGTATACTAATTCGAGCTGAATTAGGACACCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCATCTTTAACCCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613478 Paratanytarsus sp. water mite diet isolate 6809-BHL032417-GBD13779_27712-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCGTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCACTTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613479 Paratanytarsus sp. water mite diet isolate 6814-BHL032417-GBD9351_20050-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613480 Paratanytarsus sp. water mite diet isolate 6815-BHL032417-GBD25297_24515-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCTTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATATTGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613481 Paratanytarsus sp. water mite diet isolate 6818-BHL032417-GBD25462_19545-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCCGGAACTTTTATTGGAGATGACCAATTTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613482 Paratanytarsus sp. water mite diet isolate 6821-BHL032417-GBD20743_26325-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACATCTCATGCTTTTATTATAATTTTTTTCATAGTTATCCCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCCTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAATGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613483 Paratanytarsus sp. water mite diet isolate 6824-BHL032417-GBD16797_28086-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTTGGTGCCTGATCAGGAATACTAGGAACTTCCCTAAGATTATTATTTCGAGCTGAACTAGGACATCCTGAAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTCTATTTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTATCAAATAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613484 Paratanytarsus sp. water mite diet isolate 6826-BHL032417-GBD23841_24125-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGTAACTTCCTTAAGAATCTTAATTCGAGCCGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613485 Paratanytarsus sp. water mite diet isolate 6827-BHL032417-GBD5273_14979-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTCGGTGCCTGATCGGGAATAGTGGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCATTAACCCTTTTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613486 Paratanytarsus sp. water mite diet isolate 6828-BHL032417-GBD26331_13188-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGTCCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATCGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACCACTTCCCCCCTCTTTAACTCTATTACTATCAAGTGGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613487 Paratanytarsus sp. water mite diet isolate 6831-BHL032417-GBD4964_11447-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAACTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACCTCATTACTATCAAGGAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613488 Paratanytarsus sp. water mite diet isolate 6836-BHL032417-GBD17203_21977-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGTGTCTGATCAGGTATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613489 Paratanytarsus sp. water mite diet isolate 6837-BHL032417-GBD15877_18507-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTCATTTTTGGTGCCTGATCAGGTATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATAGGAGGGTTTGGGAACTGATTATTGCCTTTAATATTAGGTGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCTATTACCATCAAGTAGAATAGCGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613490 Paratanytarsus sp. water mite diet isolate 6841-BHL032417-GBD15863_27895-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCCTCTTTAACTCTTCTTCTTTCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613491 Paratanytarsus sp. water mite diet isolate 6842-BHL032417-GBD24574_18986-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGACATCCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCATTAACTCTTTTACTATCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613492 Paratanytarsus sp. water mite diet isolate 6844-BHL032417-GBD20401_17998-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGACATCCTGGTTCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACTCTATTACTATCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613493 Paratanytarsus sp. water mite diet isolate 6847-BHL032417-GBD17232_8600-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGACCCAGATATAGCTTTTCCTCGAATAAAGAATATAAGATTTTGACTTCTTCACACCTCTTTAACGCGGTGACGTTCAAGTAGAATAGTGGAAAATGGCGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613494 Paratanytarsus sp. water mite diet isolate 6848-BHL032417-GBD26107_7878-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTTTACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAATAATACTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTGCTGCTCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613495 Paratanytarsus sp. water mite diet isolate 6849-BHL032417-GBD6185_5581-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTCGGTGCCTGATCAGGAATAGTGGGCACTTCCCTAATAATATTAATTCGAGCTGAGTTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACACTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613496 Paratanytarsus sp. water mite diet isolate 6852-BHL032417-GBD19005_11919-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAGTTGGAGGATTTGGAAATTGATTATTACCTCTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAGAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR294834, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613497 Paratanytarsus sp. water mite diet isolate 6861-BHL032417-GBD25889_7132-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCTAAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR772535, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613498 Paratanytarsus sp. water mite diet isolate 6863-BHL032417-GBD24867_22202-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCCAAGAATATTAATTCGAACTGAACTAGCACATCTTGGAACATTTATTGGAGATGACCAAATTTATAATGTACTTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTACCTTTAAGATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCTTTTACTTTCAAGTAGAATAGTGGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR294834, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613499 Paratanytarsus sp. water mite diet isolate 6865-BHL032417-GBD21832_16983-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATACTTCATTTTTGGTGCCTGATCAGGTATAGTAGGAACTTCCCTGAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTGTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCTATTACCATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613500 Paratanytarsus sp. water mite diet isolate 6868-BHL032417-GBD15869_11606-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGAGCCTGATCAGGCATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATACTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTATTATAATTTTTTTCATAGTTATGCCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCATTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613501 Paratanytarsus sp. water mite diet isolate 6869-BHL032417-GBD20393_21630-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGTTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACCCTATTTCTATCAAATACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613502 Paratanytarsus sp. water mite diet isolate 6870-BHL032417-GBD11450_27299-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCTGAACTAGGACACCCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTATAGCTCATGCTTTTATTATAATTTTTTTCATAGTGATACCTATTTTAATTGGGGGATTTGGGAATTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613503 Paratanytarsus sp. water mite diet isolate 6872-BHL032417-GBD28145_17869-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCAGTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGTAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGATGATTTGGGAACTGATTATTGCCTTTAATACTCAGAGCCCCAGATATAGCTTTTCCTCGACAAAATAATATAAGATTTTGACTTCTCCCCCCCACTTTAACTCTTTTACTTTCAAGTAGAATAGAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613504 Paratanytarsus sp. water mite diet isolate 6879-BHL032417-GBD8154_6755-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTAATTGGAGACGAACAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613505 Paratanytarsus sp. water mite diet isolate 6883-BHL032417-GBD9769_10954-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATACTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCTGAATTAGGATATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTCCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTCTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR772535, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613506 Paratanytarsus sp. water mite diet isolate 6884-BHL032417-GBD5097_12300-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAAATCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCTTTTAATATTAGGAGCCCCAGATAAAGCTTTCCCTCGAAAAAAAAAAATAAGATTTTGCCTTCTTCCCGCCTCTTTAACTCTTTTACTTTCAAATAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613507 Paratanytarsus sp. water mite diet isolate 6889-BHL032417-GBD18233_13206-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCAGAACTAGGACATCCTGGATCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613508 Paratanytarsus sp. water mite diet isolate 6890-BHL032417-GBD14874_13165-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTAAATTAGGACATCCTGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGTGGATTTGGAAACTGATTATTGCCTTTAATATTAGGTGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACACTATTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613509 Paratanytarsus sp. water mite diet isolate 6891-BHL032417-GBD14128_20383-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGACCCAGATATAGCTTTTCCTCGACTAAATAATATAAGATTTTGACTGCATCCCACCTCTGTAACACTGTTCCTTTCAAGTAGAATAGTGGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613510 Paratanytarsus sp. water mite diet isolate 6893-BHL032417-GBD15127_6502-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGCAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTAGTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGGTTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613511 Paratanytarsus sp. water mite diet isolate 6894-BHL032417-GBD19565_11065-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTCGGAACTTCTTTAAGTTTACTAAATCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGCTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTAGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613512 Paratanytarsus sp. water mite diet isolate 6895-BHL032417-GBD25239_19789-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATGCTGGATCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGTTTTGGAAAATGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613513 Paratanytarsus sp. water mite diet isolate 6897-BHL032417-GBD13482_11923-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACTCTATTACTATCAAACAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613514 Paratanytarsus sp. water mite diet isolate 6902-BHL032417-GBD7706_24257-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCTTGATCAGGAATAGTGGGAACTTCCTTAAGAATCTTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTTTCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613515 Paratanytarsus sp. water mite diet isolate 6903-BHL032417-GBD13915_21788-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGACAAAGATATAGCTTTTCCTCCAATAAATAATAAAAGATTTTGACTTCATCACCCCTCTTTAAAACTGTTACTTTCAAGTAGAAGAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613516 Paratanytarsus sp. water mite diet isolate 6907-BHL032417-GBD7016_10364-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGAACCTGATCAGGAATAGTTGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTCTTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTTCTTCTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613517 Paratanytarsus sp. water mite diet isolate 6909-BHL032417-GBD22050_14873-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATTAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGTATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAACAATATAAGATTTTGACTACTACCCCCCTCTTTAACCCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613518 Paratanytarsus sp. water mite diet isolate 6910-BHL032417-GBD25889_22922-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGTCATACTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTACTTCCTTTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613519 Paratanytarsus sp. water mite diet isolate 6916-BHL032417-GBD21224_23101-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTACCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAAGAGCCCCAGAGATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCAGCACCCCGCTTTAACGCGGTTACTGTCAAGTAGAATAGTGGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613520 Paratanytarsus sp. water mite diet isolate 6919-BHL032417-GBD12768_6863-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613521 Paratanytarsus sp. water mite diet isolate 6920-BHL032417-GBD22606_17627-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTCATTTTTGGAGCCTGATCAGGCATAGTAGGAACTTCCCTAAGAATTTTAATTCGAGCTGAACTAGGACATACTGGTACCTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613522 Paratanytarsus sp. water mite diet isolate 6923-BHL032417-GBD22380_24968-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCTTAATAATGTTTATTCGAGCTGAGCTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTCCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613523 Paratanytarsus sp. water mite diet isolate 6928-BHL032417-GBD23017_16577-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATACTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCATTAAGAATATTAATTCGAGCAGAACTAGGACATCCTGGAACTTTAATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTCTAACTCTTTTACTTTCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613524 Paratanytarsus sp. water mite diet isolate 7390-BHL032417-GBD20787_10658-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAGGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCATTAATATTAGGAGCCCCAGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGACTATTACCACCATCTCTTACTCTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613525 Paratanytarsus sp. water mite diet isolate 7556-BHL040517-GBD22351_18122-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613526 Paratanytarsus sp. water mite diet isolate 7581-BHL040517-GBD6195_9414-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGTTTGATCCGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTCTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613527 Paratanytarsus sp. water mite diet isolate 7591-BHL040517-GBD17337_8644-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR757714, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613528 Paratanytarsus sp. water mite diet isolate 7700-BHL040517-GBD27286_12323-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.9% identical to accession ID KR757714, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613529 Paratanytarsus sp. water mite diet isolate 7723-BHL040517-GBD7444_14852-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTATAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613530 Paratanytarsus sp. water mite diet isolate 7856-BHL040517-GBD15750_3054-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATGTAAGATTTTGACTTCTTCACCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KM905578, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613531 Paratanytarsus sp. water mite diet isolate 7879-BHL040517-GBD11384_22287-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAACTAGGACATCCCGGAACTTTAATTGGAGATGACCAAATTTATAATGTAATTGTTATAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCTTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR757714, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613532 Paratanytarsus sp. water mite diet isolate 7889-BHL040517-GBD17365_3170-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTTTTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613533 Paratanytarsus sp. water mite diet isolate 7909-BHL040517-GBD27107_13005-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTTATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGTATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613534 Paratanytarsus sp. water mite diet isolate 7912-BHL040517-GBD3839_21402-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCTTTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGTATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613535 Paratanytarsus sp. water mite diet isolate 7924-BHL040517-GBD27171_18298-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGCTCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGGTACAGCTCATGCATTTATTATAATTTTTTTCATAATTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613536 Paratanytarsus sp. water mite diet isolate 7930-BHL040517-GBD16749_28882-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCTGAACTAGAACATCCTGGATCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613537 Paratanytarsus sp. water mite diet isolate 7964-BHL040517-GBD16825_13080-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCCTTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTAATGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613538 Paratanytarsus sp. water mite diet isolate 7966-BHL040517-GBD8586_24625-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGTTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACACGGAACTTTCATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTCTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTACTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613539 Paratanytarsus sp. water mite diet isolate 8014-BHL040517-GBD29419_16874-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCGGTAACGCGGGGACGGGCAAGGAGAAGAGGGGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613540 Paratanytarsus sp. water mite diet isolate 8056-BHL040517-GBD26604_20223-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTTGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613541 Paratanytarsus sp. water mite diet isolate 8088-BHL040517-GBD13963_27415-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGAGTCTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCAGAACTAGGACATCCTGGATCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613542 Paratanytarsus sp. water mite diet isolate 8097-BHL040517-GBD6169_5132-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTCGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACACCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGTGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCTCCTCTTTAACCCTTTTACTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613543 Paratanytarsus sp. water mite diet isolate 8185-BHL040517-GBD27903_13362-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGTGTCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGTTGAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613544 Paratanytarsus sp. water mite diet isolate 8205-BHL040517-GBD19224_28586-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAAGAATAGTGGAAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTAGTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATT-CCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613545 Paratanytarsus sp. water mite diet isolate 8234-BHL040517-GBD12420_24263-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCAGTGCCTGATCAGGAATAGTGGGAACTTCCATAAGAATATTAATTCGAGCTGAACTAGGACGTCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGGCTTGTCCCCCTAATACTTGGAGCACCTCACATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613546 Paratanytarsus sp. water mite diet isolate 8257-BHL040517-GBD4325_16581-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTTATTTTCGGAGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATTTTAATTCGAGCAGAACTCGGACATCCCGGATCTTTTATCGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613547 Paratanytarsus sp. water mite diet isolate 8287-BHL040517-GBD3712_20509-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGAACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATGGTTATACCAATTCTAATTGGAGGATTCGGACATTGATTAGTCCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCGATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613548 Paratanytarsus sp. water mite diet isolate 8303-BHL040517-GBD2207_13903-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTCCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAGTATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTTCTTCCCCCCTCTTTTACTCTTCTTCTTTCTAAATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613549 Paratanytarsus sp. water mite diet isolate 8342-BHL040517-GBD8630_20805-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATTTTAATTCGAGCTGAACTAGGACATCCTGGCACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613550 Paratanytarsus sp. water mite diet isolate 8889-BHL032417-GBD12567_26367-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTACTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613551 Paratanytarsus sp. water mite diet isolate 8985-BHL032417-GBD21335_6956-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGACTTTTACCCCCCTTTCGTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613552 Paratanytarsus sp. water mite diet isolate 9013-BHL032417-GBD13377_17080-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGAAATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACCTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613553 Paratanytarsus sp. water mite diet isolate 9232-BHL032417-GBD7391_20185-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGTAGAGCTGGGTCGACCTGGAACTTTTATTGGCGATGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTACTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR628998, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613554 Paratanytarsus sp. water mite diet isolate 9344-BHL032417-GBD25076_16158-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAGATTGACTTGTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGAATAAATAATATAAGTTTTTGATTACTACCCCCATCTTTAACCCTACTTCTATCAAGAACATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613555 Paratanytarsus sp. water mite diet isolate 9379-BHL032417-GBD13648_7897-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACTTCCTTAAGTATATTAATTCGAGCAGAATTAGGTCACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTCTACCATTAATATTAGGAGCCCCCGATATAGCTGTTCCACGAATAAATAATATAAGATTTTGATTACTACCCCCATCTTTAACCCTACTACTATCAAGAAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613556 Paratanytarsus sp. water mite diet isolate 9394-BHL032417-GBD23364_15047-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATAGGAACTTCTTTAAGTATATTAATTCGAACAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGACTATTACCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCATCTTTAACCCTACTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613557 Paratanytarsus sp. water mite diet isolate 9401-BHL032417-GBD16597_28998-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCCTTATATTTTATTTTCGGAGCTTGATCAGGAATAATAGGAACATCCCTAAGTATATTAATTCGAGCAGAACTAGGACACCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTACTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613558 Paratanytarsus sp. water mite diet isolate 9657-BHL032417-GBD23719_9027-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAAAATTAGGGCACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR740890, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613559 Paratanytarsus sp. water mite diet isolate 9704-BHL032417-GBD28220_10086-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTCGGTGTTTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGAAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATATCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCTTCTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613560 Paratanytarsus sp. water mite diet isolate 9879-BHL040517-GBD15524_15801-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATATTATTTTTGGTGCTTGGTCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.4% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613561 Paratanytarsus sp. water mite diet isolate 9890-BHL040517-GBD23261_13306-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCATTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613562 Paratanytarsus sp. water mite diet isolate 9905-BHL040517-GBD8985_3710-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTATGTTTTACTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR757714, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613563 Paratanytarsus sp. water mite diet isolate 9910-BHL040517-GBD17839_13581-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATT-CCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613564 Paratanytarsus sp. water mite diet isolate 9922-BHL040517-GBD4910_11911-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATACGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTCTAATTGGAGGATTTGGGAACTGATTATTGCATTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613565 Paratanytarsus sp. water mite diet isolate 9924-BHL040517-GBD5902_21175-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613566 Paratanytarsus sp. water mite diet isolate 9935-BHL040517-GBD27644_10852-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGATATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCA--TCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613567 Paratanytarsus sp. water mite diet isolate 9945-BHL040517-GBD23039_5545-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTTCATTATACTTCATTTTCGGTGTCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR292109, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613568 Paratanytarsus sp. water mite diet isolate 9968-BHL040517-GBD3940_8398-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGCGCCTGATCTGGGATAATAGGGACTTCTCTAAGAATGCTTGTTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR757714, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613569 Paratanytarsus sp. water mite diet isolate 9998-BHL040517-GBD13902_10229-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGATATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTGTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR292109, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613570 Paratanytarsus sp. water mite diet isolate 10002-BHL040517-GBD25626_11941-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCTGAACTAGGATATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAACTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCGTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613571 Paratanytarsus sp. water mite diet isolate 10027-BHL040517-GBD13436_16963-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCACGGATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613572 Paratanytarsus sp. water mite diet isolate 10063-BHL040517-GBD4647_17312-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTACTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAAGAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTCACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613573 Paratanytarsus sp. water mite diet isolate 10082-BHL040517-GBD6386_8884-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCCTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID KR772535, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613574 Paratanytarsus sp. water mite diet isolate 10095-BHL040517-GBD27618_20242-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGTGCTTGACCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGTTGAATTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279360, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613575 Paratanytarsus sp. water mite diet isolate 10137-BHL040517-GBD13438_27681-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGGATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCATTTAATATTAGGAGCCCCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613576 Paratanytarsus sp. water mite diet isolate 10143-BHL040517-GBD15143_22806-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGTCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCAGGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613577 Paratanytarsus sp. water mite diet isolate 10170-BHL040517-GBD8103_11861-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTGATTCGAGCTGAACTAGGATATCCCGGAACTTTTATTGGAGGTGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGTCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613578 Paratanytarsus sp. water mite diet isolate 10182-BHL040517-GBD26306_6749-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATACTTTATTTTTGGTGCTTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGATATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTCCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613579 Paratanytarsus sp. water mite diet isolate 10197-BHL040517-GBD19976_20407-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTACTACCACCATCTCTAACTTTATTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613580 Paratanytarsus sp. water mite diet isolate 10206-BHL040517-GBD5306_9351-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGACTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAGTTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGA-TTATTACCCCCTCCATTAAC---CTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.7% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613581 Paratanytarsus sp. water mite diet isolate 10235-BHL040517-GBD22255_12276-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCAGTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATTTTAATTCGAGCTGAACTAGGATATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTCGTAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACACTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613582 Paratanytarsus sp. water mite diet isolate 10250-BHL040517-GBD19268_3834-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTACATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATACTAATTCGAGCTGAACTAGGACATCCCGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTGCCCCCCTCTTTAACTTTATTACTTTCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613583 Paratanytarsus sp. water mite diet isolate 10257-BHL040517-GBD22566_25638-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGTGCTTGATCAGGTATAGTGGGAACTTCTCTAAGTATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613584 Paratanytarsus sp. water mite diet isolate 10266-BHL040517-GBD3441_16870-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACATTATTTTTCGGGGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATAGTAGTGCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTTGAGGATTTGGGACCTGATTATTGCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTCAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613585 Paratanytarsus sp. water mite diet isolate 10270-BHL040517-GBD21394_10628-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTCATTTTCGGTGCCTGATCAGGGATAGTGGGCACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGTCATCCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613586 Paratanytarsus sp. water mite diet isolate 10272-BHL040517-GBD11868_16128-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTCGGAGCCTGATCAGGAATAGTGGGAACTTCTCTAAGAATATTAATTCGAGCTGAATTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACTTTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613587 Paratanytarsus sp. water mite diet isolate 10280-BHL040517-GBD16456_14830-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTTATTTTCGGTGCTTGATCAGGAATAGTGGGAACTTCCTTAAGAATACTTATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTTTTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613588 Paratanytarsus sp. water mite diet isolate 10289-BHL040517-GBD14055_6680-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATACTTTATTTTTGGTGCTTGATCAGGAATAGTCGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCATTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAACATAAGATTTTGACTTCTTCCCCCATCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613589 Paratanytarsus sp. water mite diet isolate 10303-BHL040517-GBD23130_8936-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGACTTGAACTAGGACACCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCATTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613590 Paratanytarsus sp. water mite diet isolate 10314-BHL040517-GBD19174_8296-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCTCTAAGAATTTTAATTCGAGCTAAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCGTCATTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613591 Paratanytarsus sp. water mite diet isolate 10328-BHL040517-GBD11124_11257-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGATCATTATATTTTATTTTCGGAGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTCGGACATCCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613592 Paratanytarsus sp. water mite diet isolate 10342-BHL040517-GBD9242_24118-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACTTCATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCCTTAAGAATATTTATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGTAACTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTCTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613593 Paratanytarsus sp. water mite diet isolate 10354-BHL040517-GBD25709_23873-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGCAACTTCTCTAAGAATTTTAATTCGAGCTGAACTAGGACATCCCGGATCTTTTATTGGAGATGACCAAATTTATATTGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613594 Paratanytarsus sp. water mite diet isolate 10359-BHL040517-GBD24096_5288-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACCTCTTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATCATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCATTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613595 Paratanytarsus sp. water mite diet isolate 10360-BHL040517-GBD18091_5823-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR282105, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613596 Paratanytarsus sp. water mite diet isolate 10387-BHL040517-GBD26653_22072-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGCACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613597 Paratanytarsus sp. water mite diet isolate 10401-BHL040517-GBD21702_2686-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTAGAGATGACCAAATTTATAATGTAATTGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATGGCTTTTCCTCGAATAGATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613598 Paratanytarsus sp. water mite diet isolate 10409-BHL040517-GBD22512_22631-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGATTTTGACTGCTGCCCCCATCATTAACTCTATTATTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613599 Paratanytarsus sp. water mite diet isolate 10416-BHL040517-GBD23980_14171-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTCATTTTCGGTGCCTGATCAGGTATAGTGGGTACTTCCTTAAGAATTTTAATTCGAGCTGAACTAGGTCATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTATTATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613600 Paratanytarsus sp. water mite diet isolate 10425-BHL040517-GBD28578_13815-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTCGGAACTTCCTTAAGTATACTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613601 Paratanytarsus sp. water mite diet isolate 10430-BHL040517-GBD25301_25141-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGAGCCTGATCAGGAATAGTGGGAACTTCTTTAAGAATATTAATTCGAGCTGAACTAGGACATGCCGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTATAGTTATACCTATTCTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613602 Paratanytarsus sp. water mite diet isolate 10432-BHL040517-GBD4179_11181-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTTTATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTGCTTCCCCCATCTTTAACTCTATTACTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613603 Paratanytarsus sp. water mite diet isolate 10437-BHL040517-GBD28235_12360-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATGCTTCATTCTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGGGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTCAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613604 Paratanytarsus sp. water mite diet isolate 10440-BHL040517-GBD24692_25080-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGTACTTCCCTAAGAATCTTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTCTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613605 Paratanytarsus sp. water mite diet isolate 10464-BHL040517-GBD26578_13681-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGCACTTCCCTAAGTCTATTAATTCGAGCTGAACTAGGATATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGAGTTTGACTTCTTCCCCCCTCGGTAACTCATTTACTTGCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613606 Paratanytarsus sp. water mite diet isolate 10468-BHL040517-GBD18937_14177-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTTATTTTCGGAGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGTAACTGATTCTTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACACTATTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR282105, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613607 Paratanytarsus sp. water mite diet isolate 10482-BHL040517-GBD12027_22837-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTGGGAACTTCTTTAAGAATATTAATTCGACCTGAACTTGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCATTAACTCTTTTACTTTCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613608 Paratanytarsus sp. water mite diet isolate 10487-BHL040517-GBD1873_14677-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR757714, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613609 Paratanytarsus sp. water mite diet isolate 10488-BHL040517-GBD23247_9165-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAGCTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGCACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTACATTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTTTTACTATCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613610 Paratanytarsus sp. water mite diet isolate 10518-BHL040517-GBD23037_10360-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGACTTATCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613611 Paratanytarsus sp. water mite diet isolate 10537-BHL040517-GBD7388_10888-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613612 Paratanytarsus sp. water mite diet isolate 10539-BHL040517-GBD28524_11036-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGATCATTATATTTCATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTCCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR293963, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613613 Paratanytarsus sp. water mite diet isolate 10541-BHL040517-GBD15707_11123-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATCTTAGGAGTTTGAGCTGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTCTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTCTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613614 Paratanytarsus sp. water mite diet isolate 10550-BHL040517-GBD28811_17684-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTACATTATACTTTATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTAGGATATCCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613615 Paratanytarsus sp. water mite diet isolate 10552-BHL040517-GBD12502_13835-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTCATTTTCGGTGCCTGATCAGGTATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGATCAAATTTATCACGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCTTTTACCATCAAGTAGAATAGCGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613616 Paratanytarsus sp. water mite diet isolate 10567-BHL040517-GBD12510_12936-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTTATTTTCGGTGCCTGATCAGGCATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGTTCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCATTAACTCTTTTACTATCAAGTAGAACAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613617 Paratanytarsus sp. water mite diet isolate 10577-BHL040517-GBD19190_27453-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTTATTTTTGGTGCTTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTTATTCGAGCTGAACTAGGACTTCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTTCTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613618 Paratanytarsus sp. water mite diet isolate 10584-BHL040517-GBD6868_21087-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCTTTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTACCTTTAATATTAGGAGCCCCAGATATAGCCTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613619 Paratanytarsus sp. water mite diet isolate 10590-BHL040517-GBD9133_16903-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTGATTTTACTTCATTTTCGGTGCCTGATCCGGAATATTGGGAACTTCCCTAAGAATATTAATTCGAGCTGTACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACACTTTATCAATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613620 Paratanytarsus sp. water mite diet isolate 10602-BHL040517-GBD23008_10523-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGTTGAACTAGGACATCCCGGATCTTTTATTGGAGATGATCAAATTTATAATGTACTTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATATTAATTGGAGGATTTGGGAACTGATTACTGCCATTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCATCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613621 Paratanytarsus sp. water mite diet isolate 10609-BHL040517-GBD26367_11413-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGCACTTCCCTAAGAATATTAATTCGAGTTGAACTAGGACATCCTGGATCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGTGCCCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCATTAACCCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613622 Paratanytarsus sp. water mite diet isolate 10611-BHL040517-GBD21351_10062-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTTATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCATTTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613623 Paratanytarsus sp. water mite diet isolate 10614-BHL040517-GBD4204_12300-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTATCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613624 Paratanytarsus sp. water mite diet isolate 10626-BHL040517-GBD25075_7571-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCGGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCACCCTCTTTAACTTTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613625 Paratanytarsus sp. water mite diet isolate 10632-BHL040517-GBD21798_7552-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGATCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTTGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTACTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTATGACTACTTCCCCCCTCTTTAACTCTTCTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR293963, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613626 Paratanytarsus sp. water mite diet isolate 10635-BHL040517-GBD8954_11835-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTCGGTGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTATTACCCCCATCTCTAACATTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613627 Paratanytarsus sp. water mite diet isolate 10639-BHL040517-GBD7474_7996-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCTTTAAGAATTTTAATTCGAGCTAAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTTCTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613628 Paratanytarsus sp. water mite diet isolate 10642-BHL040517-GBD14289_19181-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGCTCTTTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAGCTTTTATTGGAGATGACCAAATTTATAATGCAATTGTTACAGCACATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTACTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613629 Paratanytarsus sp. water mite diet isolate 10644-BHL040517-GBD5560_17219-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGACTACTTCCCCCATCTTTAACTTTATTACTTTCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613630 Paratanytarsus sp. water mite diet isolate 10650-BHL040517-GBD20560_26004-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTTATTTTCGGAGCCTGATCAGGAATAGTAGGAACTTCCTTAAGTATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATCTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACGATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613631 Paratanytarsus sp. water mite diet isolate 10654-BHL040517-GBD7721_8253-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTTATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCACTTCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613632 Paratanytarsus sp. water mite diet isolate 10669-BHL040517-GBD4872_10421-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGATCATTTTATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTGCCCCCCTCTTTAACTTTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613633 Paratanytarsus sp. water mite diet isolate 10685-BHL040517-GBD9802_13628-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGATCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCACGCATTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAAATGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTTTTTTATTATCAAGTAGACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613634 Paratanytarsus sp. water mite diet isolate 10687-BHL040517-GBD22754_13651-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTTTATTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCCGAACTAGGACATACTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTGCTGCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613635 Paratanytarsus sp. water mite diet isolate 10696-BHL040517-GBD4250_17567-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGTCATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613636 Paratanytarsus sp. water mite diet isolate 11034-BHL110116-GBD20224_10166-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTAAACTAGGACATCTCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCACCCTCTTTAACGCTTTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613637 Paratanytarsus sp. water mite diet isolate 11044-BHL110116-GBD20244_14589-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTCATTTTTGGTGCCTGTTCAGGATTAGAAGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAATTTTATAATGCAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACGTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613638 Paratanytarsus sp. water mite diet isolate 11058-BHL110116-GBD24183_7900-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGGAACTGACTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGACTACTTCCCCCATCTTTAACCCTTTTACTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613639 Paratanytarsus sp. water mite diet isolate 11077-BHL110116-GBD12387_18022-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAGCGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATACTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAA-TCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613640 Paratanytarsus sp. water mite diet isolate 11082-BHL110116-GBD13211_6170-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KR283251, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613641 Paratanytarsus sp. water mite diet isolate 11117-BHL110116-GBD21357_16119-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAGCTTCCCTAAGCATATTAATTCGAGCTGACCTAGGACATCCCGGAACTTTTATTGGCGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTCCATAGTTATACCTATTTTAATTGGGTTATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACATTCAAGTAGAATAGTGGAAAATAGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613642 Paratanytarsus sp. water mite diet isolate 11132-BHL110116-GBD5214_8111-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR293963, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613643 Paratanytarsus sp. water mite diet isolate 11137-BHL110116-GBD11438_6092-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAGCTAGGACATCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCGTTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID KR283251, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613644 Paratanytarsus sp. water mite diet isolate 11138-BHL110116-GBD24707_20819-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGAGGCTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613645 Paratanytarsus sp. water mite diet isolate 11142-BHL110116-GBD23717_22455-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTCATTTTTGGTGCCTGATCAGGAATACTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTCGGACATCCCGGATCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613646 Paratanytarsus sp. water mite diet isolate 11143-BHL110116-GBD12919_21755-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGAGGATTTGGAAACTGATTATTGCCATTAATATTAGGAGCCCCAGATATGGCTGTTCCTCGAATAAATAATATAAGATTTTGACTACTACCACCATCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR293963, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613647 Paratanytarsus sp. water mite diet isolate 11159-BHL110116-GBD13876_2795-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTCGGAGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTGATCCGAGCTGAACTAGGACATCCCTGAACTTTTATTGGAGATGACCATATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGTAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613648 Paratanytarsus sp. water mite diet isolate 11171-BHL110116-GBD17600_2220-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTGTACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGCGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAACATAAGATTCTGGTTACTACCTCCGTCTATTTCTTTGCTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613649 Paratanytarsus sp. water mite diet isolate 11175-BHL110116-GBD20655_26914-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACATTATACTTTATTTTTGGGGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACGACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613650 Paratanytarsus sp. water mite diet isolate 11185-BHL110116-GBD11199_27293-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAAAATTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTCTTCCCCCTTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.1% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613651 Paratanytarsus sp. water mite diet isolate 11188-BHL110116-GBD12313_13512-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAGCTAGGACAACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGTGGGTTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTTTTACCATCAAGTAGAATAGCGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613652 Paratanytarsus sp. water mite diet isolate 11193-BHL110116-GBD17972_3412-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAAC---CTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR757972, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613653 Paratanytarsus sp. water mite diet isolate 11199-BHL110116-GBD6249_6632-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGACGACCAAGTTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCACCATCTCTAA-TCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.4% identical to accession ID KR276243, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613654 Paratanytarsus sp. water mite diet isolate 11202-BHL110116-GBD10048_20357-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGAGGCTTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACCTTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613655 Paratanytarsus sp. water mite diet isolate 11205-BHL110116-GBD4849_15760-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTAAACTAGGACATCCCGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGTGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR293963, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613656 Paratanytarsus sp. water mite diet isolate 11215-BHL110116-GBD21682_8762-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTTTACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGTGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTGCCGCCCCCATCATTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613657 Paratanytarsus sp. water mite diet isolate 11218-BHL110116-GBD8417_14375-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.4% identical to accession ID KR757972, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613658 Paratanytarsus sp. water mite diet isolate 11221-BHL110116-GBD22231_21337-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGATTTGGAAACTGATTATTACCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACCCTTTTACTATCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR294834, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613659 Paratanytarsus sp. water mite diet isolate 11228-BHL110116-GBD10555_14054-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACGGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCACCCTCTCTAACTTTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613660 Paratanytarsus sp. water mite diet isolate 11250-BHL110116-GBD23439_4960-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGAGCCTGAGCAGGAATAGTAGGAACTGCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGAAACTGATTATTACCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCATCTTTAACTCTATTACTTGCAAGTAGACCAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613661 Paratanytarsus sp. water mite diet isolate 11255-BHL110116-GBD24002_11047-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGTGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACTCTATTACTGTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613662 Paratanytarsus sp. water mite diet isolate 11263-BHL110116-GBD4395_19488-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTTTATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTAGGACATCCCGGATCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACAAATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTGCTGCCCCCATCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613663 Paratanytarsus sp. water mite diet isolate 11275-BHL110116-GBD26576_12104-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGCGCTGAACTAGGACATCCCGGAACTTTTATTGGAGCTGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGCTATAGCCTGTCCTCGAATAAATAATATAAGATTTTGACTTCGTCCCCCCGCGTTAACGCTTTTACGTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR276243, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613664 Paratanytarsus sp. water mite diet isolate 11277-BHL110116-GBD23646_13992-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTCGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATCTTTTAATTGGGGGATTTGGTAACTGATTATTGCCTTTAATATTAGGAGCTCCAGAGATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTGCTTCCCCCCGCTTTAACTCGTTTACGTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613665 Paratanytarsus sp. water mite diet isolate 11279-BHL110116-GBD2813_20439-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGTTGAACTATGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGCAATTGTTACTGCTCATGCATTCATTATAATTTTTTTCATAGTTATACATATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613666 Paratanytarsus sp. water mite diet isolate 11285-BHL110116-GBD15051_26733-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTTCATTATATTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACAACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTTCAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAACTGATTATTTCCTTTAATATTAGGAGACCCAGACATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTTTAACTCTTTTACTTTCTAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR283845, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613667 Paratanytarsus sp. water mite diet isolate 11290-BHL110116-GBD22787_22055-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCACCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAAAGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR757972, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613668 Paratanytarsus sp. water mite diet isolate 11301-BHL110116-GBD23276_26655-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGTGGGATTTGGAAACTGATTTTTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613669 Paratanytarsus sp. water mite diet isolate 11303-BHL110116-GBD12715_13080-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTTATAGTGATACATATTTTAATTGGAGGATTTGGAAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613670 Paratanytarsus sp. water mite diet isolate 11324-BHL110116-GBD22726_18073-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGTGGGAATTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGAAATAGCCTTTCCTCCAATAAATAAAATAAGAATTTGACCTCTTCCCCCCTCTTTAACTCCTTTACCTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613671 Paratanytarsus sp. water mite diet isolate 11342-BHL110116-GBD19607_9009-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATACTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCTGAACTCGGACATCCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGTAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCGTCTTTAACTCTATTACTATCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613672 Paratanytarsus sp. water mite diet isolate 11346-BHL110116-GBD12668_27969-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTTATTCGAGCTGAATTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGTGGATTAGGTAACTGATTTTTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTTCTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613673 Paratanytarsus sp. water mite diet isolate 11360-BHL110116-GBD19194_25623-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGAGCATGATCAGGAATAGTAGGAACTTCCTTAAGAATATTTATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCCCCAGACATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613674 Paratanytarsus sp. water mite diet isolate 11365-BHL110116-GBD20743_25631-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTCTTCCTCGAATAAATAACATAAGATTTTGACTACTTCCCCCCTCTTTAACACGTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613675 Paratanytarsus sp. water mite diet isolate 11483-BHL101516-GBD15192_12418-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCACCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACATCCCCCCTCTCTAACCCTTCGACTTTCAAGTAGAATAGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613676 Paratanytarsus sp. water mite diet isolate 12677-BHL040517-GBD8884_18892-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTTCCTTTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCCTCTTTAACTTTTTTACTATCAAGTAGACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613677 Paratanytarsus sp. water mite diet isolate 13211-BHL040517-GBD14253_9239-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGCAACATTTATTGGAGATGTCCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGAGTTCTGGGAATTGACCTCTTCCTTTAATATTAGGAACTCCCGATATAGCTTTTCCCCGTAAAAATAACAAAAGTTTTTGATCACTTCCCCCATCTTTAACCCTTCTTCCATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613678 Paratanytarsus sp. water mite diet isolate 13240-BHL040517-GBD15634_29054-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACTTCCTTAAGTATATTAATTCGAGCTGAATTAGGGCATCCTGGAACATTTATTGGAGATGACCAAATATATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTACTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCCCGAATAAATAACATAAGATTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR672858, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613679 Paratanytarsus sp. water mite diet isolate 13250-BHL040517-GBD23333_21142-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATACTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCTCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTGCTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613680 Paratanytarsus sp. water mite diet isolate 13252-BHL040517-GBD7702_10729-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAGTATTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGCGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTATTATAATTTTTTTTATAGTTATTCCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR740890, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613681 Paratanytarsus sp. water mite diet isolate 13256-BHL040517-GBD26497_8130-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCCGGAATAATCGGAACTTCCTTAAGTATACTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCGGATATAGCTTTTCCCCGAATAAATAACAAAAGTTTTGGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR672858, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613682 Paratanytarsus sp. water mite diet isolate 13270-BHL040517-GBD24712_13270-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTCTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGACTTCTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCCCGAATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTACTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613683 Paratanytarsus sp. water mite diet isolate 13276-BHL040517-GBD3678_13212-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACTTCCTTAAGTATATTAATTCGAGCAGAATTAGGTCACCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGGCTTCTTCCATTAATATTAGGAGCTCCCGATATAGCTTTTCCACGTATAAATAACATAAGATTTTGATTACTACCCCCATCTTTAACCCTACTTCTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KM994688, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613684 Paratanytarsus sp. water mite diet isolate 13278-BHL040517-GBD14933_12578-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGCTATACCTATTTTAATTAGGGGTTTTGGGTATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACGGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR740890, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613685 Paratanytarsus sp. water mite diet isolate 13280-BHL040517-GBD14375_19709-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAACTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTAAAATTTCTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGTATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAGATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR672858, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613686 Paratanytarsus sp. water mite diet isolate 13284-BHL040517-GBD12310_26822-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGTATAATCGGAACTTCCTTAAGTATATTAATTCGAGTAGAATTAGGGCACCCTGGAACATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGTAATTGACTTCTACCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGAATAAATAACATAAGATTTTGATTACTTCCCCCATCTTTAACCCTACTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR672858, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613687 Paratanytarsus sp. water mite diet isolate 13293-BHL040517-GBD8785_6567-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGGTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTGGAGTACGTCCCCCAGCGTTAACCCTTCTGCGATCAAGAAGATTAGTGGAAAAGGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613688 Paratanytarsus sp. water mite diet isolate 13303-BHL040517-GBD4148_11821-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAGTCGGAACTTCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACAGCTCATGCCTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCATTCCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTACTACTATCAAGAAGACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR672858, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613689 Paratanytarsus sp. water mite diet isolate 13306-BHL040517-GBD14500_27492-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613690 Paratanytarsus sp. water mite diet isolate 13312-BHL040517-GBD11518_13146-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATACAGCTTTTCCCCGTATAAATAACATAAGTTATTGATTACTTCGCCCATCTTTAACCCGTCTGCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR672858, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613691 Paratanytarsus sp. water mite diet isolate 13337-BHL040517-GBD7294_12769-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACTTCCTTAAGTATACTAATTCGAGCTGAATTAGGGCACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGACTACTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGAATAAATAACATAAGTTTTTGATTACTACCCCCATCTTTAACCCTTCTTCTATCAAGGAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR672858, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613692 Paratanytarsus sp. water mite diet isolate 13346-BHL040517-GBD24232_11121-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACTTCCTTAAGTATACTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGACCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGATTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCGCGAATAAATAACATAAGATTTTGACTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613693 Paratanytarsus sp. water mite diet isolate 13351-BHL040517-GBD25147_10792-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACTTCCTTAAGTATTCTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGACTTCTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCCCGAATAAATAACATAAGTTTTTGATTGCTGCCCCCATCTTTAACCCTACTACTATCAAGAACATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR672858, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613694 Paratanytarsus sp. water mite diet isolate 13353-BHL040517-GBD20957_3744-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGTGCTTGGTCAGGAATAGTCGGAACTTCCTTAAGTATATTAATTCGAGCTGAATTAGGTCATCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGGAATTGATTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR672858, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613695 Paratanytarsus sp. water mite diet isolate 13359-BHL040517-GBD29154_14943-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGCCAGGAATAATCGGCACTTCCTTAAGTATACTAATTCGACTAGAATTAGGGCACCCTGGCACATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGAATAAATAACATAAGTTTTTGATTACTACCCCCATCATTAACCCTTCTTCTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR672858, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613696 Paratanytarsus sp. water mite diet isolate 13367-BHL040517-GBD28403_15372-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAGTCGGAACTTCTTTAAGTATACTAATTCGAGCAGAATTAGGGCAACCTGGAACATTTATTGGAGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGAAATTGACTTCTTCCTCTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGACTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613697 Paratanytarsus sp. water mite diet isolate 13374-BHL040517-GBD3856_16564-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACTTCTTTAAGTATATTAATTCGAGCGGAATTAGAGCACCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTACTTCCTTTAATATTAGGAGTTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGATTTTGATTACTACCCCCATCTTTAACCCTACTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613698 Paratanytarsus sp. water mite diet isolate 13375-BHL040517-GBD26672_18740-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTCGGAACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACACCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGAATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAACATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR740890, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613699 Paratanytarsus sp. water mite diet isolate 13378-BHL040517-GBD7377_12311-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACTTCTTTAAGTATACTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTCTTCCTCTAATATTAGGAGCACCCGATATAGCATTTCCCCGTATAAATAACATAAGATTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM994688, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613700 Paratanytarsus sp. water mite diet isolate 13388-BHL040517-GBD22036_22726-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTTGGAGCTTGGTCAGGAATAATAGGAACTTCTTTAAGTATATTAATTCGAGCAGAATTAGGTCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGATTTTTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTACCCCCATCTCTAACCCTACTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613701 Paratanytarsus sp. water mite diet isolate 13390-BHL040517-GBD22418_26953-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTTGGAGCTTGGTCAGGAATAATCGGAACATCATTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTCTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCCTCTTTAACCCTTCTTCTATCTAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613702 Paratanytarsus sp. water mite diet isolate 13391-BHL040517-GBD24586_25407-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTCTATATTTATTTTCGGAGCTTGGTCAGGAATAATTGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTCTTCCTTTAATATTAGGTGCTCCCGATATAGCTTTTCCCCGAATAAATAACATAAGATTTTGATTACTTCCCCCATCTTTAACCCTACTACTATCAAGAAGAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613703 Paratanytarsus sp. water mite diet isolate 13393-BHL040517-GBD10063_7580-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGTTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTCTTCCTTTAATATTAGGAGCACCCGATATAGCTTTTCCACGAATAAATAACATAAGTTTTTGATTACTGCCCCCATCATTAACCCTACTACTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613704 Paratanytarsus sp. water mite diet isolate 13399-BHL040517-GBD22857_24537-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACTTCCTTAAGTATATTAATTCGAGCAGAATTAGGGCATCCTGGATCATTTATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTCTTGGAAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTACTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR672858, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613705 Paratanytarsus sp. water mite diet isolate 13400-BHL040517-GBD17482_8901-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTTTATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACTTCCTTAAGTATACTAATTCGAGCAAAATTAGGACACCCTGGATCATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTACTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGAATAAATAACATAAGTTTTTGATTGCTGCCCCCATCTTTAACCCTACTACTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613706 Paratanytarsus sp. water mite diet isolate 13402-BHL040517-GBD23720_7565-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTTAGTATATTAATTCGAGCTGAATTAGCGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGCAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGAAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGAATAAATAACATAAGATTTTGATTACTTCCCCCATCTTTAACCCTACTGCTATCAAGAAGAGTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR742514, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613707 Paratanytarsus sp. water mite diet isolate 13403-BHL040517-GBD2734_17919-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTCTATTTTCGGGGCTTGGTCCGGAATAATCGGAACTTCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTCATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGACTACTACCCCCATCTCTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613708 Paratanytarsus sp. water mite diet isolate 13407-BHL040517-GBD29068_18245-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACTTCCTTAAGTATATTAATTCGAGCAGACTTAGGTCACCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGGATAAATAACATAAAGTTTTGATTACTTCCCCCATCTTTAACCCTACTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613709 Paratanytarsus sp. water mite diet isolate 13409-BHL040517-GBD18689_24745-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTATTTTTGGAGCTTGGTCAGGAATAATCGGAACTTCCTTAAGTATACTAATTCGAGCAGAATTAGGTCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGTTTTGGGAATTGACTTCTTCCTTTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR628998, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613710 Paratanytarsus sp. water mite diet isolate 13410-BHL040517-GBD6707_8435-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGTATAATCGGAACTTCCTTAAGTATTCTAATTCGAGCAGAATTCGGGCACCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGAAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTACTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR672858, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613711 Paratanytarsus sp. water mite diet isolate 13422-BHL040517-GBD24376_25445-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTTGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGAAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCTCGAATAAATAACATAAGTTTTCGATTACTTCCCCCATCTTTAACCCTACTTCTATCAAGAACATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR672858, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613712 Paratanytarsus sp. water mite diet isolate 13423-BHL040517-GBD2364_15972-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTTGGTGCCTGGTCAGGAATAATAGGAACTTCCTTAAGAATATTAATTCGAGCAGAACTAGGGCATCCTGGAACTTTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGATTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR672858, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613713 Paratanytarsus sp. water mite diet isolate 13429-BHL040517-GBD25199_10954-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGTCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAACTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCACCCGATATAGCATTTCCCCGAATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTACTATTATCAAGAACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM994688, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613714 Paratanytarsus sp. water mite diet isolate 13453-BHL040517-GBD22831_11084-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTTTATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGACACCCTGGCACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAGTTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGAATAAATAACATAAGTTTTTGATTACTTCCCCCATCATTAACCCTACTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613715 Paratanytarsus sp. water mite diet isolate 13458-BHL040517-GBD23851_8964-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCCGGAATAGTCGGAACTTCCTTAAGTATACTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTCTTCCTTTAATATTAGGAGCACCCGATATAGCTTTTCCCCGAATAAATAACATAAGTTTTTGATTACTTCCCCCATCTATAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613716 Paratanytarsus sp. water mite diet isolate 13468-BHL040517-GBD23267_25573-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTTAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAGTTGACTACTTCCTCTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGATTTTGATTACTACCCCCATCTTTAACCCTACTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613717 Paratanytarsus sp. water mite diet isolate 13472-BHL040517-GBD22738_3966-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACTTCCTTAAGTATTCTAATTCGAGTAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTCTACCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGAATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM994688, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613718 Paratanytarsus sp. water mite diet isolate 13475-BHL040517-GBD15077_11332-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCATTACGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTGTGATCATGTCCCCCATCTTTAACCCTTCATAAAGCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613719 Paratanytarsus sp. water mite diet isolate 13479-BHL040517-GBD11289_7229-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAGTAGGAACTTCCTTAAGTATACTAATTCGAGCTGAATTAGGACACCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGACTATTGCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGAATAAATAACATAAGATTTTGATTACTTCCCCCATCTTTAACCCTTTTTCTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613720 Paratanytarsus sp. water mite diet isolate 13481-BHL040517-GBD22516_12815-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACTTCCTTTAGTATATTAATTCGAGCAGAGTTAGGACACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTGTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTCCCCCGAATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM994688, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613721 Paratanytarsus sp. water mite diet isolate 13482-BHL040517-GBD5264_19525-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCCTGGTCAGGCATAATCGGAACTTCCTTAAGAATTTTAATTCGAGCAGAATTCGGGCACCCTGGTACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACCGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGAATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTACTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613722 Paratanytarsus sp. water mite diet isolate 13496-BHL040517-GBD26770_10971-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGTACTTCCTTAAGTATACTAATTCGAGCAGAATTAGGTCACGCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAACTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGTAAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTACTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613723 Paratanytarsus sp. water mite diet isolate 13498-BHL040517-GBD16394_20587-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCTGTACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGTACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTAGACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGGGTTTGATTACTTCCCCCATCTGTAACCCATCTACTATCAAGAAGATGAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613724 Paratanytarsus sp. water mite diet isolate 13499-BHL040517-GBD11961_17718-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACTTCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGATCATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGACTTTTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCCCGTATAAATAACATAAGATTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR672858, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613725 Paratanytarsus sp. water mite diet isolate 13501-BHL040517-GBD13044_25193-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGGACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTCCAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCAGCGGGAACCCGGCGGCGAGCAAGAAGAGTAGGGGAAAAGGGAGCGGGAACGGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613726 Paratanytarsus sp. water mite diet isolate 13502-BHL040517-GBD8569_9230-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTTGGAGCCTGGTCAGGAATAGTAGGAACTTCCTTAAGTATATTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGACTTCTGCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGATTTTGACTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613727 Paratanytarsus sp. water mite diet isolate 13505-BHL040517-GBD21812_3518-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTATTTTTGGAGCTTGATCAGGAATAGTCGGAACTTCCTTTAGTATATTAATTCGAGCAAAATTAGGACACCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTCTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KP043139, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613728 Paratanytarsus sp. water mite diet isolate 13506-BHL040517-GBD14527_15764-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTCGGAGCTTGATCAGGAATAATCGGAACTTCCTTAAGTATACTAATTCGAGCAGTGTTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCCATTTTAATTGGAGGTTTTGGAAATTGACTACTTCCTTTAATATTAGGAGCACCCGATATAGCTTTTCCCCGTATAAATAACATAAGATTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613729 Paratanytarsus sp. water mite diet isolate 13515-BHL040517-GBD26418_21287-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCAACCTGGAACATTTTTTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGGAATTGACTACTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGAATAAATAACATAAGATTTTGACTACTTCCCCCATCTTTAACCCTACTAATATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613730 Paratanytarsus sp. water mite diet isolate 13520-BHL040517-GBD23613_21884-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTCGGATCTTGGTCAGGAATAATCGGAACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGGGGATTTGGAAATTGACTTCTTCCTTTAATACTAGGAGCTCCCGATACAGCTTTTCCCCGAATAAATAACATAAGTTTTTGATTACTACCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613731 Paratanytarsus sp. water mite diet isolate 13521-BHL040517-GBD9350_7769-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACTTCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACTTTTATTGGAGATGACCAAATCTATAATGTAGTTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAACTGACTTCTTCCTTTAATACTAGGAGCACCCGATATAGCTTTTCCACGTATAAATAACATAAGTTTTTGATTACTACCCCCATCTTTAACCCTTCTTCTATCAAGAACATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613732 Paratanytarsus sp. water mite diet isolate 13524-BHL040517-GBD24851_25459-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTATTTTCGGAGCTTGATCAGGAATAGTCGGAACTTCCTTAAGTATACTAATTCGAGCAGAATTAGGTCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCGGTATAAATAATATAAGTTTTTGACTACTTCCCCCATCTTTAACCCTTCTGCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR740890, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613733 Paratanytarsus sp. water mite diet isolate 13525-BHL040517-GBD26170_14601-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTTGGAGCTTGGTCCGGAATAATCGGAACTTCCTTAAGTATACTAATTCGAGCAGAATTAGGACATCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCACCCGATATAGCTTTTCCCCGTATAAATAACATAAGATTTTGATTACTACCCCCATCTTTAACCCTGCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR672858, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613734 Paratanytarsus sp. water mite diet isolate 13528-BHL040517-GBD13673_27265-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTATTTTTGGAGCTTGGTCGGGAATAATAGGAACTTCTTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGCATAAATAACATAAGTTTTTGATTACTACCCCCATCATTAACCCTACTTCTATCAAGAAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR742514, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613735 Paratanytarsus sp. water mite diet isolate 13531-BHL040517-GBD20289_27442-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTTGGAGCTTGGTCAGGAATAATAGGAACTTCCTTAAGAATACTAATTCGAGCAGAATTAGGGCTACCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGAAATTGACTTTTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTACCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613736 Paratanytarsus sp. water mite diet isolate 13535-BHL040517-GBD29348_13314-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTTGGAGCCTGGTCAGGAATAATCGGAACATCCTTAAGTATTTTAATTCGAGCAGAATTAGGGCACACTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTACTTCCGTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCATTAACCCTACTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613737 Paratanytarsus sp. water mite diet isolate 13536-BHL040517-GBD25389_16827-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTTGGAGCCTGGTCAGGAATAGTCGGCACTTCTTTAAGTATTTTAATTCGAGCAGAACTAGGTCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTCTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613738 Paratanytarsus sp. water mite diet isolate 13541-BHL040517-GBD7225_14900-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTATTTTCGGAGCTTGGTCCGGAATAGTCGGAACTTCCTTAAGAATGCTTATTCGAGCAGAATTAGGGCACCCTGGAACATTCATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAATGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR742514, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613739 Paratanytarsus sp. water mite diet isolate 13542-BHL040517-GBD18410_25171-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTATTTTCGGAGCTTGGTCTGGAATAATCGGAACATCCTTTAGTATACTAATTCGAGCAGAATTAGGTCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAACTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGTAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAACATAAGATTTTGATTACTACCCCCATCTTTAACACTACTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR628998, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613740 Paratanytarsus sp. water mite diet isolate 13546-BHL040517-GBD9809_17570-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATCTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATGAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGCGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.4% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613741 Paratanytarsus sp. water mite diet isolate 13561-BHL040517-GBD16687_23223-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATCCTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613742 Paratanytarsus sp. water mite diet isolate 13585-BHL040517-GBD5770_15346-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACACTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCTAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613743 Paratanytarsus sp. water mite diet isolate 13597-BHL040517-GBD19286_3881-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCCCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGACGGGTCATTAATTGGAGACGATCAAATTTATATTGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTCATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613744 Paratanytarsus sp. water mite diet isolate 13611-BHL040517-GBD5171_15352-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGAAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTCTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATACAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613745 Paratanytarsus sp. water mite diet isolate 13619-BHL040517-GBD11966_24829-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCATATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613746 Paratanytarsus sp. water mite diet isolate 13644-BHL040517-GBD4739_23050-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTATTTCGAGCTGAACTAGGACATACCGGAACTTTTATTGGAGATTACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCACCCTCTTTCACTCTATTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613747 Paratanytarsus sp. water mite diet isolate 13650-BHL040517-GBD21742_20224-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGTAAAATTAGGACGACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGTAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.4% identical to accession ID KR664189, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613748 Paratanytarsus sp. water mite diet isolate 13661-BHL040517-GBD6565_21270-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGTTGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613749 Paratanytarsus sp. water mite diet isolate 13683-BHL040517-GBD17100_10832-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTGGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATGGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTACACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATAGAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTGCTTCCCCCCTCTTTAACTCCTTTACTATTATCTAGTTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613750 Paratanytarsus sp. water mite diet isolate 13699-BHL040517-GBD24565_13353-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTCGGGGCTTGATCCGGGATAGTAGGTACTTCCCTAAGAATCTTAATTCGAGCTGAATTAGATCATGCCGTGTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGATGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACGTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR757714, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613751 Paratanytarsus sp. water mite diet isolate 13749-BHL040517-GBD22519_10689-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGATCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613752 Paratanytarsus sp. water mite diet isolate 13771-BHL040517-GBD11815_6619-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGCACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACACCCTGGATCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCATTAACCCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613753 Paratanytarsus sp. water mite diet isolate 13775-BHL040517-GBD26583_21724-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCTTGATCAGGTATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCCTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613754 Paratanytarsus sp. water mite diet isolate 13781-BHL040517-GBD23401_14914-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGTCATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGTAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGACTAGTGGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613755 Paratanytarsus sp. water mite diet isolate 13804-BHL040517-GBD19754_23869-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACCTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613756 Paratanytarsus sp. water mite diet isolate 13807-BHL040517-GBD26921_9879-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTTCATTATACTTCATTTTAGGGGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTGTTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR283845, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613757 Paratanytarsus sp. water mite diet isolate 13824-BHL040517-GBD28247_16864-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTGCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613758 Paratanytarsus sp. water mite diet isolate 13843-BHL040517-GBD16486_27060-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTACATTATATTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTAAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTTCTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613759 Paratanytarsus sp. water mite diet isolate 13850-BHL040517-GBD5389_8403-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGGGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCAGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGACTAGTGCCTTTAATATTAGGAGCACCTGATATGGCTTTACCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATCGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613760 Paratanytarsus sp. water mite diet isolate 13887-BHL040517-GBD26312_14142-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTCATTTTTGGTGCCTGATCAGGCATAGTAGGCACTTCTCTAAGAATTTTAATTCGAGCTGAACTAGGACATCCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613761 Paratanytarsus sp. water mite diet isolate 13896-BHL040517-GBD26415_18071-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATACTTCATCTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGTCATCCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTCCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613762 Paratanytarsus sp. water mite diet isolate 13900-BHL040517-GBD26379_14896-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGTAACTTCTTTAAGAATTTTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTTCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCTTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613763 Paratanytarsus sp. water mite diet isolate 13925-BHL040517-GBD21890_17547-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGGGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGTACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGAAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCACCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613764 Paratanytarsus sp. water mite diet isolate 13945-BHL040517-GBD8057_10454-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTAAACTAGGACATCCTGGTGCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTCTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613765 Paratanytarsus sp. water mite diet isolate 14155-BHL040517-GBD20961_14962-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613766 Paratanytarsus sp. water mite diet isolate 14169-BHL040517-GBD3292_13805-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCTGCACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAATTATACCTATTTTCATTAGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCCGATATAACTGTTCCTCGAATAAATAATAATATAAGAGTTTGACTTCTTCCCCCCTCTTTAACTCTTGTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613767 Paratanytarsus sp. water mite diet isolate 14189-BHL040517-GBD7595_24538-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTCTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613768 Paratanytarsus sp. water mite diet isolate 14191-BHL040517-GBD15669_26230-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCAGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613769 Paratanytarsus sp. water mite diet isolate 14199-BHL040517-GBD25210_6920-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAAAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACCTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID KR758568, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613770 Paratanytarsus sp. water mite diet isolate 14208-BHL040517-GBD2814_15245-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATTTTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613771 Paratanytarsus sp. water mite diet isolate 14209-BHL040517-GBD7332_17437-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATGAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613772 Paratanytarsus sp. water mite diet isolate 14212-BHL040517-GBD22787_17238-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGAGCCTGATCAGGAATAGTGGGTACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGTCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613773 Paratanytarsus sp. water mite diet isolate 14234-BHL040517-GBD13485_9562-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTTACACTACTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613774 Paratanytarsus sp. water mite diet isolate 14275-BHL040517-GBD28228_13823-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATCTTTTATTTTCGGAGCTTGATCAGGAATATTCGGAACATCCTTAAGTATATTAATTCGAGCCGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAAACTATAATGTTATTGTTACAGCTCATGCTTTTATTATAAATTTTTTTATAGTAATACCTATTTTAAGTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTAAAAATAATATAAGTTTTTGATTACTACCCCCATCTTTAATCCTTCTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613775 Paratanytarsus sp. water mite diet isolate 14278-BHL040517-GBD8206_9761-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTACATTATATTTTATTTTCGGTGCCTGATCAGGAATAGTGGGCACTTCCCTAAGAATATTAATTCGAGCAGAACTAGGACATCCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCGTTTATTATAATTTTTTTCATAGTTAGACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATTTTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613776 Paratanytarsus sp. water mite diet isolate 14281-BHL040517-GBD9891_24240-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAAGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAGGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613777 Paratanytarsus sp. water mite diet isolate 14283-BHL040517-GBD21577_18288-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGAGCCTGATCAAGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGTTTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATAAAAGATTTTGTCATCTTCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613778 Paratanytarsus sp. water mite diet isolate 14285-BHL040517-GBD7644_11363-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTTGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID KR279360, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613779 Paratanytarsus sp. water mite diet isolate 14298-BHL040517-GBD19200_28809-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATATTTGGAGCTTGAGCGGGAATAGTAGGAACTTCTCTTAGTATTTTAATTCGAGCAGAATTAGGACATCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613780 Paratanytarsus sp. water mite diet isolate 14330-BHL040517-GBD27852_19653-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACTTCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAACTGACTTCTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCCCGAATAAATAATATAAGTTTTTGACTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613781 Paratanytarsus sp. water mite diet isolate 14337-BHL040517-GBD24653_5094-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACCTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTTACATTACTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613782 Paratanytarsus sp. water mite diet isolate 14339-BHL040517-GBD13499_22173-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGCTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATTTTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279360, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613783 Paratanytarsus sp. water mite diet isolate 14345-BHL040517-GBD20468_8424-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATTTTAATTCGAGCTGAACTAGGACATCCCGGATCTTTAATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAGCTGATTATTGCCTTTAATTTTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCCCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613784 Paratanytarsus sp. water mite diet isolate 14349-BHL040517-GBD19227_26958-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCTTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTAGTGCCTTTAATATTAGGTGCCCCAGATATAGCTTTTCCTCAAATAAATAATATAAGATTTTGACTACTTCCTCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613785 Paratanytarsus sp. water mite diet isolate 14374-BHL040517-GBD4469_19474-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCAGTGACAGGAGACGACCAAATCTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAGTAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR283251, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613786 Paratanytarsus sp. water mite diet isolate 14379-BHL040517-GBD20651_7319-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATCATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACTTTTCTTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATTTTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613787 Paratanytarsus sp. water mite diet isolate 14380-BHL040517-GBD12625_17933-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTTTACTTCATTTTCGGTGCCTTATCAAGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGATCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACGTCCCCCCTCTTTAACACTTTTACAATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613788 Paratanytarsus sp. water mite diet isolate 14388-BHL040517-GBD26726_11903-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCCTTAAGTATATTAATTCGACTAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTACTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTACTACCCCCATCATTAACCCTACTTCTATCAAGAAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613789 Paratanytarsus sp. water mite diet isolate 14401-BHL040517-GBD20308_10200-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATAGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGGTGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613790 Paratanytarsus sp. water mite diet isolate 14404-BHL040517-GBD15705_23288-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTCGGTGCCCGATCAAGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGGTGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATGGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613791 Paratanytarsus sp. water mite diet isolate 14427-BHL040517-GBD13337_13741-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATATTTGGAGCTTGAGCGGGAATAGTAGGAACTTCTCTTAGTATTTTAATTCGAGCAGAATTAGGACATCCAGGTGCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGCAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGTAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAGGAAGATTAATGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR758568, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613792 Paratanytarsus sp. water mite diet isolate 14431-BHL040517-GBD10892_14956-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAGTTGGAGGATTTGGGAATTGATTATTGCCTTTAATTTTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGGCTTCTTCCCCCCTCTTTAACTCTTTTACTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR282105, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613793 Paratanytarsus sp. water mite diet isolate 14435-BHL040517-GBD26470_14059-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCTTGAGCGGTAATAGTAGGAACTTCTCTTAGTATTTTAATTCGAGCAGAATTAGGACATCCAGGTGCTTTAATTGGAGATGATCAAATTTATAATGTTATTGTTCCAGCTCATGCTTTTACTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCATTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613794 Paratanytarsus sp. water mite diet isolate 14448-BHL040517-GBD25272_24078-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTCGGTGCTTGATCAAGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACTCTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613795 Paratanytarsus sp. water mite diet isolate 14461-BHL040517-GBD16218_24786-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACATCCTTAAGAATATTAATTCGAGCTGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGACTATTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCTTTAACCCTTCTACTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613796 Paratanytarsus sp. water mite diet isolate 14468-BHL040517-GBD24772_5220-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGAATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTGTGCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGAATAAATAATATAAGTTTTTGACTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.1% identical to accession ID KR758568, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613797 Paratanytarsus sp. water mite diet isolate 14469-BHL040517-GBD14670_22854-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACATCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGCCATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGCAATTGCTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATTCTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613798 Paratanytarsus sp. water mite diet isolate 14470-BHL040517-GBD9331_3098-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATGAATAATATAAGTTTTTGATTACTACCTCCTTCTCTTACCTTACTTTTAGTAAGCAGTATACTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR740890, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613799 Paratanytarsus sp. water mite diet isolate 14471-BHL040517-GBD15142_21631-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCCTTAATATTAGGAGCCCCAAATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTCTAACACTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613800 Paratanytarsus sp. water mite diet isolate 14491-BHL040517-GBD18888_5476-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATTTTAGGAGCCCCAGAAAATGCCTTTCCCCCAATAAATAAATTAAGATTTTGACCTCCTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613801 Paratanytarsus sp. water mite diet isolate 14511-BHL040517-GBD15000_17870-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACTTCCTTAAGTATATTAATTCGAGCAGAACTAGGACACCCTGGATCTTTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTACTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCATTAACCCTACTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613802 Paratanytarsus sp. water mite diet isolate 14526-BHL040517-GBD24197_19887-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTTATTTTCGGAGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTATTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATTTTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTCTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613803 Paratanytarsus sp. water mite diet isolate 14559-BHL040517-GBD17280_13537-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTTATTTTCGGTGCCTGATCAGGTATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCAGAACTAGGACATCCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTGTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613804 Paratanytarsus sp. water mite diet isolate 14623-BHL040517-GBD20083_10285-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGGACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGTTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613805 Paratanytarsus sp. water mite diet isolate 14657-BHL040517-GBD13509_19912-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAGGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR282105, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613806 Paratanytarsus sp. water mite diet isolate 14659-BHL040517-GBD11607_5483-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATTTTTTGGAGCTTGAGCTGGAATAGTAGGAACTTCCTTAAATATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTACTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR757714, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613807 Paratanytarsus sp. water mite diet isolate 14670-BHL040517-GBD3975_11882-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGTCTTTAATATTAGGGGCCCCAGATATAGCTTTTCCTCGAATAAATAATACAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR757714, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613808 Paratanytarsus sp. water mite diet isolate 14758-BHL040517-GBD13794_16869-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTCGGACATCCCGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTGCTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613809 Paratanytarsus sp. water mite diet isolate 14769-BHL040517-GBD6154_18779-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCATTTATTATAACTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTTTTACTATCAAGCAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613810 Paratanytarsus sp. water mite diet isolate 14800-BHL040517-GBD21834_5288-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAAAATATTAATTCGAACTGAACTAGGACATCACGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACACTATTATTAGCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613811 Paratanytarsus sp. water mite diet isolate 14801-BHL040517-GBD21484_2963-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATATTTTGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613812 Paratanytarsus sp. water mite diet isolate 14824-BHL040517-GBD23313_13603-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTTTACATCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCTTAAGTATATTAATTCGAGCTGAACTAGGACATCCCGAAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613813 Paratanytarsus sp. water mite diet isolate 14832-BHL040517-GBD27718_9757-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCATTAACTCTTTTACTTTCAAGCGGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613814 Paratanytarsus sp. water mite diet isolate 14876-BHL040517-GBD9667_9144-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGTCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGTGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCTAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613815 Paratanytarsus sp. water mite diet isolate 14908-BHL040517-GBD8460_10927-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGATCAAATTTATAATATAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTATTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR757714, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613816 Paratanytarsus sp. water mite diet isolate 15076-BHL040517-GBD7376_10874-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTACCACTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTATTACCACCATCTCTAACTTTATTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR293963, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613817 Paratanytarsus sp. water mite diet isolate 15081-BHL040517-GBD18990_12689-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAAC---CTTACTTTTATCAAAATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR292109, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613818 Paratanytarsus sp. water mite diet isolate 15138-BHL040517-GBD9306_9083-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTTTATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGTTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTTCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTGCTGCCCCCCTCATTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613819 Paratanytarsus sp. water mite diet isolate 15151-BHL040517-GBD25588_22529-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGTACTTCCTTAAGAATTTTAATTCGAGCTGAACTAGGACATCCCGGATCTTTTATGGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACTCTTTTACTATCAAGTAGAATAGCGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613820 Paratanytarsus sp. water mite diet isolate 15196-BHL040517-GBD27923_11248-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCTCTAAGAATATTAATCCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACTCTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613821 Paratanytarsus sp. water mite diet isolate 15212-BHL040517-GBD24665_20185-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTTTTTTGGTGCTTGATCAGGAATAGTGGGAACTTCTTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTCTAACTCTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613822 Paratanytarsus sp. water mite diet isolate 15253-BHL040517-GBD16806_7754-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAATCAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTCTCCACGAATAAATAATATAAGATTTTGACTTCTTCCCCCATCTTTAACTCTATTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613823 Paratanytarsus sp. water mite diet isolate 15266-BHL040517-GBD22264_3041-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTAGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGGTACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID KM905578, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613824 Paratanytarsus sp. water mite diet isolate 498-BHL040517-GBD12788_15995-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGTAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGGA	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613825 Paratanytarsus sp. water mite diet isolate 704-BHL072216-GBD5883_13917-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613826 Paratanytarsus sp. water mite diet isolate 746-BHL040916-GBD17286_28907-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAAGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613827 Paratanytarsus sp. water mite diet isolate 1092-BHL100916-GBD8913_12438-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTCCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGTCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCCTCCCCCCTCTTTAACCCTTTTACTCTCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613828 Paratanytarsus sp. water mite diet isolate 1283-BHL110116-GBD16053_7394-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613829 Paratanytarsus sp. water mite diet isolate 1400-BHL110116-GBD10158_22852-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTACTTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCTCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACTCTTTTACTTTCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613830 Paratanytarsus sp. water mite diet isolate 1457-BHL110116-GBD15886_21077-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGAATACTTCCCCCATCTTTAACACGACATCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613831 Paratanytarsus sp. water mite diet isolate 1553-BHL110116-GBD27524_16888-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTAAACTAGGACATCCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613832 Paratanytarsus sp. water mite diet isolate 1679-BHL110116-GBD15135_3505-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATTTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTTGAGGTTTTGGCAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATACGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTACTGGAAAATGGTGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613833 Paratanytarsus sp. water mite diet isolate 1767-BHL110116-GBD14067_7781-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATTTTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCCTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613834 Paratanytarsus sp. water mite diet isolate 1826-BHL022317-GBD20682_26375-Ldc88 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCAGCTTTAACCCTTCTACGATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613835 Paratanytarsus sp. water mite diet isolate 1837-BHL072216-GBD17014_27546-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGATATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613836 Paratanytarsus sp. water mite diet isolate 1849-BHL072216-GBD6694_17151-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTCTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613837 Paratanytarsus sp. water mite diet isolate 1863-BHL072216-GBD26319_12594-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATACTTATTCGAGCAGAATTAGGACAACCTGGAACATTTATTGGAGATGACCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCACCCGATATAGCTTTTCCCCGAATAAATAATATAAGCTTTTGATTACTTCCCCCATCTTTAACCCTCCTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613838 Paratanytarsus sp. water mite diet isolate 1869-BHL022317-GBD20618_6800-Ldc89 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTTAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTGTTGGGAATTGACTTATTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613839 Paratanytarsus sp. water mite diet isolate 2209-BHL072216-GBD2098_12451-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAACAATAGAAGATTTTGACTACATCCCCCCTCTTTAACTCTTTTACGGACAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613840 Paratanytarsus sp. water mite diet isolate 2223-BHL072216-GBD18772_23244-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCACCCGATATAGCTTTTCCACGTATAAATAATATAAGTTTTTGATTACTGCCCCCATCTTTAACCCTACTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613841 Paratanytarsus sp. water mite diet isolate 2285-BHL072216-GBD18734_17515-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGGACTTCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGATTTTGATTACTTCCCCCATCTTTAACCCTACTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR672858, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613842 Paratanytarsus sp. water mite diet isolate 2329-BHL072216-GBD12448_13633-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTCATTTTCGGTGCCTGATCAAGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCATTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCATTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR282105, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613843 Paratanytarsus sp. water mite diet isolate 2512-BHL072216-GBD10868_13429-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACGTCCCCCCTCATTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613844 Paratanytarsus sp. water mite diet isolate 2522-BHL072216-GBD17745_25329-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGAGTTTGACTTCTTCCCCGATCTGTAACTCTGTCACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613845 Paratanytarsus sp. water mite diet isolate 2651-BHL072216-GBD10189_4233-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGGTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTGTTGATTACTTACCCCATCTTTAACCCTTATTCGATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613846 Paratanytarsus sp. water mite diet isolate 3218-BHL032417-GBD6946_18051-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCTTTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCTAATAAAAAATATAAGATTTTGACTACTACCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613847 Paratanytarsus sp. water mite diet isolate 3281-BHL032417-GBD5014_13620-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAAGACATCCCGGAACTTTTATTGGAGATGACCAATTTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAGCTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTCTAACTCTTTTACTTTCAAGTAGAATGGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613848 Paratanytarsus sp. water mite diet isolate 3572-BHL032417-GBD9584_5448-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCATCTTTAACACTTCTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613849 Paratanytarsus sp. water mite diet isolate 3632-BHL032417-GBD21771_8249-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCCGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGAAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATGATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613850 Paratanytarsus sp. water mite diet isolate 3744-BHL032417-GBD15582_12436-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCATTAACTCTTTTACTATCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613851 Paratanytarsus sp. water mite diet isolate 4243-BHL032417-GBD9484_7972-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAGATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAACATAAGATTTTGACTACTTCCCCCATCTTTAACTCTTTTACTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613852 Paratanytarsus sp. water mite diet isolate 4506-BHL032417-GBD23315_15012-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAAAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTGTTCCTCGAATAAATAATATAAGATTTTGGCTTCTACCCCCCTCTTTAACTCTACTACTTTCAAGTAGAATAGTGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613853 Paratanytarsus sp. water mite diet isolate 4510-BHL032417-GBD11064_14319-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGGACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATACAATATTTTGACATCATCACCCCTCTTTAACACTTTTACTGTCAAGTAGAATAGTGGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613854 Paratanytarsus sp. water mite diet isolate 4518-BHL032417-GBD26354_19599-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCCTGATCAGGACTAGTAGGAACTTCCCCAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGAGCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTAGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613855 Paratanytarsus sp. water mite diet isolate 4525-BHL032417-GBD27535_19283-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTAGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCATTAACTCTATTACTATCAAGTAGAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613856 Paratanytarsus sp. water mite diet isolate 4528-BHL032417-GBD17345_8258-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGACCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTCATACCACCCTCTGTAACTCGGTTACTTTCAAGGAGAATAGTGGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613857 Paratanytarsus sp. water mite diet isolate 4533-BHL032417-GBD25796_20879-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTATGAATATTAATTCGAGCTGAACTAGGCCATCCTGGCACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGAGTTGGGAACTGATTATTGCCTTTAATATTAGGAACCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCGTTAACTCTTTTACTTTCAAGTAGAAAAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613858 Paratanytarsus sp. water mite diet isolate 4536-BHL032417-GBD13157_13902-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGATTTGGGAATTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613859 Paratanytarsus sp. water mite diet isolate 4543-BHL032417-GBD3481_20765-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTAATGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCCGTTCCTCGAAAAAATAATATAAGATTTTGAATTCTTCCCCCCTCTTTAACTCTTTTACTTTCCAGTAGAATAGTGGAAAAAGGAGCTGGAACCGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613860 Paratanytarsus sp. water mite diet isolate 4555-BHL032417-GBD6641_22976-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCATGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCCGTTTTAATTGGAGGATTTGTGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCCTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTGTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGATGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613861 Paratanytarsus sp. water mite diet isolate 4558-BHL032417-GBD17397_3339-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGGGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAGTGTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTACTGTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGGCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGTGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613862 Paratanytarsus sp. water mite diet isolate 4564-BHL032417-GBD27328_12775-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGACACACTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAGATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613863 Paratanytarsus sp. water mite diet isolate 4572-BHL032417-GBD18504_8183-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTTCATTATACTTCATTTCTGGTGCCTGATCAGGAATAGTCGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAACATAAGATTTTGACTACTTCCCCCATCCTTAACCCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR292109, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613864 Paratanytarsus sp. water mite diet isolate 4575-BHL032417-GBD21928_19567-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCACCTCTTTAACGCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613865 Paratanytarsus sp. water mite diet isolate 4576-BHL032417-GBD26180_17601-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGTCATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACCCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613866 Paratanytarsus sp. water mite diet isolate 4582-BHL032417-GBD28523_14858-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGACCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613867 Paratanytarsus sp. water mite diet isolate 4584-BHL032417-GBD17993_7021-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTAGAGCTGAACTAGGACATCCTGAAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCCTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACTCTGTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613868 Paratanytarsus sp. water mite diet isolate 4585-BHL032417-GBD12271_3342-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCTTGATCAGGAATAGTAGGCACTTCCCTAAGAATGTTAATTCGAGCTGAACTAGGACATCCTGGCACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTTATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACCCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613869 Paratanytarsus sp. water mite diet isolate 4587-BHL032417-GBD10232_9385-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGTCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGACCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCATCCTCCCTCTTTAACACTTTTACGTTCAAGTAGAATAGTGGAAAATGGAGCAGCAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613870 Paratanytarsus sp. water mite diet isolate 4588-BHL032417-GBD14124_5125-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACCTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGCACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGCCTAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACACTTTTCCTTTCAAGTAGAATAGTGGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613871 Paratanytarsus sp. water mite diet isolate 4593-BHL032417-GBD24357_15879-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTTCCTTTAATATTATGTGCCCCAGATAAAGCCTTTCCTCGAATAAATAATATAAGATTTTGACTTCCTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613872 Paratanytarsus sp. water mite diet isolate 4596-BHL032417-GBD22455_11410-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGTTGAACTAGAACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCACTCTTTAACCCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613873 Paratanytarsus sp. water mite diet isolate 4601-BHL032417-GBD20348_5958-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTATTGCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACCCTTTTTCTTTCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613874 Paratanytarsus sp. water mite diet isolate 4608-BHL032417-GBD13617_5765-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TAGACTTCATTTTTGGGGCCTGATCAGGAAGAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCGTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGCGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613875 Paratanytarsus sp. water mite diet isolate 4612-BHL032417-GBD2524_14454-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTTCTTCCCCCCTCTTTAACTCTATTACTATCAAGCAGAATAGTGGGAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613876 Paratanytarsus sp. water mite diet isolate 4613-BHL032417-GBD17943_11270-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTTGGTGCCTGATCAGGATTAGCAGGAACTTCTCTAAGAATATTATTTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAACATAAGATTTTGACTTCTTCCCACCTCTTTAACCCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613877 Paratanytarsus sp. water mite diet isolate 4617-BHL032417-GBD27450_21475-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGTAACTGATTATTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTTTATTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR294834, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613878 Paratanytarsus sp. water mite diet isolate 4618-BHL032417-GBD11916_8046-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCCTGATCAGGTATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGTACATCCTGGAACTTTTATTGGAGATGACCAAATTTCTAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACGTCTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613879 Paratanytarsus sp. water mite diet isolate 4620-BHL032417-GBD22077_12503-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGATCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCGTCCCTCCTCTTTAACACTTCTTCAATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613880 Paratanytarsus sp. water mite diet isolate 4621-BHL032417-GBD18984_16801-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTATGAACTTCCCTACGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTCTAACGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGTGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613881 Paratanytarsus sp. water mite diet isolate 4623-BHL032417-GBD7727_21064-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTTATTTTTGGTGCCTGATCGGGAATAGTAGGAACTTCCCTAAGTATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTCTTCTGTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613882 Paratanytarsus sp. water mite diet isolate 4626-BHL032417-GBD18497_28842-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGCAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGTGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGAAATAGCTTTTCCTCGAAAAAAAAAAAAAAATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613883 Paratanytarsus sp. water mite diet isolate 4631-BHL032417-GBD2602_16444-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTGGGTGCCTGATCAGGATTAGTAGGAACTTCTCTAAGAAGATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTTCCTTTAATATTGGGAGCCCCAGACATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613884 Paratanytarsus sp. water mite diet isolate 4637-BHL032417-GBD17338_3094-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATACTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCATAAGAATACTAATTCGAGCTGAACTAGGACATCCTGGAACTTTAATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTACCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR764064, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613885 Paratanytarsus sp. water mite diet isolate 4638-BHL032417-GBD10434_18746-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGACCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTAGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAAGAAAAGATTTTGACTTCTTCCCCCATCTTTAACTCTGTTACTTGCAAAAAGAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613886 Paratanytarsus sp. water mite diet isolate 4639-BHL032417-GBD4791_14224-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCATTAATATTAGGAGCCCCAGACATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTCTAACTCTTCTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613887 Paratanytarsus sp. water mite diet isolate 4646-BHL032417-GBD15301_16797-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATATTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACACCCTGGAACTTTTATTGGTGATGACCAAATTTCTAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTCCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613888 Paratanytarsus sp. water mite diet isolate 4647-BHL032417-GBD26900_10126-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGTCCCAGATATAGCTTTTCCTCGCATAAATAATAAAAGATTTTCACCTCATCCCCCCTCTTTAACTCTTTTACATTCAAGTAGAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613889 Paratanytarsus sp. water mite diet isolate 4648-BHL032417-GBD27673_21981-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGCACTTCCCTAAGAATATTAATTCGAGTTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTACCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTAGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR294834, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613890 Paratanytarsus sp. water mite diet isolate 4650-BHL032417-GBD25571_13252-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTTTACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGCACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCATCTTTAACTCTATTACAACCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613891 Paratanytarsus sp. water mite diet isolate 4651-BHL032417-GBD29051_17846-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGTAGCCCCAGATATAGCTTTTCCTCGAAAAAATAATAAAAGATTTGGACTTCTTCCCCCCTCTTTAACACATTTACTTACAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613892 Paratanytarsus sp. water mite diet isolate 4652-BHL032417-GBD4029_14330-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTCCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613893 Paratanytarsus sp. water mite diet isolate 4658-BHL032417-GBD28110_15706-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACATTATACTTCATTTTTGGGGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCAGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCCTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTTGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613894 Paratanytarsus sp. water mite diet isolate 4659-BHL032417-GBD18918_16946-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTACTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGATCTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACATCCACCCACTGTAACGCTTTTACTTTCAAGTAGAATAGGGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613895 Paratanytarsus sp. water mite diet isolate 4663-BHL032417-GBD20988_19196-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTACCTGATCAGGAATAGTAGGAACTTTCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGCACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTGCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCGCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613896 Paratanytarsus sp. water mite diet isolate 4665-BHL032417-GBD3781_22390-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTTGGTGCCTGATCAGGAATAGTAGGATCTTCCCTAAGTATATTAATTTGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCTTAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTACCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTAGACTACTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR294834, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613897 Paratanytarsus sp. water mite diet isolate 4666-BHL032417-GBD26310_11879-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGTATAGTAGAAACTTCCCTAAGAATATTAATTCGAGCTGAACTCGGCCATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAGTATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTGTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613898 Paratanytarsus sp. water mite diet isolate 4674-BHL032417-GBD26442_11242-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATCTTTTGGTGCTTGATCAGGATTAGTAGGACCTTCCCTAAGAATATTATTTCGAGCTGAACTAGGCCATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613899 Paratanytarsus sp. water mite diet isolate 4678-BHL032417-GBD24662_7989-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTCATTTTTGGGGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGGACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCTTTTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613900 Paratanytarsus sp. water mite diet isolate 4684-BHL032417-GBD15177_2565-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCATATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTACCTCTTTTACTTTCAAATAGAATCGTGGAAAATGGAGCTGGTCCAG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR747869, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613901 Paratanytarsus sp. water mite diet isolate 4686-BHL032417-GBD13912_5137-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTATTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATGCGAGCTGAACTAGGACATCCTGTAACTTTTAGTGGAGATGACCATATTTATAATGTAATTGGTACAGCTCATGCAATTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATGGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613902 Paratanytarsus sp. water mite diet isolate 4689-BHL032417-GBD15887_2525-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACAACCCGTAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCCCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGACCCCGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR747869, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613903 Paratanytarsus sp. water mite diet isolate 4691-BHL032417-GBD13810_4225-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACACCCTGGAACATTTATTGGAGATGACCAAATGTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCACAAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCTTTTTCTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613904 Paratanytarsus sp. water mite diet isolate 4694-BHL032417-GBD22323_23318-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCCTTTCCTCGAATAAATAATATAAGATTTTGAATTCTTCCCCCATCTTTAACTCTGTTACTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613905 Paratanytarsus sp. water mite diet isolate 4695-BHL032417-GBD25308_19055-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTCTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGTATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATACTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTTTTACTTTCAAGTACAATAGTGGAAAATCGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613906 Paratanytarsus sp. water mite diet isolate 4701-BHL032417-GBD10994_4127-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGTGACTGATCAGGAGTAGTAGGAACTTCAATAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613907 Paratanytarsus sp. water mite diet isolate 4704-BHL032417-GBD16321_6438-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATACTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGAAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTTTTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTTTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613908 Paratanytarsus sp. water mite diet isolate 4707-BHL032417-GBD29053_17603-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCCTATGTATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTTCCTTTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613909 Paratanytarsus sp. water mite diet isolate 4709-BHL032417-GBD27808_10600-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATGGTAGGAACTTCCCTAAGAATGTTAATTCGCGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGTATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAAAAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCAGTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613910 Paratanytarsus sp. water mite diet isolate 4712-BHL032417-GBD4222_23207-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTACATTATATTTTATTTTCGGAGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCCTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613911 Paratanytarsus sp. water mite diet isolate 4720-BHL032417-GBD20956_19641-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTTGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACATCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGAATATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCACCATCTTTAACTCTTTTACTTTCAAGTAGAATAGCGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613912 Paratanytarsus sp. water mite diet isolate 4725-BHL032417-GBD19035_27252-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTTATTTTTGGTGCCTGATCAGGAATATTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTATTACCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGACTTCTTCCCCCATCTTTAACCCTTCTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR294834, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613913 Paratanytarsus sp. water mite diet isolate 4726-BHL032417-GBD23650_7281-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTATGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATCGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTACTTCCACCCTCTTTAACTCTATTACTTTCAAGTAGGATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613914 Paratanytarsus sp. water mite diet isolate 4729-BHL032417-GBD23166_8814-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATTTTAATTCGAGCTGAACTAGGTCATGCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCATCTTTAACTTTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613915 Paratanytarsus sp. water mite diet isolate 4730-BHL032417-GBD24861_6401-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGATCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCGTCCCCTCGCTTTAACTAGTTTGCTGTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613916 Paratanytarsus sp. water mite diet isolate 4734-BHL032417-GBD23812_7110-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGTACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATAAAGCTTTTCCTCGAATAAATAAAAAAAGATTTTGACCTCTTCCCCCCTCATTAACCCCTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613917 Paratanytarsus sp. water mite diet isolate 4735-BHL032417-GBD10846_14873-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGAGCATGATCAGAAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGTCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACACTGTTACTAGCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613918 Paratanytarsus sp. water mite diet isolate 4739-BHL032417-GBD20966_13306-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTACATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTTATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613919 Paratanytarsus sp. water mite diet isolate 4742-BHL032417-GBD11959_8302-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTGTCCTTCATTTTTTGGTGCCTGATCAGGAATAGTAGTAACTTCCCTAAGATTATTAATTCGAGCTGAACTAGGACATCCTGTAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGAAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTGTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTGTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613920 Paratanytarsus sp. water mite diet isolate 4745-BHL032417-GBD29582_13659-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACCTCATTTTTGGGGCCTGATCAGGAATAGTAGGGACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACGTCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTTGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613921 Paratanytarsus sp. water mite diet isolate 4746-BHL032417-GBD21246_27244-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTTATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTATAATTGGAGGATTTGGGGACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613922 Paratanytarsus sp. water mite diet isolate 4747-BHL032417-GBD24195_16641-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTGTACTTCATTTTTGGTGCCTGGTCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGATCTAGGACATCCTGGAACTTTTATTGGAGATGACCATATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGAATTTGACTTCTTCCCCCCTCGTTAACTCGTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613923 Paratanytarsus sp. water mite diet isolate 4751-BHL032417-GBD26620_12732-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGACTATTAATTCGAGCTGAACTAGGATATCCTGGAACTTTTATAGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTGTTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTCTAACTCTATTACTTGCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613924 Paratanytarsus sp. water mite diet isolate 4769-BHL032417-GBD18429_15607-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATCTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATCGTTACAGCACATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613925 Paratanytarsus sp. water mite diet isolate 4770-BHL032417-GBD26998_13001-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGGGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGATCTAGGACATCCTGGAACTTTTTTTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGTATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCCTCTCTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613926 Paratanytarsus sp. water mite diet isolate 4772-BHL032417-GBD16509_4621-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTGTTGGAGCCTGATCAGGAATGGTAGGAACTTCCCTAAGAATATTAATCCGAGCTGAACTAGGACATCCTGTAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCGTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613927 Paratanytarsus sp. water mite diet isolate 4773-BHL032417-GBD9240_22325-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGTTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGGAACTGATTACTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGGATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613928 Paratanytarsus sp. water mite diet isolate 4776-BHL032417-GBD24018_6055-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGTGATGACCATATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATCTGGAAATTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACACTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR293963, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613929 Paratanytarsus sp. water mite diet isolate 4777-BHL032417-GBD21164_23107-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTAAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTGGCAGGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613930 Paratanytarsus sp. water mite diet isolate 4778-BHL032417-GBD5444_6440-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTTATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTCCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613931 Paratanytarsus sp. water mite diet isolate 4783-BHL032417-GBD19957_23586-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTTGTAACTTCCCTTAGACTATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCACTGTAACTCTGTTACTTTCACGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613932 Paratanytarsus sp. water mite diet isolate 4788-BHL032417-GBD25426_8423-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGCGTCTGATCAGGAATAGTAGGAACTTCCTTATGAATATTACTTCGAGTTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGTCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGAGTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR757714, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613933 Paratanytarsus sp. water mite diet isolate 4792-BHL032417-GBD8594_14649-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTGTATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATAATAATTTTTTTCATAGTTATACCTATTTTAATTAGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTTCCCCCTCTTTAACCCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613934 Paratanytarsus sp. water mite diet isolate 4796-BHL032417-GBD10424_19214-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCTTTATACTTCATTTTTGGTGCCTGATCCGGAATAGTAGGAACTTCCCTAAGAATATTTATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCAAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAATGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613935 Paratanytarsus sp. water mite diet isolate 4797-BHL032417-GBD28259_14186-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCGTTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCATTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTGTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCCTTTTCTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613936 Paratanytarsus sp. water mite diet isolate 4799-BHL032417-GBD20704_22500-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGTGTCTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCTGAACTATGACATCCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTACTTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCATCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613937 Paratanytarsus sp. water mite diet isolate 4802-BHL032417-GBD2433_12835-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTATGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCATTTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACACTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613938 Paratanytarsus sp. water mite diet isolate 4803-BHL032417-GBD25215_23750-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTTCTTTATACTTTATTTTTGGGGCCTGATCAGGAATTGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTCTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR283845, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613939 Paratanytarsus sp. water mite diet isolate 4806-BHL032417-GBD27732_17666-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTACACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATAATAATTCGACCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGTCCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTCTAATATTAGGAGCCCTAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCCTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613940 Paratanytarsus sp. water mite diet isolate 4807-BHL032417-GBD13857_18255-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGCTCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAAGTAGGACATCCTGGAACATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTAATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGATCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACACTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613941 Paratanytarsus sp. water mite diet isolate 4817-BHL032417-GBD18436_6945-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCATGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATATTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCATTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCACCATCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613942 Paratanytarsus sp. water mite diet isolate 4818-BHL032417-GBD15257_26576-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGAGCATGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGAATTTGGGAATTGATTATTACCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR294834, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613943 Paratanytarsus sp. water mite diet isolate 4826-BHL032417-GBD14514_6642-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTTATTCGAGTTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAGATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTCTTCCCCCCTCTCTAACTCTTTCACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613944 Paratanytarsus sp. water mite diet isolate 4829-BHL032417-GBD23938_5120-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTATGAATATTAATTCGAGCTGAACTAGGACACCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATCTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTCTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTCTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613945 Paratanytarsus sp. water mite diet isolate 4833-BHL032417-GBD2909_10631-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTGAATTTTTGGAGACTGATCAGGAATAGTAGGAACTTCCCGAAGAATATTAATTCGAGTTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613946 Paratanytarsus sp. water mite diet isolate 4839-BHL032417-GBD15564_27515-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGGGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAACAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATCGCGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613947 Paratanytarsus sp. water mite diet isolate 4842-BHL032417-GBD3266_9626-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATACATCATTTTTGGTGCATGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGGCCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTTGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTCTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613948 Paratanytarsus sp. water mite diet isolate 4844-BHL032417-GBD25838_19795-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAGCTTCCTTAAGAATATTAATTCGAGTTGAACTAGGACATCATGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGAGTTCTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613949 Paratanytarsus sp. water mite diet isolate 4846-BHL032417-GBD18958_25988-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTACACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTATGATCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACGTCCCCCCGCTTTAACTCGTTTACGTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613950 Paratanytarsus sp. water mite diet isolate 4849-BHL032417-GBD21947_8608-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTTATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGTGACTGATTATTGACTTTAATATTAGGAGCCCCAGGTATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613951 Paratanytarsus sp. water mite diet isolate 4852-BHL032417-GBD28123_19275-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATACTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCAGAACTAGGACATGCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTCCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAAGAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613952 Paratanytarsus sp. water mite diet isolate 4853-BHL032417-GBD19096_27802-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTATGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGCATAAATAATATAAGAATTTGACTTCTTCCCCCCTCTTTAACTCATTTAATTGCAAGTAGAATAGTGGAAAATGGAGCTG	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613953 Paratanytarsus sp. water mite diet isolate 4854-BHL032417-GBD25770_5741-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGCACTTCCTTAAGAATATTAATTCGAGCTAAACTAGGACATCCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTGCCTCGAATAAATAATATAAGATTTTGACTACTGCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613954 Paratanytarsus sp. water mite diet isolate 4864-BHL032417-GBD26660_20244-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGACCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGTGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTTTAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATATTGACATCTTCCCCCCGCTTTAACTCATTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613955 Paratanytarsus sp. water mite diet isolate 4868-BHL032417-GBD19132_23051-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTATGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCGGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGCTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAAGATTAGGAGCCCCAGATATAGCCTTTCCTCGAATAAATAATATAAGATTTTGACTTCGTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613956 Paratanytarsus sp. water mite diet isolate 4870-BHL032417-GBD27420_20980-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCAGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCCTTTCTTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613957 Paratanytarsus sp. water mite diet isolate 4871-BHL032417-GBD5822_21312-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAACTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTCTTCCTCGCATAAATAATATAAGATTTTGACTTCTTCCCCCCTCGATAACTCGATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613958 Paratanytarsus sp. water mite diet isolate 4873-BHL032417-GBD25927_19309-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGCGCCTGATCAGGAATGGTAGGAACTTCCCTAAGTATATTAATTCGAGTTGAACTATGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTCTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCATTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR295226, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613959 Paratanytarsus sp. water mite diet isolate 4875-BHL032417-GBD17854_15301-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGGAATGACTATTGCCTTTAATATTAGTAGCCCCAGATATAGCTTTTCCTCGAATAAATAATAAAAGATTTTGACTTCCTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613960 Paratanytarsus sp. water mite diet isolate 4878-BHL032417-GBD23791_10229-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGTAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGTAGCCCAAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTGCTTCCAACCTCTTTAACGCGGTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613961 Paratanytarsus sp. water mite diet isolate 4879-BHL032417-GBD14616_4562-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGGGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACATGCAATTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTTATTATTGCCTTTAATATTAGGAGCCCAAGATATAACTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613962 Paratanytarsus sp. water mite diet isolate 4883-BHL032417-GBD27788_12801-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTAATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAACGCAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTTTTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTACCTCTATTACTTACAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613963 Paratanytarsus sp. water mite diet isolate 4884-BHL032417-GBD8748_12886-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTACATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAACTGAACTATGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTACTTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCACCCTCTCTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613964 Paratanytarsus sp. water mite diet isolate 4885-BHL032417-GBD26469_20512-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCCTTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGCACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCACTTTAACTCTTTTACTTGCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613965 Paratanytarsus sp. water mite diet isolate 4891-BHL032417-GBD18373_27746-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGTACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGTATTTGGGAACTGATTATTGCCTTTAATATTAGGGGCACCAGATATAGCTTTTCCTCGAATAAAAAATATAAGATTTTGACTTCGTCCCCCCGCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613966 Paratanytarsus sp. water mite diet isolate 4897-BHL032417-GBD6890_8024-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGTGCCTGATCAGGTATAGTAGGAACTTCCCTAAGAATACTAATTCGAGCTGAACTAGGACGTCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCATTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR664189, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613967 Paratanytarsus sp. water mite diet isolate 4900-BHL032417-GBD24127_18182-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGTGCCTGATCAGGTATAGTAGGTACTTCCCTAAGTATGTTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATGCCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGACCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613968 Paratanytarsus sp. water mite diet isolate 4903-BHL032417-GBD20041_8591-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGTGCCTGCTCAGGAATAGTAGTAACTTCCCTAAGAATATTAATTCGAGCTGAACTCGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCGTTAACTCTGGCACTTGCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613969 Paratanytarsus sp. water mite diet isolate 4905-BHL032417-GBD8205_13397-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGACCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGCTTTGGTAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCTTTTACTTTCAAGTAGACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613970 Paratanytarsus sp. water mite diet isolate 4908-BHL032417-GBD28165_20995-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCACCCGCGGAAACTCTTTTACTTTCAAGTAGAATCGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613971 Paratanytarsus sp. water mite diet isolate 4912-BHL032417-GBD15947_3038-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACATTTATTGGAGATGACCATATTTATAATGAAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGACCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTCACTCTTTTACTTTCAAATACAATCGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613972 Paratanytarsus sp. water mite diet isolate 4914-BHL032417-GBD12629_9259-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGATTATACTTCATTTTTGGTGCCTGATCAGGAATCGTAGGAACTTCCCTCAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCGGCCCCCCTCGTTAACTCTTTTACTAGCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613973 Paratanytarsus sp. water mite diet isolate 4916-BHL032417-GBD6393_22030-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATTTTAATTCGAGCTAAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAAGATTTGGGAGCTGATTATTGCCTTTAATATTAGGAGTCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613974 Paratanytarsus sp. water mite diet isolate 4919-BHL032417-GBD12221_4944-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATCGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTCTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTTCAAATAGAATAGTGGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613975 Paratanytarsus sp. water mite diet isolate 4920-BHL032417-GBD28662_12224-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTTTTCCCTTTAATATTAGGAGCCCCAGATATGGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613976 Paratanytarsus sp. water mite diet isolate 4923-BHL032417-GBD25612_24105-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGGGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGATCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTTCCTTTAATATTAGGAGACCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTTTTTTACCTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613977 Paratanytarsus sp. water mite diet isolate 4926-BHL032417-GBD27704_10395-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCGGGAATAGTAGGAACTTCATTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTTCACATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGACTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613978 Paratanytarsus sp. water mite diet isolate 4933-BHL032417-GBD19931_24938-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATATCAATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613979 Paratanytarsus sp. water mite diet isolate 4938-BHL032417-GBD16355_24275-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGTAACTGATTATTGCCTTTAATATTTGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTGCTTCCCCCCTCTCTAACACCTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613980 Paratanytarsus sp. water mite diet isolate 4941-BHL032417-GBD23509_25232-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATTCTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTCAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGAGATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCACTTTAACTCATTTACTACCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613981 Paratanytarsus sp. water mite diet isolate 4942-BHL032417-GBD7530_22189-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATAACTATTTTAATTAGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCACCCACGTTAACTCTGTTACTTTCAAGTAGAATAGTGGGAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613982 Paratanytarsus sp. water mite diet isolate 4943-BHL032417-GBD11084_3768-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTAATTTTTGGTGCCTGATCAGGAATAGTAGGAACATCTCTAAGAATATTAATTCGAGCTGAACTAGGACATACTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTGTTTCATAGTGATACCTATTTTAATTGGAGGATTTGGGATCTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613983 Paratanytarsus sp. water mite diet isolate 4944-BHL032417-GBD10542_25839-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACCTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTAGGAACTGATTATTGCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCATCTGTAACTCTATTACTGTCAAGTAGAATAGTGGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613984 Paratanytarsus sp. water mite diet isolate 4946-BHL032417-GBD15160_2179-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGATCATTATACTTCATTTTGGGGGCCGGATCGGGAATAGAAGGAACTTCCCTAGGAATATTAATTCGAGCGGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613985 Paratanytarsus sp. water mite diet isolate 4950-BHL032417-GBD24728_14761-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTTTACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCACTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGTGAACTGATTATTTCCTTTAATATTATGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACAATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613986 Paratanytarsus sp. water mite diet isolate 5071-BHL032417-GBD23352_7987-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTTACATCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613987 Paratanytarsus sp. water mite diet isolate 5083-BHL032417-GBD15581_5521-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCAGATCAGGAATAGTGGGAGCTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGTAACTTTTATTGGAGATGACCAAATTTATAGTGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCACAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613988 Paratanytarsus sp. water mite diet isolate 5089-BHL032417-GBD20832_7658-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTGCTGCCCCCATCATTAACTCTATTACTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613989 Paratanytarsus sp. water mite diet isolate 5096-BHL032417-GBD18872_14668-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATCATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGATCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCCTCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613990 Paratanytarsus sp. water mite diet isolate 5102-BHL032417-GBD22180_17314-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCTTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTAATGGAGATGACCAAATTTATAATATAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACCTCATCCCCCCTCTTTAACTCGTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613991 Paratanytarsus sp. water mite diet isolate 5115-BHL032417-GBD27677_15188-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGAGCCTGATCAGGAATAGTGGGCACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAATTTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCTCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613992 Paratanytarsus sp. water mite diet isolate 5131-BHL032417-GBD7202_11871-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGATCTTTATATTTTATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613993 Paratanytarsus sp. water mite diet isolate 5144-BHL032417-GBD11271_19828-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTCCATTTTACTTCATTTTCGGTGCCTGATCAGGAATAATGAGAACTTCCCTAAGAATCTTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACGTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613994 Paratanytarsus sp. water mite diet isolate 5157-BHL032417-GBD18229_2839-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTCTCGGTGCCTGATCAGAAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTACTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCCTTTACTTTCAAGTAGAATAGTGGAAAATGGCGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613995 Paratanytarsus sp. water mite diet isolate 5186-BHL032417-GBD13882_12929-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTCGGAGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGATACGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGACTCTTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613996 Paratanytarsus sp. water mite diet isolate 5227-BHL032417-GBD7641_22879-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGTTCAGGAATAGTGGGAACTTCCTTAAGATTATTAATTCGAGCTGACCTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGATCCCCAGATACAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW613997 Paratanytarsus sp. water mite diet isolate 5253-BHL032417-GBD3843_10033-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATCTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTGGAGCTGAACTAGGACATCCCGGAACTTTTATTGGGGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAACTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCTTGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613998 Paratanytarsus sp. water mite diet isolate 5255-BHL032417-GBD13975_8319-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTCATTTTTGGTGCTTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTACGGCCCCCCTCTTTAACTCTTTTACTAGCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279360, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW613999 Paratanytarsus sp. water mite diet isolate 5290-BHL032417-GBD9628_24687-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATCCTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTACGACTATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGATCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCGTTAACTCTGTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614000 Paratanytarsus sp. water mite diet isolate 5312-BHL032417-GBD3658_15816-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATTTTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCCTTAATATTAGGAGCCCCAGATATAGCCTTTCCTCGAATAAATAATGTAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAGGTAGAATAATGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614001 Paratanytarsus sp. water mite diet isolate 5327-BHL032417-GBD10333_26597-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGAGAATGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTCCTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCCTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614002 Paratanytarsus sp. water mite diet isolate 5357-BHL032417-GBD22595_26837-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATCTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGATATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTACTATTAGGAGCCCCAGATACAGCTTTTCCTCGAATGAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614003 Paratanytarsus sp. water mite diet isolate 5372-BHL032417-GBD20074_23656-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGGATAGTGGGAACTTCCCTGAGAATATTAATTCGAGCTAAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATAAAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTCCATTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614004 Paratanytarsus sp. water mite diet isolate 5394-BHL032417-GBD29287_13649-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAATGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGATCAACTTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTAGTACCTTTAATATTAGGAGCCCCAGATATAGCTTTGCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614005 Paratanytarsus sp. water mite diet isolate 5414-BHL032417-GBD26635_22384-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGACCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGCACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCATTAATATTAGGATCCCCAGAGATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCGCTTTAACTCGTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614006 Paratanytarsus sp. water mite diet isolate 5429-BHL032417-GBD19580_18401-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGTATATTTATTCGAGCTGAACTAGGACATCCTGGCACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGTGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACTCTTTTACTGTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614007 Paratanytarsus sp. water mite diet isolate 5449-BHL032417-GBD18673_28053-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGTACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCGTTTACTATCAAGTAGAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614008 Paratanytarsus sp. water mite diet isolate 5461-BHL032417-GBD23118_15416-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTCTACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGCATATTAATTCGAGCTGAACTAGCACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGAATTGGTAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCACCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614009 Paratanytarsus sp. water mite diet isolate 5465-BHL032417-GBD27647_18022-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACATCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGGTTATTGCCTTTAATATTAGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCACCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614010 Paratanytarsus sp. water mite diet isolate 5505-BHL032417-GBD18869_17909-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGATGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATACTAATTCGTGCTGAACTAGGACATCCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614011 Paratanytarsus sp. water mite diet isolate 5510-BHL032417-GBD27342_10282-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGGCTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR772535, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614012 Paratanytarsus sp. water mite diet isolate 5533-BHL032417-GBD20533_14798-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTGTACTTCATTTTCGGTGCCTGATCAGGTAGAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGCACTAGGACATCCCGAAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGATACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614013 Paratanytarsus sp. water mite diet isolate 5545-BHL032417-GBD26248_10439-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTTTCCTTCATTTTCGGTGCCTGATCAGGAACAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCACTTTAACTCTTTTACTAGCAAGTAGAATAGTGGAAAATGGAGCTGGAACGGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614014 Paratanytarsus sp. water mite diet isolate 5546-BHL032417-GBD25399_16263-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGATATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGTCCCAGATATAGCTTTTCATCGAATAAATAATATAAGATTTTGACTCCTTCCCCCCTCTTTAACGCGTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614015 Paratanytarsus sp. water mite diet isolate 5550-BHL032417-GBD24367_16143-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGAGCCTGGTCTGGGATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACAGCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614016 Paratanytarsus sp. water mite diet isolate 5552-BHL032417-GBD9290_23228-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCCCGAATAAATAACATAAGATTTTGACTACCTCCCCCATCTTTAACCCTTCTTCTATCAAGTAGAATAGTGGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614017 Paratanytarsus sp. water mite diet isolate 5595-BHL032417-GBD17035_4101-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614018 Paratanytarsus sp. water mite diet isolate 5793-BHL032417-GBD5843_24279-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTGATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTACTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCCTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614019 Paratanytarsus sp. water mite diet isolate 5869-BHL032417-GBD13977_26773-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGAGCATGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAGTATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614020 Paratanytarsus sp. water mite diet isolate 6414-BHL032417-GBD11447_13478-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGAGATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCATCCACCCTCTTTAACACGTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614021 Paratanytarsus sp. water mite diet isolate 6660-BHL032417-GBD4640_21341-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614022 Paratanytarsus sp. water mite diet isolate 6685-BHL032417-GBD16009_8897-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTCATTTTCGGTGCCTGATCTGGTATAGTGGGAACTTCCCTAATAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAACTGGAAAAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614023 Paratanytarsus sp. water mite diet isolate 6689-BHL032417-GBD26059_7905-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGCACTTCCCTAAGTATCTTAATTCGAGCTGAACTAGGACATCCTGGATCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTCTAACCCTATTACTTTCAAGTAGAATAGTGGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614024 Paratanytarsus sp. water mite diet isolate 6695-BHL032417-GBD12866_11331-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAACCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614025 Paratanytarsus sp. water mite diet isolate 6708-BHL032417-GBD15177_3476-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTCGGAGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTTCTTCCAAGTAGAATAGCGGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614026 Paratanytarsus sp. water mite diet isolate 6712-BHL032417-GBD20265_9887-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGATGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614027 Paratanytarsus sp. water mite diet isolate 6740-BHL032417-GBD21101_23719-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTGTCCTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAATTTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCTAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTGTAACTCAGTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614028 Paratanytarsus sp. water mite diet isolate 6751-BHL032417-GBD19166_11847-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTTAGAATATTAATTCGAGTTGAACTAGGACATCCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTTTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATATGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614029 Paratanytarsus sp. water mite diet isolate 6759-BHL032417-GBD15012_4418-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAGTTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAAGTTGAGGATTTGGGAACTGATTATGGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614030 Paratanytarsus sp. water mite diet isolate 6762-BHL032417-GBD7751_5452-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCTTAATAATATTTATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAGTTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTTTTCCCTCTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614031 Paratanytarsus sp. water mite diet isolate 6766-BHL032417-GBD14747_5599-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTAGGACATCCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTGACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGACCTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGCATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTCCTTTCAAGTAGAATAGTGGAAACTGGAGCTGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614032 Paratanytarsus sp. water mite diet isolate 6769-BHL032417-GBD12275_20392-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAATAATGTTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAGCTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614033 Paratanytarsus sp. water mite diet isolate 6784-BHL032417-GBD24288_23320-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTATTAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTTGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGTGGATTTGGGAACTGATTCTTGCCTTTAATATTAGTAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCACTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614034 Paratanytarsus sp. water mite diet isolate 6789-BHL032417-GBD23390_23212-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAATGTTTACTTCCCTAATAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTGCCTCGAATAAATAAAATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTGTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614035 Paratanytarsus sp. water mite diet isolate 6790-BHL032417-GBD19322_4750-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTAGGACATCCCGGAACTTTTATTGGAGATGACCAATTTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAACATAAGATTTTTACTTCTTCCCCCATCTTTAACCCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614036 Paratanytarsus sp. water mite diet isolate 6797-BHL032417-GBD15275_7917-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTTTACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGTATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTCCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACCCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614037 Paratanytarsus sp. water mite diet isolate 6799-BHL032417-GBD17699_3515-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATTACCAAATTTATAATGTAATTGTTACAGCACATGCATTTATTATAATTTTTTTCATAATTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614038 Paratanytarsus sp. water mite diet isolate 6807-BHL032417-GBD15887_4575-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATGCGAGCTGAACTAGGACAACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCGCTTGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGCAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGACTAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGCGCTGGCCCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614039 Paratanytarsus sp. water mite diet isolate 6811-BHL032417-GBD13774_24574-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGTTGCCTGATCAGGAATAGTGAGAACTTCCTTCGGAATATTAATTCGGGCTGAACTAGGACTTCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614040 Paratanytarsus sp. water mite diet isolate 6819-BHL032417-GBD26741_23354-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGTAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGTCCCAGATATAGCTTTTCCTCGCATAAATAATATAAGATTTTGACTTCTCCCCCCCTCTGCAACTCTTTCACTTTCAAGTAGAATAGTGGAAAATGGCGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614041 Paratanytarsus sp. water mite diet isolate 6822-BHL032417-GBD16459_28028-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTACATTATATTTCATTTTCGGAGCCTGATCAGGAATAGTGGGAACTTCCCTTATAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614042 Paratanytarsus sp. water mite diet isolate 6825-BHL032417-GBD23487_5456-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGGCCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGACTTCATCCCACCGCTGTAACTCTTTTACTTACAAGTAGAATAGTGGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614043 Paratanytarsus sp. water mite diet isolate 6835-BHL032417-GBD24575_19331-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTCGGTGCCTGCTCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAATTTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGGGCCCCAGATATAGCTTTTCCTCAAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACTGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR283336, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614044 Paratanytarsus sp. water mite diet isolate 6839-BHL032417-GBD28858_17906-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGTAATAGTGTGAACTTCCCTAAGACTATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATAACTATTTTAATTGGAGGATATGGGAACTGATTATTGCCTTTAATATTAGGATCCCCAGATATAGCTTTTCCTCGAAAAAATAATATAAGATTTTGACTTCTTCCACCCGCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614045 Paratanytarsus sp. water mite diet isolate 6840-BHL032417-GBD27961_17374-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGAGCTTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCAGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTACTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614046 Paratanytarsus sp. water mite diet isolate 6845-BHL032417-GBD27554_20817-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTCGGAGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATACTAATTCGAGCTGAACTAGGACATCCCGAAACTTTTATTGGAGATGACCAATTTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614047 Paratanytarsus sp. water mite diet isolate 6850-BHL032417-GBD25205_9998-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGACACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACTCTTTTAATTTCTAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614048 Paratanytarsus sp. water mite diet isolate 6851-BHL032417-GBD27045_9492-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGATGCCTGATCAGGAATAGTGGGAACTTCCTTAATAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTAATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614049 Paratanytarsus sp. water mite diet isolate 6857-BHL032417-GBD15253_6289-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAATAATATTAATTCGAGCTGAACTAGGACGGCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGGTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCACAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAACTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614050 Paratanytarsus sp. water mite diet isolate 6866-BHL032417-GBD12507_13117-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTAGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGACCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCAGCACCCCTCTTTAACACTTTTACTTTCAAGTAGAAAAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614051 Paratanytarsus sp. water mite diet isolate 6877-BHL032417-GBD24683_8121-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGTCTGATCAGGAATAGTGGGAATTTCACTAAGAATATTAATTCGAGCTGATTTAGGACACCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614052 Paratanytarsus sp. water mite diet isolate 6892-BHL032417-GBD13641_10720-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTCATTTTTGGTGCCTGATCAGAAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATATCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTTTAACTCTTTTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614053 Paratanytarsus sp. water mite diet isolate 6900-BHL032417-GBD22553_19927-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACCTCATTTTCGATGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGGCCAAATTTATAATGTAATTGCTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGACCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACGTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614054 Paratanytarsus sp. water mite diet isolate 6904-BHL032417-GBD4124_20649-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTGCCTTTAATATTAGGTGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614055 Paratanytarsus sp. water mite diet isolate 6908-BHL032417-GBD17269_28003-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAATAATATTAATTCGAGCTGAGCTAGGACATCCCGAAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTTTTATAATTTTTTCCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGGCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614056 Paratanytarsus sp. water mite diet isolate 6911-BHL032417-GBD8831_17894-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTTAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.1% identical to accession ID KR757714, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614057 Paratanytarsus sp. water mite diet isolate 6912-BHL032417-GBD26164_21676-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAATAATATTAATTCGAGCTGAACTAGGACGTCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTAGTGCCTTTAATATTAGGTGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCGCGTTAACTCGTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614058 Paratanytarsus sp. water mite diet isolate 6915-BHL032417-GBD9374_22131-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATACTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGCACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTGTAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTTTTACTTTCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614059 Paratanytarsus sp. water mite diet isolate 6921-BHL032417-GBD25263_24722-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATCCTTTATTTTCGGTGCCTGATCAGGAATAGTGGGTACTTCCTTAATAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGTCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614060 Paratanytarsus sp. water mite diet isolate 6924-BHL032417-GBD26340_19348-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTAAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAATTTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATATTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAATGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614061 Paratanytarsus sp. water mite diet isolate 6925-BHL032417-GBD8398_18753-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCCTTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTATTTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCCTCTTTAACACTATTCCTTTCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614062 Paratanytarsus sp. water mite diet isolate 6930-BHL032417-GBD2294_11743-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACCTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAATAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCATATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATACTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614063 Paratanytarsus sp. water mite diet isolate 7022-BHL032417-GBD10285_14198-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGCCTCCTTCCCCCCTCTTTAACCCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614064 Paratanytarsus sp. water mite diet isolate 7660-BHL040517-GBD20821_2428-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCCTTTACTTTCAAGTTCTAATGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614065 Paratanytarsus sp. water mite diet isolate 7736-BHL040517-GBD8426_8558-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGGACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACCCTATTTCTTTCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614066 Paratanytarsus sp. water mite diet isolate 7783-BHL040517-GBD19227_8843-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACATTATTTTTGGGGCTTGATCAGGAATTGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACTTCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGATGATTTGGGAGCTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTGCTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614067 Paratanytarsus sp. water mite diet isolate 7812-BHL040517-GBD19619_27507-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATACTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTAGGACTACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCGTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614068 Paratanytarsus sp. water mite diet isolate 7853-BHL040517-GBD20388_19583-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATTAGATTTTGATTACTACCCCCATCTTTAACCCTACTTCGATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614069 Paratanytarsus sp. water mite diet isolate 7898-BHL040517-GBD2535_16439-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATACTTTATTTTTGGTGCTTGATCCGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCCGGAACTTTTATTGGAGATGACCAAACTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTTTTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614070 Paratanytarsus sp. water mite diet isolate 7947-BHL040517-GBD20186_27777-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCCATAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTGTACCTATTTTAACTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614071 Paratanytarsus sp. water mite diet isolate 7972-BHL040517-GBD6186_14218-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTACCTGATCAGGAATAGTAGGAACTCCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCGTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACCTCTTCCCCCCTCTTTAACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614072 Paratanytarsus sp. water mite diet isolate 7985-BHL040517-GBD22028_17556-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATCGTAGGAACTCCCCTTAGTATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACACATTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614073 Paratanytarsus sp. water mite diet isolate 8059-BHL040517-GBD28023_9820-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTCCTCTAAGAATATTAATTCGAGCAGAACTAGGACATCCTGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614074 Paratanytarsus sp. water mite diet isolate 8129-BHL040517-GBD28317_15932-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAATTTTTGACTACTTCCCCCATCTTTAACCCGTCTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR672858, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614075 Paratanytarsus sp. water mite diet isolate 8197-BHL040517-GBD5436_14449-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGTGCCTGATCAGGTATAGTAGGAACTCCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCTATTACCATCAAGTAGAATAGCGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614076 Paratanytarsus sp. water mite diet isolate 8410-BHL101416-GBD8376_15337-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTGAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614077 Paratanytarsus sp. water mite diet isolate 8861-BHL101416-GBD9567_20330-Lq60 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGCGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTCTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAGAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR295226, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614078 Paratanytarsus sp. water mite diet isolate 8867-BHL101416-GBD13772_28171-Lq60 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCATTTAATAATAGGAGCCCCAGATATAGCTTTTCCTCCAATAAAAAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCGTTGACGTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614079 Paratanytarsus sp. water mite diet isolate 9056-BHL032417-GBD27193_10787-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACTTCCTTAAGTATATTAATTCGAGTAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCATTAACCCTTCTTCTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR740890, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614080 Paratanytarsus sp. water mite diet isolate 9121-BHL032417-GBD22634_19271-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTAATTCGAGCAGAATTAGGACACCCTGGACCATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614081 Paratanytarsus sp. water mite diet isolate 9549-BHL032417-GBD15551_13208-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCGCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614082 Paratanytarsus sp. water mite diet isolate 9560-BHL032417-GBD16018_19963-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGTAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGGCACTCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATATCCATTTTAATGGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGTGCACCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGAGTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614083 Paratanytarsus sp. water mite diet isolate 9723-BHL040517-GBD25015_10230-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCGTTTACGATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614084 Paratanytarsus sp. water mite diet isolate 9930-BHL040517-GBD14295_28426-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTACATTATACTTCATTTTCGGTGCCTGATCAGGCATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACAACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGATGATTTGGGAACTGATTATTGCCTTTAATATTAGGAACCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614085 Paratanytarsus sp. water mite diet isolate 9947-BHL040517-GBD13807_3796-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGATATCCCGTAACTTTTATTGGATATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGCAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614086 Paratanytarsus sp. water mite diet isolate 9950-BHL040517-GBD12260_5308-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGATATCCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614087 Paratanytarsus sp. water mite diet isolate 9952-BHL040517-GBD17235_9061-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACAACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATGGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTACTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCATCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614088 Paratanytarsus sp. water mite diet isolate 9963-BHL040517-GBD21606_13064-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATCCTTCATTTTCGGTGTCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATAAAAGATTTTGACTTCTTCCCCCCTCTTTAACTCAGTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614089 Paratanytarsus sp. water mite diet isolate 9970-BHL040517-GBD19042_23837-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGGACTTCCTTAAGTATATTAATTCGAGCTGAACTAGGACATCCTGGAGCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614090 Paratanytarsus sp. water mite diet isolate 9979-BHL040517-GBD7910_8189-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCACTAAGAATATTAATTCGAGCTGAACTAAGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTTGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCCTCTTTAACTCTTTTTCTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614091 Paratanytarsus sp. water mite diet isolate 9994-BHL040517-GBD2419_12910-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGTGCTGAACTAGGATATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614092 Paratanytarsus sp. water mite diet isolate 10088-BHL040517-GBD18129_24927-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGCTCATTATACTTCATTTTCGGAGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTATGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTATTACTTTCTAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614093 Paratanytarsus sp. water mite diet isolate 10103-BHL040517-GBD4275_15812-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTTATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTTGGAGCCCCAGATATAGCTTTTCCTCGAATAAAAAATAAAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614094 Paratanytarsus sp. water mite diet isolate 10104-BHL040517-GBD4020_17860-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTCATTTTCGGTGTCTGATCAGGAATAGTGGGAACTTCCCCTAGAATATTAATTCGAGTTGAATTATGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614095 Paratanytarsus sp. water mite diet isolate 10136-BHL040517-GBD10502_13524-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCATTAACTCTATTACTATCAAGTAGAATAGTGGAGAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614096 Paratanytarsus sp. water mite diet isolate 10138-BHL040517-GBD27369_15775-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATTCTTTATTTTCGGTGCCTGATCCGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAAAAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTCAACTCTTTTACAATCAAGTAGAATAGTGGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614097 Paratanytarsus sp. water mite diet isolate 10141-BHL040517-GBD16595_3692-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATGTTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCTAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCACAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGCGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR282105, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614098 Paratanytarsus sp. water mite diet isolate 10147-BHL040517-GBD23545_25103-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTTTTGGTGCTTGATCAGGAATAGTAGGTACTTCCCTTAGAATATTCATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTGTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR747869, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614099 Paratanytarsus sp. water mite diet isolate 10153-BHL040517-GBD23552_19851-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTCCCTCTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCGCTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614100 Paratanytarsus sp. water mite diet isolate 10156-BHL040517-GBD14578_3255-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATGCGAGCTGAACTAGGACGTCCCTTAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATGATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATGAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614101 Paratanytarsus sp. water mite diet isolate 10161-BHL040517-GBD14665_7190-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTTATTCGAGCTGAACTAGGACGTCCCGGAACTTTTATTGGAGATGACCAAGTTTATAATGTAATTGTTACTGCTTATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614102 Paratanytarsus sp. water mite diet isolate 10166-BHL040517-GBD27590_10895-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGAGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTCGGTTATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614103 Paratanytarsus sp. water mite diet isolate 10168-BHL040517-GBD4887_22407-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGAGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTAGGATATCCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTCTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614104 Paratanytarsus sp. water mite diet isolate 10169-BHL040517-GBD4477_13070-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR757714, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614105 Paratanytarsus sp. water mite diet isolate 10175-BHL040517-GBD20943_7499-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCTTTATACTTTATTTTCGGTGCCTGATCCGGAATAGTGGGAACTTCCCTAAGAATATTTATTCGAGCTGAATTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614106 Paratanytarsus sp. water mite diet isolate 10194-BHL040517-GBD16082_5960-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTCGGAGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGTAACTTTTATTGGAGATGACCAAATTTATAATGCAATTGTTACAGCACATGCATTAATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614107 Paratanytarsus sp. water mite diet isolate 10216-BHL040517-GBD23216_25154-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTCATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCACTTTAACTCTTTTACTTGCAAGTAGAATAGTGGAAAATGGAGCTGAAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614108 Paratanytarsus sp. water mite diet isolate 10234-BHL040517-GBD6448_14384-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCATGACTAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGATATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTCTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTGTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614109 Paratanytarsus sp. water mite diet isolate 10236-BHL040517-GBD17316_2252-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGAGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCAGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTACTGCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAATAGAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614110 Paratanytarsus sp. water mite diet isolate 10253-BHL040517-GBD11049_22712-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTGATTATACTTCATTTTCGGTGCCTGATCAGGAAGAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGATCTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATACAAGATTTTGACTTCTTCCCCCCTCTTTAACACGATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614111 Paratanytarsus sp. water mite diet isolate 10261-BHL040517-GBD13203_6066-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGATATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGACTATTGCCTTTAATCTTAGGATCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCCTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614112 Paratanytarsus sp. water mite diet isolate 10264-BHL040517-GBD15393_28713-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTTATTTTTGGTGCCTGATCCGGAATAGTAGGAACTTCATTAAGAATATTAATTCGAGCTGAATTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR747869, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614113 Paratanytarsus sp. water mite diet isolate 10273-BHL040517-GBD23806_10662-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCCTTATACTTCATTTTCGGTGCCTGATCAGGAATATTGGGAACTTCCCTAAGAATATTTATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGTATTTGGGAACTGATTACTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCGTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614114 Paratanytarsus sp. water mite diet isolate 10276-BHL040517-GBD27559_22226-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATACATTATTTTTGGGGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTTATTCGAGCTGAACTAGGATATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614115 Paratanytarsus sp. water mite diet isolate 10278-BHL040517-GBD3620_20570-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATACTTCATTTTAGGTGCATGATCAGGAATAGTGGGAACTTCGCTAAGAATATTAATTCGAGCTGAACTATGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTACTTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614116 Paratanytarsus sp. water mite diet isolate 10282-BHL040517-GBD6688_18699-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTTATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACGCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614117 Paratanytarsus sp. water mite diet isolate 10306-BHL040517-GBD22260_17529-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGGACTTCCCTAAGAATATTAATTCGTGCTGAACTAGGACATCCCGGAACTTTTATCGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCTTCTCTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR292109, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614118 Paratanytarsus sp. water mite diet isolate 10316-BHL040517-GBD19974_19768-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTTTACTTCATTTTCGGTGCCTGATCAGGGATAGCGGGAACTTCCCTAAGAATATTAATTCGAGTTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTACTGCCTTTAATATTGGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACATTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614119 Paratanytarsus sp. water mite diet isolate 10323-BHL040517-GBD4715_16911-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATGTTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCCTTAATATTAGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTTCTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614120 Paratanytarsus sp. water mite diet isolate 10330-BHL040517-GBD9970_4972-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATACTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTACTTGTTACTGCTCATGCATTTATTATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTCCCCTTAATACTAGGAGCCCCAGACATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614121 Paratanytarsus sp. water mite diet isolate 10335-BHL040517-GBD18247_3554-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACGTCATTTTCGGAGCCTGATCAGGAATAGGGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACAGCCCTGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTGCAGCTCATGCATTTATTATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTCTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614122 Paratanytarsus sp. water mite diet isolate 10336-BHL040517-GBD17927_3285-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTCGGGACCTGATCAGGAATAGGGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACACCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGAAATTGTTACGGCTCATGCATTTATTATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614123 Paratanytarsus sp. water mite diet isolate 10366-BHL040517-GBD4733_22508-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGATATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCGTTTATTATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATCTGGGAACTGGTTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTCTCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCCTCTTTAACTCGTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614124 Paratanytarsus sp. water mite diet isolate 10372-BHL040517-GBD15707_14339-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATGCTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTACTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATATTGACTTCTTCCCCCCTCTTTAAAAGTGTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614125 Paratanytarsus sp. water mite diet isolate 10373-BHL040517-GBD5310_21899-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGTATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTCGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTACTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTCTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614126 Paratanytarsus sp. water mite diet isolate 10402-BHL040517-GBD22632_21372-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGAGCTTGATCAGGGATAGTGGGAACTTCTTTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAAGTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACCTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614127 Paratanytarsus sp. water mite diet isolate 10443-BHL040517-GBD5077_12921-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGATCATTATACTTTATTTTCGGGGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTCTTCCCCCCTCCTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614128 Paratanytarsus sp. water mite diet isolate 10457-BHL040517-GBD26491_18380-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGCACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTGTCCTCGAATAAATAATATAAGATATTGACTTCTTCCCCCCTCTGTAACTCGGTTACTGTCAAGTAGAACAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614129 Paratanytarsus sp. water mite diet isolate 10463-BHL040517-GBD25761_10824-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTTATTTTCGGAGCTTGATCAGGAATAGTGGGAACTTCCTTAAGTATATTAATTCGAGCTGAACTAGGACATCCAGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTCTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614130 Paratanytarsus sp. water mite diet isolate 10510-BHL040517-GBD25933_8082-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTTTTCTTCCTTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTTAGCATATTACTTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCGTCCCCCCTCTTTAACACTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614131 Paratanytarsus sp. water mite diet isolate 10530-BHL040517-GBD18099_5808-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGATCATTATACTTCATTTTCGGTGTCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACCTCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATACTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTACAATCGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614132 Paratanytarsus sp. water mite diet isolate 10573-BHL040517-GBD25130_16209-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTACATTATACTTCATTTTTGGTGCTTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAACCAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCCTCTTTAACTCTTTTTCTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614133 Paratanytarsus sp. water mite diet isolate 10574-BHL040517-GBD28871_11629-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTCAGAATATTAATTCGAGTTAAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614134 Paratanytarsus sp. water mite diet isolate 10598-BHL040517-GBD26414_15832-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATCTTAATTCTAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAAGTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATCTTAGGAGACCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTGCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614135 Paratanytarsus sp. water mite diet isolate 10608-BHL040517-GBD9349_5054-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGTAACTGATTATTGCCATTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTCTACCACCATCTTTAACTCTATTACTTTCAAATAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614136 Paratanytarsus sp. water mite diet isolate 10627-BHL040517-GBD25563_17120-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTTAGAATATTAATTCGAGCTGAACTAGCACATCCCGGAACATTTATTGGAGATGACCAAATTTATAATATAATTGTTACAGCTCATGCATTTTTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614137 Paratanytarsus sp. water mite diet isolate 10641-BHL040517-GBD28385_19024-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACATTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGAATTGGGAACTGATTATTGCCTTTAATATTAGGATCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAAGAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614138 Paratanytarsus sp. water mite diet isolate 10643-BHL040517-GBD24327_13178-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACATCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAAAAAAAGATTTTGACTTCTTCCCCCCTCTTTAACCCCTTTTCTTTCCAGTAGAATAGGGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614139 Paratanytarsus sp. water mite diet isolate 10655-BHL040517-GBD16405_6234-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCTTAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCAATTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGAATTGGGAACTGATTATGGACTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGCGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614140 Paratanytarsus sp. water mite diet isolate 10667-BHL040517-GBD15214_4212-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATGCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAATTTTATAGTGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCATTTAATATTAGGAGACCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614141 Paratanytarsus sp. water mite diet isolate 10677-BHL040517-GBD17074_5538-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATGTTCGGTGCCTGAGCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGATATCCCTGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGGTATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614142 Paratanytarsus sp. water mite diet isolate 10678-BHL040517-GBD19353_2124-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTCTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCATTAACGCTATTACTATCAAGTAGAATAGGGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614143 Paratanytarsus sp. water mite diet isolate 10695-BHL040517-GBD23868_8539-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCTGGAATATTGGGAACTTCCCTAAGTATATTAATTCGAGCTGAACTAGGACATCCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATCCCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCATTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614144 Paratanytarsus sp. water mite diet isolate 10754-BHL101516-GBD21661_22823-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACACTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614145 Paratanytarsus sp. water mite diet isolate 10933-BHL101516-GBD27749_8357-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACCTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGAAACTGATTATTGCCTCTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614146 Paratanytarsus sp. water mite diet isolate 11003-BHL110116-GBD19745_20487-Lq74 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGTGGATTTGGGAACTGATTCTTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACACTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614147 Paratanytarsus sp. water mite diet isolate 11016-BHL110116-GBD6630_8741-Lq75 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACAGATTATTGCCTTTAATATTAGGAGTCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614148 Paratanytarsus sp. water mite diet isolate 11047-BHL110116-GBD17123_4722-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTAATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGTGGATTTGGTAACTGATTATTGCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR757972, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614149 Paratanytarsus sp. water mite diet isolate 11049-BHL110116-GBD25415_13482-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGCACTTCTCTAAGAATATTAATTCGAGTTGAACTAGGACATCCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACCCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614150 Paratanytarsus sp. water mite diet isolate 11052-BHL110116-GBD17075_10037-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGAGGGTTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTATTATCAAGCAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614151 Paratanytarsus sp. water mite diet isolate 11053-BHL110116-GBD18493_16435-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGCCATCCCGGAACTTTTATTGGAGATGACCAGATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCACCCTCTTTAACACGATTACTGTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614152 Paratanytarsus sp. water mite diet isolate 11056-BHL110116-GBD16557_19190-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGAGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGAAATAACTTTTCCCCGAATAAATAATATAAGAATTTGGCTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614153 Paratanytarsus sp. water mite diet isolate 11059-BHL110116-GBD14864_5365-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGGGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTCGACTTCTTCCCCCCTCTTTAACTCTTTTTCTTTCTAGTAGAATCGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR757714, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614154 Paratanytarsus sp. water mite diet isolate 11063-BHL110116-GBD14912_17946-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACATTTATTGGAGATGACCAAATTTATAATGTCATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACCCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR747869, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614155 Paratanytarsus sp. water mite diet isolate 11065-BHL110116-GBD20462_14090-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTACGTATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGAGATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTGCTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614156 Paratanytarsus sp. water mite diet isolate 11074-BHL110116-GBD10332_23934-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCATGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGTTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGTGTGATTTGTGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614157 Paratanytarsus sp. water mite diet isolate 11078-BHL110116-GBD16599_19515-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTCTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGACCTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACTTATTTTAATTGGTGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTCTACCCCCCTCTGTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614158 Paratanytarsus sp. water mite diet isolate 11083-BHL110116-GBD11203_5785-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACCTTTATTGGAGATGACCAAATTTATAACGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTCAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR757972, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614159 Paratanytarsus sp. water mite diet isolate 11084-BHL110116-GBD13658_28872-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACAAGGACATCCCGGAACTTTTATTGGAGATGACAAAATTTATAATGTAATTGTTACAGCTCATGCCTTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614160 Paratanytarsus sp. water mite diet isolate 11091-BHL110116-GBD26537_19139-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGTGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCGCGTTAACTCGTTTACTGGCAAGTAGAAGAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614161 Paratanytarsus sp. water mite diet isolate 11093-BHL110116-GBD9922_24832-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTCTAATTGGGGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATGATATAAGATTTTGACTACTACCCCCCTCTTCAACTCTATTACTGTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614162 Paratanytarsus sp. water mite diet isolate 11098-BHL110116-GBD25556_7611-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACAGATTTTAATTGGAGGATTTGGGAACTGATTATTCCCTTTAATATTAGGAGCCCCAGACATAGCTTTTCCTCGAATAAATAATATAAGATTATGACTTTTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATCGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614163 Paratanytarsus sp. water mite diet isolate 11099-BHL110116-GBD21648_26377-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCACTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAGCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAACTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614164 Paratanytarsus sp. water mite diet isolate 11103-BHL110116-GBD26839_11742-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATTTTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGGCCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCAAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTACTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614165 Paratanytarsus sp. water mite diet isolate 11104-BHL110116-GBD1927_15167-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCACGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAACTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGTGGAGTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCACTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614166 Paratanytarsus sp. water mite diet isolate 11106-BHL110116-GBD12077_8719-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGTGGATTTGGAAACTGATTATTGCCTGTAATATTAGGTGCCCCAGATATGGCTTTTCCTCGAATAAATAATATAAGATTTTGACGTATTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614167 Paratanytarsus sp. water mite diet isolate 11107-BHL110116-GBD12649_2108-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGGATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGGGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACACTTTTACTATCAAGGAGAATAGGAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614168 Paratanytarsus sp. water mite diet isolate 11113-BHL110116-GBD7929_8525-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAAGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTCATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCACCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTTGCATGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614169 Paratanytarsus sp. water mite diet isolate 11118-BHL110116-GBD27204_22791-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATTTTAATTCGAGCTGAACTAGGACATCCCGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTATCAAGTACAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614170 Paratanytarsus sp. water mite diet isolate 11126-BHL110116-GBD23427_10631-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCATATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCACTTCCTCGAATAAATAATATAAGAATTTGACTTCCTCCCCCCGCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614171 Paratanytarsus sp. water mite diet isolate 11127-BHL110116-GBD21333_3178-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGATCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGTGTATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACGTCTTCCACCCTCTTGAACTCTTGTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614172 Paratanytarsus sp. water mite diet isolate 11133-BHL110116-GBD2420_17215-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATGTTAATTCGAGCTGAACTAGGACGTCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAGTTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTCTTCCCCCCTCTCTAACTCTTCTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614173 Paratanytarsus sp. water mite diet isolate 11140-BHL110116-GBD21711_23019-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTCTACTTCATTTTTGGTGCCTGATCATGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGGTTATTGCCTTTAATATTAGGAGAACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTGAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614174 Paratanytarsus sp. water mite diet isolate 11146-BHL110116-GBD8767_23899-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTCTAATTGGTGGATTTGGGAACTGATTAATGCCTTTAATATTAGGAGCCCCAGATATGGCTTTTCCTCGAATAAATAATAGAAGATTTTGGCTTCTTCCCCCCTCTTTAACTCGTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614175 Paratanytarsus sp. water mite diet isolate 11148-BHL110116-GBD22216_21348-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCGGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACACTTTTTCAATCAAGTAGAATAGTGGAAAATGGCGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614176 Paratanytarsus sp. water mite diet isolate 11150-BHL110116-GBD24703_8254-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGCAATTGTTACAGCTCATGCATTTCTTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTACCTTTAATATTAGGAGCACCAGATATAGCTTGTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614177 Paratanytarsus sp. water mite diet isolate 11161-BHL110116-GBD26777_11985-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCAGGAACTTTTATTAGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTTTAACTCTTTTACTTTCAAGTAGGATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR292109, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614178 Paratanytarsus sp. water mite diet isolate 11166-BHL110116-GBD3634_8277-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGATCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAACTGATTAGTGCCTTTAATATTAGGAGCCACAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTCGACTACTTCCCCCCTCTTTAACTCGTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614179 Paratanytarsus sp. water mite diet isolate 11179-BHL110116-GBD15094_4506-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCTGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGTGGATTTGGGACCTGATTATTGCCTTTAATATTAGGAGCCACAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGTGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR757972, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614180 Paratanytarsus sp. water mite diet isolate 11180-BHL110116-GBD17084_16115-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGGACTAGGACATCCCGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGTGGATTTGGGAACTGATTATTGCCTTTAATATTAGTAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTTCTTTCTAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614181 Paratanytarsus sp. water mite diet isolate 11183-BHL110116-GBD21716_13815-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACACATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTTGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTCTAACTCTTTTTCTTTCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614182 Paratanytarsus sp. water mite diet isolate 11198-BHL110116-GBD11690_23389-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTCATTGGAGATGAACAAATCTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATATTAATTGGGGGATTTGGGAACTGATTATTTCCTTTAATATTAGGATCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCACCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614183 Paratanytarsus sp. water mite diet isolate 11200-BHL110116-GBD24346_18179-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATACCTGAACTTTTATTGGAGATGACCAATTTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTTGGGGATTTGGGAACTGATTAGTGCCTTTAATATTAGTAGCCCCAGATATAGCTTTTCCTCGAATAGATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACGTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614184 Paratanytarsus sp. water mite diet isolate 11204-BHL110116-GBD18414_27381-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGACCTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGCAATTGTTGCAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCAGTTACTTGCAAGTAGAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614185 Paratanytarsus sp. water mite diet isolate 11207-BHL110116-GBD20213_4261-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGATCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACCTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGAGGATTTGGAAACTGATTTGTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTCTTCCCCCCTCTTTAACTCTTTTTCTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614186 Paratanytarsus sp. water mite diet isolate 11214-BHL110116-GBD26140_10344-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTTTACTTCCTTTTTGGTGCCTGATCAGGAATAGTAGGCACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGTGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGATCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCGCTTTAACCCGTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614187 Paratanytarsus sp. water mite diet isolate 11229-BHL110116-GBD26207_23533-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCCGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGATCTGAACTAGGACATACCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGGTTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTGGCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614188 Paratanytarsus sp. water mite diet isolate 11236-BHL110116-GBD22176_12188-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGTGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGACCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCGCTTTAACACTTTTACTATCAAGTAGAATAGTGGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614189 Paratanytarsus sp. water mite diet isolate 11244-BHL110116-GBD6637_8698-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGTAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAGCTGATTATTGCCTTTAATATTAGGAGTCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGGTTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTGTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR757972, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614190 Paratanytarsus sp. water mite diet isolate 11245-BHL110116-GBD7968_10073-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAACAAATAATATAAGATTGTGGCTTCTTCCCCCCTCTTTAACTCTTTTACAATCAAGTAGAAGAGTGGAAAATGGAGCCGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614191 Paratanytarsus sp. water mite diet isolate 11247-BHL110116-GBD7524_16186-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAATAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCATCCTTAACCCTATTACCATCAAGTAGAATAGCGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614192 Paratanytarsus sp. water mite diet isolate 11249-BHL110116-GBD2506_12943-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGGGCCTGATCAGGAATAGTAGGAACTTCACTAAGAATATTAATTCGAGCTGAATTAGGACATCCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGAGGATTTGGAAACTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614193 Paratanytarsus sp. water mite diet isolate 11252-BHL110116-GBD25766_17009-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGTCATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTGTTATAATTTTTTTCATAGTTATACATATTTTAATTGGAGGATTTGGGAACTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATATTGACTACTTCCCCCCTCTTTAACACTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614194 Paratanytarsus sp. water mite diet isolate 11254-BHL110116-GBD28095_15584-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATGTTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGTACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGGAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614195 Paratanytarsus sp. water mite diet isolate 11264-BHL110116-GBD10647_23456-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCAGAACTAGGACATCCCGGAACTTTTATTGGAGATGACAAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTTTTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614196 Paratanytarsus sp. water mite diet isolate 11268-BHL110116-GBD11023_11621-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGATTTTCCTCGAATAAATAATATAAGAGTTTGTCTTCTTCCCCCCTCTTTAACTATGTTACTTTCAAATAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR757972, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614197 Paratanytarsus sp. water mite diet isolate 11284-BHL110116-GBD16513_3304-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCGTTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGTAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTACTTTAATTGGCGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAATAGAATAGTGGAAAATGGAGCTGG	Using NCBI BLASTN in June 2018, this sequence was 98.1% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614198 Paratanytarsus sp. water mite diet isolate 11294-BHL110116-GBD6151_7565-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCATTTATTATCATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAACTGATTGTTGCCTTTAATATTAGGCGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTCTAACTCTGTTACTTTCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614199 Paratanytarsus sp. water mite diet isolate 11330-BHL110116-GBD20690_23870-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTAGGACATTCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATACTAGGTGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTGTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614200 Paratanytarsus sp. water mite diet isolate 11334-BHL110116-GBD4884_11128-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATGGGAGATGACCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATCTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCGTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614201 Paratanytarsus sp. water mite diet isolate 11348-BHL110116-GBD2452_11900-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAAGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTATGACATCCCGGAACCTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATCATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCGTTAACTCTTTTACGGTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614202 Paratanytarsus sp. water mite diet isolate 11352-BHL110116-GBD6503_4798-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTACCCCACTTCCTTCCAAGTAGAATAGAGGAAAATGGAGCTCGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614203 Paratanytarsus sp. water mite diet isolate 11356-BHL110116-GBD26669_7617-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATTTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGTGGGATTTGGGAACTGATTATTGCCTTGAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCGCTTTAACTCGTTTACGTTCAAATAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614204 Paratanytarsus sp. water mite diet isolate 11358-BHL110116-GBD24915_23377-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCCTAAGTATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAGCTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTATTCCCCCATCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614205 Paratanytarsus sp. water mite diet isolate 11359-BHL110116-GBD6830_8139-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGTTGAATTAGGACATCCCGGATCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTCCTACCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614206 Paratanytarsus sp. water mite diet isolate 11373-BHL110116-GBD2017_16315-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATACTAATTCGAGCTGAATTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAATTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAACATAAGATTTTGACGTCTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614207 Paratanytarsus sp. water mite diet isolate 11383-BHL110116-GBD15601_4683-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTAAACTAGGACATCCCTGAACTTTTATTGGAGATGACAAAATTTATAAGGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGCAACTGATTATGGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR757972, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614208 Paratanytarsus sp. water mite diet isolate 11387-BHL110116-GBD14275_4207-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACCTCCCTAAGAATATTAATTCGAGCTGAACTAGGACAGCCCTTAACTTTTATTGGAGATGACCATATTTATAATGTAATGTTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAATATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614209 Paratanytarsus sp. water mite diet isolate 11409-BHL101516-GBD15345_13204-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTGGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCGTCCCCCCTCTTTAACACTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614210 Paratanytarsus sp. water mite diet isolate 11448-BHL101516-GBD7068_14686-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614211 Paratanytarsus sp. water mite diet isolate 11496-BHL101516-GBD27851_11496-Lq80 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614212 Paratanytarsus sp. water mite diet isolate 11554-BHL101516-GBD27405_17599-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTACCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACACTATTACGTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614213 Paratanytarsus sp. water mite diet isolate 11782-BHL101516-GBD3942_12250-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGCACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCGTCCCCCCTCTTTAACTCGTTTGCTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614214 Paratanytarsus sp. water mite diet isolate 12049-BHL040517-GBD8376_15337-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTGAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614215 Paratanytarsus sp. water mite diet isolate 12550-BHL040517-GBD5670_9064-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCAGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGCAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAATATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614216 Paratanytarsus sp. water mite diet isolate 12980-BHL040517-GBD11964_21913-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACCTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTTATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614217 Paratanytarsus sp. water mite diet isolate 12990-BHL040517-GBD24391_16283-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCTGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCAATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614218 Paratanytarsus sp. water mite diet isolate 13015-BHL040517-GBD17084_17560-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACGTCCTTAAGTATACTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTATAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTCCCCCGTATAAATAACATAAGTTTTTGATTACTTCCGCCATCATTAACCCTTCTTCTATCAACAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614219 Paratanytarsus sp. water mite diet isolate 13091-BHL040517-GBD8012_26327-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTTATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGCGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATAAATATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR742514, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614220 Paratanytarsus sp. water mite diet isolate 13200-BHL040517-GBD21482_18918-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614221 Paratanytarsus sp. water mite diet isolate 13233-BHL040517-GBD25435_11024-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGAATAAATAACATAAGATTTTGATTACTACCCCCATCTTTAACCCTACTTCTATCAAGAACATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR742514, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614222 Paratanytarsus sp. water mite diet isolate 13358-BHL040517-GBD19562_20059-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGTCACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTCCCCCGAATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTTTTCTATCAAGAACATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR628998, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614223 Paratanytarsus sp. water mite diet isolate 13413-BHL040517-GBD12422_14596-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCTGAATTATGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTTTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGATTTTGATTACTTCCCCCATCTTTAACCCTACTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR753366, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614224 Paratanytarsus sp. water mite diet isolate 13440-BHL040517-GBD10746_13901-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTATATTTTCGGAGCTTGGTCAGGAATAGTCGGTACTTCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR753366, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614225 Paratanytarsus sp. water mite diet isolate 13443-BHL040517-GBD3529_18658-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTATTTTTGGAGCTTGGTCAGGAATAATAGGAACATCCTTAAGTATATTAATTCGAGTAGAATTAGGACACCCAGGAACATTAATTGGAGATGATCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR740890, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614226 Paratanytarsus sp. water mite diet isolate 13487-BHL040517-GBD25641_18750-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGTAGAATTAGCTCACCCTGGAACATTTCTTGGAGATGATCAACTCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCACCCGATATAGCTTTTCCCCGTATAAATAACATAAGATTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR753366, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614227 Paratanytarsus sp. water mite diet isolate 13533-BHL040517-GBD17254_2734-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTTTAACATTTATTGGATATGACCAAATCTATAATGTAAGTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAAAAGATTAGTGGAAAATGGCGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR742514, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614228 Paratanytarsus sp. water mite diet isolate 13557-BHL040517-GBD15437_2013-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACTTTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACATATTCTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614229 Paratanytarsus sp. water mite diet isolate 13588-BHL040517-GBD20018_16515-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGAGCCTGATCAGGAATAGTAGGAACTTCCTTAAGTATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTTTTACTATCAAGTAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614230 Paratanytarsus sp. water mite diet isolate 13589-BHL040517-GBD25559_8635-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACATTATTTTTTGGTGCCTGATCAGGAATAGTAGGAATTTCCCTAAGATTATTAATTCGCGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614231 Paratanytarsus sp. water mite diet isolate 13668-BHL040517-GBD10275_27043-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCATTTAATATTAGGAGCCCCAGATATAGCTTTTCTTCGAATAAATAATATAAGATTTTGACTACGTCCCCCCACTTTAACTCATTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614232 Paratanytarsus sp. water mite diet isolate 13694-BHL040517-GBD28059_10663-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACCAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCCCGAAAAAAAAATATAAGATTTTGACTTCTTCCCCCCTCCTTAACCCTTTTACTTTCAAGGAGAATAGGGGAAAAAGGAGCTGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614233 Paratanytarsus sp. water mite diet isolate 13701-BHL040517-GBD17109_17643-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGAGTTGGAAATTGATTATTGCCTTTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614234 Paratanytarsus sp. water mite diet isolate 13709-BHL040517-GBD12324_4066-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACACCCTGGAACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTAGTGCCTTTAATATTAGGAGCCACAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTTCTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614235 Paratanytarsus sp. water mite diet isolate 13713-BHL040517-GBD9612_4748-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCGTTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGTAACTTTTATTGGAGATGACCATATTTATAATGTAATTGTTACAGCTCATGCATTTATTACAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTATTTAACGCTTTTACTTCCAAGTAGAATAGTGGAAAATGGATCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614236 Paratanytarsus sp. water mite diet isolate 13719-BHL040517-GBD16562_8900-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATACTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614237 Paratanytarsus sp. water mite diet isolate 13724-BHL040517-GBD9964_2679-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTTATTTTCGGTGCCTGATCAGGAATAGTCGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATTGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTATTATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCATCTTTAACCCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614238 Paratanytarsus sp. water mite diet isolate 13768-BHL040517-GBD13855_13099-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTACCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATCGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGACCCATATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACACTTTGACTTTCAAGGAGAATAGTGGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614239 Paratanytarsus sp. water mite diet isolate 13769-BHL040517-GBD6916_8042-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACTTCCTTAAGTATATTAATTCGAGCAAAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAATTAATATAAGTTTTTGATCACTACCCCCAGCTTTAACCCTGCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614240 Paratanytarsus sp. water mite diet isolate 13866-BHL040517-GBD19567_25287-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTCATTTTTGGTGCCTGATCAGGTATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGCAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATCGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTATTACTACCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614241 Paratanytarsus sp. water mite diet isolate 13891-BHL040517-GBD17305_3934-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTCGGAGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAGTTGGAGGATTTGGCAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGTTTTTCCTCGAATAAATAATATAAGATTTTGAGTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614242 Paratanytarsus sp. water mite diet isolate 13923-BHL040517-GBD26675_16922-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGCACATTATATTTTATTTTCGGGGCCTGATCAGGCATAGTAGTAACTTACCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614243 Paratanytarsus sp. water mite diet isolate 14000-BHL040517-GBD26723_13848-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATCGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCCTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGAATACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614244 Paratanytarsus sp. water mite diet isolate 14133-BHL040517-GBD22694_26258-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTAATGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTGTAAATCGGGTATTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614245 Paratanytarsus sp. water mite diet isolate 14161-BHL040517-GBD8900_22854-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCCTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614246 Paratanytarsus sp. water mite diet isolate 14205-BHL040517-GBD22649_24224-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGATTGATCAGGAATAGTCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACTCCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGACTACTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCTCGTATAAATAATATAAGATTTTGACTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614247 Paratanytarsus sp. water mite diet isolate 14217-BHL040517-GBD29230_18535-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAACAATATAAGTTTTTGAATATTACCCCCATCTTTAACCCTTCTTCTAGCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614248 Paratanytarsus sp. water mite diet isolate 14224-BHL040517-GBD26832_15376-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATACTTCATTTTCGGTGCCTGATCCGGAATAGTGGGAACTTCCTTAAGAATATTTATTCGAGCTGAACTAGGACATCCCGGAACCTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614249 Paratanytarsus sp. water mite diet isolate 14227-BHL040517-GBD14074_20219-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTTTATTAATTCGAGCAGAATTAGGACACCCAGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGAATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTACTACTATCAAGAACATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR758568, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614250 Paratanytarsus sp. water mite diet isolate 14228-BHL040517-GBD19236_6488-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTATTTTCGGAGCTTGATCAGGAATAGTCGGAACTTCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGCTATACCTATTTTAATTGGAGGATTTGGGAATTGACTTCTTCCTTTAATATTAGGGGCCCCCGATATAGCTTTTCCCCGTATAAATAATAAAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614251 Paratanytarsus sp. water mite diet isolate 14230-BHL040517-GBD9971_25435-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACTTCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTCATAGTTATACCTATCTTAATTGGAGGATTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTAAAAATAATATAAGTTTTTGATTACTACCCCCATCTTTAACCCTTCTTCTATCAGGAAGATTAGTGGAGAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614252 Paratanytarsus sp. water mite diet isolate 14233-BHL040517-GBD23836_9730-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTCGATCCGGAATAATCGGAACTTCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTGCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCATCTATCAAGAAGATTAGTGGAAAATGTAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614253 Paratanytarsus sp. water mite diet isolate 14235-BHL040517-GBD24899_13678-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGATTTAGGACCTCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTCCAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614254 Paratanytarsus sp. water mite diet isolate 14236-BHL040517-GBD6188_9903-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTTATTTTCGATGCCTGATCCGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATTTTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTTTAACTCTGTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614255 Paratanytarsus sp. water mite diet isolate 14238-BHL040517-GBD14294_2138-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTATTTTCGGAGCTTGATCAGGAATAATAGTAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGTTGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATCATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCACCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614256 Paratanytarsus sp. water mite diet isolate 14247-BHL040517-GBD25571_9574-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGGACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTGTTATTGGAGATGACCAACTTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGTAGCCCCAGATATAGCTTTTCCTCGAATAAATAAAATAAGATTTTGACTTCGTCCCCCCTCTTTAACTCTTTTACATTCAAGTAGAATAGTGGAAAATGGAGCTGGAACGGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614257 Paratanytarsus sp. water mite diet isolate 14251-BHL040517-GBD24931_25019-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATATTCGGACCATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACTTCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGAATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614258 Paratanytarsus sp. water mite diet isolate 14255-BHL040517-GBD24825_19250-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGTATATTAATTCGAGCCGAACTAGGACATCCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCTCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614259 Paratanytarsus sp. water mite diet isolate 14262-BHL040517-GBD21709_10554-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTGAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTCACTCTTTTTCTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614260 Paratanytarsus sp. water mite diet isolate 14277-BHL040517-GBD14796_10860-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGTTAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTATAGCTCATGCATTACTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATTTTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACCTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614261 Paratanytarsus sp. water mite diet isolate 14282-BHL040517-GBD21860_12872-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCTGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTACTACTATCAAGTAGAATAGTGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614262 Paratanytarsus sp. water mite diet isolate 14289-BHL040517-GBD20424_5797-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTTGGAGCTTGATCAGGAATAATCGGTACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCTAGAAGACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KM994688, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614263 Paratanytarsus sp. water mite diet isolate 14290-BHL040517-GBD29468_17934-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATTTTTTATTTTTGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGACTAGAATTAGGACACCCTGGCACATTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCATTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614264 Paratanytarsus sp. water mite diet isolate 14291-BHL040517-GBD17213_21563-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTGGGAACTTCTTTAAGAATATTAATTCGAGCTGGACTAGGACAACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTATTGCCTTTAATTTTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279360, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614265 Paratanytarsus sp. water mite diet isolate 14308-BHL040517-GBD23738_14955-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATCATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCGTTTCCCCGAATAAATAATATAAGGTTTTGATTACGTCCCCCATCTTTAACCCGTCTTCTATCAAGAAGATTAGTGGACAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614266 Paratanytarsus sp. water mite diet isolate 14314-BHL040517-GBD11306_10440-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATACTTCATTTTCGGTGCCTGATCAGGAATAGTTGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTAGTGCCTTTAATATTAGGATCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614267 Paratanytarsus sp. water mite diet isolate 14315-BHL040517-GBD17342_10590-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTTGTTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGTTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTATAGCTCATGCATTTATTATAACTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614268 Paratanytarsus sp. water mite diet isolate 14323-BHL040517-GBD25563_5454-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACTTCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGCACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAAGATCCCCCGATATAGCTTTTCCCCGGATAAATAAAATAAGGTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614269 Paratanytarsus sp. water mite diet isolate 14327-BHL040517-GBD7244_20208-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGCAACTTTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGTTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACCTCCCACATCTTTAACCCCTCTTCTATCAAGAAGATTAGTGGAAAAAGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614270 Paratanytarsus sp. water mite diet isolate 14328-BHL040517-GBD18573_25084-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGTCTGATCAGGAATAGTTGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGTTTTGGTAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614271 Paratanytarsus sp. water mite diet isolate 14331-BHL040517-GBD24734_20605-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTGACTCTTCTACTATCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR282105, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614272 Paratanytarsus sp. water mite diet isolate 14336-BHL040517-GBD29132_17598-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTCTATTTTATTTTCGGAGCTTGATCGGGAATAATCGGAACATCCTTAAGTATATTAACTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGTTATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTTTCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614273 Paratanytarsus sp. water mite diet isolate 14340-BHL040517-GBD26437_21049-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAATTCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTATTTGATTACTTCCCCCATCTTTAACCCGGCATCAATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR740890, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614274 Paratanytarsus sp. water mite diet isolate 14342-BHL040517-GBD12943_26150-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAAAATTAGGACACCCTGGAACATTTATTGGGGGTGATCAAATCTATAATGTTATCGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACGTTCCCCATCTTTAACCCTTCTTCTATCAAGATGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614275 Paratanytarsus sp. water mite diet isolate 14352-BHL040517-GBD23976_10512-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACTTCTTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGTGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGACTTCTTCCTTTAATATTAGGTGCCCCCGATATAGCTTTTCCCAGGATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614276 Paratanytarsus sp. water mite diet isolate 14353-BHL040517-GBD13163_12522-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATTTATAATGTTGTTGTTACAGCTCATGCTTTTATTTTAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGATTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTACCCCCATCATTAACCCTACTACTATCAAGAAGATTAATGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614277 Paratanytarsus sp. water mite diet isolate 14355-BHL040517-GBD26209_20774-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGACTATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTTTTGCCTCTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTGTAACTCGTTTACTTACAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614278 Paratanytarsus sp. water mite diet isolate 14362-BHL040517-GBD18165_4195-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGTAACATTTATTGGAGATGATCAAATCTATAATGATATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATAACTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATACAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGCGCTGGAAAAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614279 Paratanytarsus sp. water mite diet isolate 14364-BHL040517-GBD8855_5158-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGTATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTCGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATTTTAGGAGTACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACGCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614280 Paratanytarsus sp. water mite diet isolate 14366-BHL040517-GBD13741_20367-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTCGGTGTCTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGATCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614281 Paratanytarsus sp. water mite diet isolate 14402-BHL040517-GBD22843_24354-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACTTCTTTAAGTATATTAATTCGAGCAGAATTAGGACATCCTGGAACATTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGTGGTTTTGGAAATTGACTACTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGAATAAATAATATAAGTTTTAGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614282 Paratanytarsus sp. water mite diet isolate 14419-BHL040517-GBD26424_8027-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATTGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGATACCCTGGAACATTCATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTACATCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614283 Paratanytarsus sp. water mite diet isolate 14422-BHL040517-GBD18925_26481-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATATTATTTTTGGAGCTTGATCTGGAATAATAGGAACTTCCTTAAGTATATTAATTCGAGCAGAACTAGGACGCCCTGGAACTTTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614284 Paratanytarsus sp. water mite diet isolate 14423-BHL040517-GBD14078_19186-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATATTCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTATGGGTCCCCGATATAGCTTTACCCCGCATAAATAATATAAGTTTTTGATTACTTCCCACATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614285 Paratanytarsus sp. water mite diet isolate 14428-BHL040517-GBD10885_6637-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTGATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTCGAGGATTTGGGAACTGATTATTGCCTTTAATTTTAGGAGCCCCAGATGTAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614286 Paratanytarsus sp. water mite diet isolate 14429-BHL040517-GBD9968_26860-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATTTTAGGCGCCCCAGATATGGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACGCTTTTACGTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614287 Paratanytarsus sp. water mite diet isolate 14434-BHL040517-GBD2369_14957-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTAGGCACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATCTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614288 Paratanytarsus sp. water mite diet isolate 14440-BHL040517-GBD9537_14467-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTCGGTGCTCGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATTTTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATACAAGATTTTGACTACTTCCCCCCTCTTTAACACTTTTTCAATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614289 Paratanytarsus sp. water mite diet isolate 14445-BHL040517-GBD3220_16335-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAAATTTTATTGGAGATGACCATATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATTTTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTCTTCCCCCCTCTCTAACTCTTTTACTTTCAAGTAGAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614290 Paratanytarsus sp. water mite diet isolate 14472-BHL040517-GBD24862_25554-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATACTTCATTTTCGGAGCATGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTAACAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614291 Paratanytarsus sp. water mite diet isolate 14476-BHL040517-GBD24464_15220-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTCGGTGCCTGATCAGGTATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACAACCCGGAACTTTTATTGGGGATGATCAAATTTATAATGCAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTATTACTAACAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614292 Paratanytarsus sp. water mite diet isolate 14480-BHL040517-GBD9811_6050-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGTTTGATCAGGAATAATCGGAACATCCTTAATTATATTAATTCGAGCAGAATTATGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATCATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTTTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614293 Paratanytarsus sp. water mite diet isolate 14483-BHL040517-GBD22801_13418-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCGGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTGGAATGTTATTGTTACAGCTCATGCTTTTTTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAGTTGACTTCTTCCCTTAATATTAGGAGCCCCCGATATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCTATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614294 Paratanytarsus sp. water mite diet isolate 14492-BHL040517-GBD6432_16403-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACTTCATTAAGTATATTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTTTTGTTACTGCTCATGCTTTTATTATAATGTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTCTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614295 Paratanytarsus sp. water mite diet isolate 14496-BHL040517-GBD21874_6041-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTTCTTCCTTTAATACTAGGAGCACCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTCTGACTACTACCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614296 Paratanytarsus sp. water mite diet isolate 14503-BHL040517-GBD26637_14308-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTTATTCGAGCAGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAGTGTAATCGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614297 Paratanytarsus sp. water mite diet isolate 14507-BHL040517-GBD16757_16235-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACTTCCTTAAGTATACTAATTCGAGCAGAATTAGGACACCTTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCCTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR742514, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614298 Paratanytarsus sp. water mite diet isolate 14509-BHL040517-GBD29036_15373-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACTTCCTTAAGTATATTTATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGAATAAATAATATAAGTTTTTGATTACTACCCCCATCTATAACCCTTCTTCTATCAAGAAGATTAGTAGAAAATGTAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614299 Paratanytarsus sp. water mite diet isolate 14510-BHL040517-GBD24600_25314-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTTGGAGCTTGATCAGGAATAATCGGAACTTCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTGTTCCTTTAATATTAGGAGCCCCCGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCTAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614300 Paratanytarsus sp. water mite diet isolate 14517-BHL040517-GBD23066_20240-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTCTATATTTTATTTTCGGAGCTTGATCAGGAATAATAGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACATCCTGGAACATTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGTGAATTGACTTCTTCCTTTAATATTAGTAGCCCTCGATATAGCGTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614301 Paratanytarsus sp. water mite diet isolate 14521-BHL040517-GBD6939_21098-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATTGGAACTTCCTTAAGTATATTAATTCGAGTTGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCCTATAAATAATAAAAGTTTTTGATTACGTCCACCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614302 Paratanytarsus sp. water mite diet isolate 14529-BHL040517-GBD19738_11976-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCCTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGTAGAATTAGGACACCCTGGTACATTTATTGGAGAAGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCATTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTACTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614303 Paratanytarsus sp. water mite diet isolate 14531-BHL040517-GBD14674_17444-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTTTATTTTATTTTCGGAGCTTGACCAGGAATAATCGGAACTTCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGGAACTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACCTCCCCCATCATTAACCCTACTACTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614304 Paratanytarsus sp. water mite diet isolate 14532-BHL040517-GBD25739_11895-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTCGGTGCCTGATCAAGAATAGTGGGAACTTCTTTAAGTATATTAATTCGAGCTGAACTAGGACATCCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATTCCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614305 Paratanytarsus sp. water mite diet isolate 14534-BHL040517-GBD20871_26681-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATGGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGCAATTGACTTCTTCCTTTAATATTTGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTTCTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614306 Paratanytarsus sp. water mite diet isolate 14535-BHL040517-GBD25245_23330-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGCACATCCTTAAGTATATTCATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTACTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAAAAAAAGTTTTGGATTACCTTCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614307 Paratanytarsus sp. water mite diet isolate 14537-BHL040517-GBD6598_11758-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACTTCCTTAGGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGATTACTTCCTTTAATATTAGGAGTACACGATATAGCTTTTCCCCGTATAAATAATATAAGATTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAACATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614308 Paratanytarsus sp. water mite diet isolate 14538-BHL040517-GBD13167_12896-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTACAGTTATACCTATTTTAATTGGAGGTTTTGGGAAATGACTTCTTCC	Using NCBI BLASTN in June 2018, this sequence was 99.0% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614309 Paratanytarsus sp. water mite diet isolate 14548-BHL040517-GBD20475_18623-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACTTCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACTTTCATTGGAGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGTTTTCGGAATTGACTTGTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTTTCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614310 Paratanytarsus sp. water mite diet isolate 14555-BHL040517-GBD28853_12556-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGCATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTGCCCCGTATAAATAATATAAGTTGTTGATTACGTCCCCCAGCTTTAACCCGACATCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614311 Paratanytarsus sp. water mite diet isolate 14556-BHL040517-GBD11421_25406-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGATTAATCGGAACTTCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACTGCTAATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCCCGTATAAATAATATAAGATTTTGATTACTACCCCCATCTTTAACCCTTCTTCTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614312 Paratanytarsus sp. water mite diet isolate 14561-BHL040517-GBD11470_13559-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTTTACTTTATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTTAGTATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614313 Paratanytarsus sp. water mite diet isolate 14967-BHL040517-GBD3806_9400-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCCTAAGAATATTTATTCGAGCTGAACTAGGCCATCACGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACATGCCTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR757714, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614314 Paratanytarsus sp. water mite diet isolate 15144-BHL040517-GBD27046_22359-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGATCACTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGTAAACTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614315 Paratanytarsus sp. water mite diet isolate 15238-BHL040517-GBD26019_16320-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCTTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATCATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGAATACTTCCCCCATCTTTAACCCTACTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614316 Patrobus sp. water mite diet isolate 15009-BHL040517-GBD6766_9914-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCATCCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTTTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID MF458986, identified in GenBank as Patrobus longicornis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614317 Pentaneura sp. water mite diet isolate 2222-BHL072216-GBD8661_11156-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTCCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACACTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGTGGATTTGGTAATTGACTAGTACCCCTTATACTAGGAGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTACTACCCCCTTCTTTAACCTTACTATTATCTAGCTCTATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID MG067468, identified in GenBank as Pentaneura sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614318 Phaenopsectra sp. water mite diet isolate 7475-BHL032417-GBD9800_12045-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614319 Phaenopsectra sp. water mite diet isolate 8423-BHL101416-GBD21196_16836-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATACATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTGACATTAATATTAGGAGCACCTGATATGGCATTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCTTCCTTAACATTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR289424, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614320 Phaenopsectra sp. water mite diet isolate 8451-BHL101416-GBD8695_11395-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTGTTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614321 Phaenopsectra sp. water mite diet isolate 8506-BHL101416-GBD20291_22515-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAAATGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATAAAACATTTCCTCGAAAAAATAATAAAAGGTTTTGACTTTTACCCCCTTCTTTAACCTCACTACTTTCTAGTACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614322 Phaenopsectra sp. water mite diet isolate 8518-BHL101416-GBD15453_14273-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGATCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTCTTGACTTCTCCCCCCATCCTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614323 Phaenopsectra sp. water mite diet isolate 8537-BHL101416-GBD16374_22773-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTAATTGGAGATGATCAAATTTATGATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTTTCTTTACTTCTTTCTAGTTCAATCTTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.7% identical to accession ID KR723136, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614324 Phaenopsectra sp. water mite diet isolate 8552-BHL101416-GBD22033_10834-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGAACTTCTTTTAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAACATAAGATTTTGACTATTACCCCCTTCTTTAACATTACTTCTATCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614325 Phaenopsectra sp. water mite diet isolate 8585-BHL101416-GBD23129_6417-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTAGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR289424, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614326 Phaenopsectra sp. water mite diet isolate 8597-BHL101416-GBD19522_27979-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAAATTTAATTGGAGATGATCAAATTTATAATGTTATTGTAACAACCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTGCCATTAATATTAGGAGCACCTGATATGGCATTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614327 Phaenopsectra sp. water mite diet isolate 8653-BHL101416-GBD18136_8092-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTCGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGACTAGTACCTTTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAACATAAGTTTTTGACTATTACCCCCATCTTTAACCCTACTTCTATCTAGAACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR723136, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614328 Phaenopsectra sp. water mite diet isolate 8694-BHL101416-GBD24607_4771-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGTTTAGTACATCTAATATTAGGAGCCCCTGATATAGCATTTCTTCGAATAAATAATATAAGTTTTTGACTTCTACCCCCATCTTTGACTCTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614329 Phaenopsectra sp. water mite diet isolate 8696-BHL101416-GBD12794_8419-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATTTTAATTCGAGTTGAATTAGGTCACCCAGGAACATTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGTAATTGATTAGTACCTCTAATATTAGGATCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTATTACCCCCTTCATTAACCTTACTTCTATCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614330 Phaenopsectra sp. water mite diet isolate 8703-BHL101416-GBD6598_7516-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTCAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614331 Phaenopsectra sp. water mite diet isolate 8707-BHL101416-GBD27397_15005-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTAAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTATTTGTAACTGCTCATGCATTTATTATATTTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGTACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614332 Phaenopsectra sp. water mite diet isolate 8708-BHL101416-GBD9960_21514-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCATTTAGAATGTTAATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGTGATGATCAAATTTATAATGGAATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTATCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.1% identical to accession ID KR723136, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614333 Phaenopsectra sp. water mite diet isolate 8729-BHL101416-GBD18937_19822-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTTAGTATATTAATTCGAGTTGAATTAGGACACCCAGGAACTTTAATTGGAGATGATCAACTTTATAATGTACTTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCACCATCTTTAACTTTACTACTTTCTAGTGCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614334 Phaenopsectra sp. water mite diet isolate 8738-BHL101416-GBD3409_13489-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCTGAATTAGGTCGCCCAGGTACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGAAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTAACTTTACTATTATCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614335 Phaenopsectra sp. water mite diet isolate 8743-BHL101416-GBD18655_28574-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATTTTAATTCGAGCTGAATTAGGTCACCCAGGCTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGTAATTGATTAGTACCTCTAATATTAGGTGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTATTACCCCCTTCATTAACTTTACTTCTATCTAGTTCAATCGTAGAAAATGGAGCTGGAACTGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614336 Phaenopsectra sp. water mite diet isolate 8775-BHL101416-GBD18138_11480-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACACTATGCTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGCTCAACCAGGAACTTTAATTGGAGGTGATCAAATTTATAATGTACTTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCTTCTTTAACCTTACTTCTTTCTAGTGCAGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR293527, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614337 Phaenopsectra sp. water mite diet isolate 8784-BHL101416-GBD20145_17184-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTATTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGACCAAATTTATAATGTAGTAGTTACAACTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAAGATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGATTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614338 Phaenopsectra sp. water mite diet isolate 8815-BHL101416-GBD2113_12770-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTTATTTTTGGAGCGTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTTATTGGGGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGAAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTATTACCACCATCTTTAACTTTACTTCTTTCTAGTACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614339 Phaenopsectra sp. water mite diet isolate 8818-BHL101416-GBD17653_20662-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGTTCATGCATTTATTATAATTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTATTACCACCTTCTTTAACCTTACTACTTTCTAGTGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614340 Phaenopsectra sp. water mite diet isolate 8825-BHL101416-GBD6156_22862-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGAAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATACTTGGAACACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614341 Phaenopsectra sp. water mite diet isolate 8831-BHL101416-GBD24413_18093-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGTTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCTTCTTTATCCTTACTACTATCTAGTACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR293527, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614342 Phaenopsectra sp. water mite diet isolate 8839-BHL101416-GBD9667_10571-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACGCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTT-TTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614343 Phaenopsectra sp. water mite diet isolate 8849-BHL101416-GBD13773_22503-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGCACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGTACCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTGTTACCCCCTTCTTTAACTTTACTACTATCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614344 Phaenopsectra sp. water mite diet isolate 12062-BHL040517-GBD21196_16836-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATACATTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTGACATTAATATTAGGAGCACCTGATATGGCATTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCTTCCTTAACATTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR289424, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614345 Phaenopsectra sp. water mite diet isolate 12090-BHL040517-GBD8695_11395-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTGTTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCATTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614346 Phaenopsectra sp. water mite diet isolate 12145-BHL040517-GBD20291_22515-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTATAGTAATACCTATTTTAAATGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATAAAACATTTCCTCGAAAAAATAATAAAAGGTTTTGACTTTTACCCCCTTCTTTAACCTCACTACTTTCTAGTACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614347 Phaenopsectra sp. water mite diet isolate 12157-BHL040517-GBD15453_14273-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGATCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTCTTGACTTCTCCCCCCATCCTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614348 Phaenopsectra sp. water mite diet isolate 12176-BHL040517-GBD16374_22773-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTAATTGGAGATGATCAAATTTATGATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTTTCTTTACTTCTTTCTAGTTCAATCTTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.7% identical to accession ID KR723136, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614349 Phaenopsectra sp. water mite diet isolate 12191-BHL040517-GBD22033_10834-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGAACTTCTTTTAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAACATAAGATTTTGACTATTACCCCCTTCTTTAACATTACTTCTATCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614350 Phaenopsectra sp. water mite diet isolate 12224-BHL040517-GBD23129_6417-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTAGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR289424, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614351 Phaenopsectra sp. water mite diet isolate 12236-BHL040517-GBD19522_27979-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAAATTTAATTGGAGATGATCAAATTTATAATGTTATTGTAACAACCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTGCCATTAATATTAGGAGCACCTGATATGGCATTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614352 Phaenopsectra sp. water mite diet isolate 12292-BHL040517-GBD18136_8092-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTCGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGACTAGTACCTTTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAACATAAGTTTTTGACTATTACCCCCATCTTTAACCCTACTTCTATCTAGAACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR723136, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614353 Phaenopsectra sp. water mite diet isolate 12333-BHL040517-GBD24607_4771-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGTTTAGTACATCTAATATTAGGAGCCCCTGATATAGCATTTCTTCGAATAAATAATATAAGTTTTTGACTTCTACCCCCATCTTTGACTCTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614354 Phaenopsectra sp. water mite diet isolate 12335-BHL040517-GBD12794_8419-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATTTTAATTCGAGTTGAATTAGGTCACCCAGGAACATTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGTAATTGATTAGTACCTCTAATATTAGGATCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTATTACCCCCTTCATTAACCTTACTTCTATCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614355 Phaenopsectra sp. water mite diet isolate 12342-BHL040517-GBD6598_7516-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTCAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614356 Phaenopsectra sp. water mite diet isolate 12346-BHL040517-GBD27397_15005-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTAAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTATTTGTAACTGCTCATGCATTTATTATATTTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGTACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614357 Phaenopsectra sp. water mite diet isolate 12347-BHL040517-GBD9960_21514-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCATTTAGAATGTTAATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGTGATGATCAAATTTATAATGGAATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTATCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.1% identical to accession ID KR723136, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614358 Phaenopsectra sp. water mite diet isolate 12368-BHL040517-GBD18937_19822-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTTAGTATATTAATTCGAGTTGAATTAGGACACCCAGGAACTTTAATTGGAGATGATCAACTTTATAATGTACTTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCACCATCTTTAACTTTACTACTTTCTAGTGCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614359 Phaenopsectra sp. water mite diet isolate 12377-BHL040517-GBD3409_13489-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCTGAATTAGGTCGCCCAGGTACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGAAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTAACTTTACTATTATCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614360 Phaenopsectra sp. water mite diet isolate 12382-BHL040517-GBD18655_28574-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATTTTAATTCGAGCTGAATTAGGTCACCCAGGCTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGTAATTGATTAGTACCTCTAATATTAGGTGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTATTACCCCCTTCATTAACTTTACTTCTATCTAGTTCAATCGTAGAAAATGGAGCTGGAACTGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614361 Phaenopsectra sp. water mite diet isolate 12414-BHL040517-GBD18138_11480-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACACTATGCTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGCTCAACCAGGAACTTTAATTGGAGGTGATCAAATTTATAATGTACTTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCTTCTTTAACCTTACTTCTTTCTAGTGCAGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR293527, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614362 Phaenopsectra sp. water mite diet isolate 12423-BHL040517-GBD20145_17184-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTATTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGACCAAATTTATAATGTAGTAGTTACAACTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAAGATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGATTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614363 Phaenopsectra sp. water mite diet isolate 12454-BHL040517-GBD2113_12770-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTTATTTTTGGAGCGTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTTATTGGGGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGAAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTATTACCACCATCTTTAACTTTACTTCTTTCTAGTACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614364 Phaenopsectra sp. water mite diet isolate 12457-BHL040517-GBD17653_20662-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGTTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTATTACCACCTTCTTTAACCTTACTACTTTCTAGTGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614365 Phaenopsectra sp. water mite diet isolate 12464-BHL040517-GBD6156_22862-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGAAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATACTTGGAACACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614366 Phaenopsectra sp. water mite diet isolate 12470-BHL040517-GBD24413_18093-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGTTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCTTCTTTATCCTTACTACTATCTAGTACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR293527, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614367 Phaenopsectra sp. water mite diet isolate 12478-BHL040517-GBD9667_10571-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACGCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTT-TTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614368 Phaenopsectra sp. water mite diet isolate 12488-BHL040517-GBD13773_22503-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGCACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGTACCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTGTTACCCCCTTCTTTAACTTTACTACTATCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614369 Phaenopsectra sp. water mite diet isolate 438-BHL040517-GBD25784_6511-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATCAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614370 Phaenopsectra sp. water mite diet isolate 1720-BHL110116-GBD29167_16355-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTATTTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTGATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCATTAACTTTACTACTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614371 Phaenopsectra sp. water mite diet isolate 1747-BHL110116-GBD11924_8387-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACTTTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTTATTCGAGCTGAATTAGGTCAACCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGTAATTGATTAGTACCTCTAATAATTGGAGCACCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTAACTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614372 Phaenopsectra sp. water mite diet isolate 2849-BHL032417-GBD8299_13839-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGGGCTGAATTAGGTCACCCATGAACTTTAATTGGAGATGATCAAATTTATGATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTGCCTCTTTCTAGTACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614373 Phaenopsectra sp. water mite diet isolate 3040-BHL032417-GBD14566_17506-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGATCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTAACTTTACTTCTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614374 Phaenopsectra sp. water mite diet isolate 5663-BHL032417-GBD20645_10642-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACATTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTAACTTTACTTCTATCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614375 Phaenopsectra sp. water mite diet isolate 5774-BHL032417-GBD18389_5372-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.7% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614376 Phaenopsectra sp. water mite diet isolate 8373-BHL101416-GBD25784_6511-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATCAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.4% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614377 Phaenopsectra sp. water mite diet isolate 8432-BHL101416-GBD23507_4418-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTTGGAGCTTGATCAGGAATACTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCTGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTATTACCCCCTTCTTTAACTTTACTTCTATCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614378 Phaenopsectra sp. water mite diet isolate 8548-BHL101416-GBD10799_14859-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGAAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCAGTTCCGCGAATAAATAATATAAGTTGTTGACTTTTACCCCCTTCTTGAACTTTACTTCGTGCTAGTTCAATCGTAGAAAATGGAGATGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614379 Phaenopsectra sp. water mite diet isolate 8553-BHL101416-GBD9782_4333-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTATTTCGAGCTGAATTAGGTCACCCAGTTACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCGTCATTAACTTTACTTCTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614380 Phaenopsectra sp. water mite diet isolate 8575-BHL101416-GBD3098_17625-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCTGAATTCGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCCTCTTTAACTTTACTTCTTTCTAGTTCACTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR723136, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614381 Phaenopsectra sp. water mite diet isolate 8632-BHL101416-GBD16986_2528-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACACTGTACTTTATTTTTGGAGCTAGATCAGGAATAGCAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGGCACCCAGGAACTTTAGTTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGTATTTCCTCGAATAAATAATATAATTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR293527, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614382 Phaenopsectra sp. water mite diet isolate 8654-BHL101416-GBD17586_8327-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACCCTTTACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTCTAACTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTAACTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614383 Phaenopsectra sp. water mite diet isolate 8655-BHL101416-GBD18098_27641-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACATTATTTTTGGGGCTTGATCCGAAATAGTGGGAACTTCTTTAAGTATATTAATTCGAGCTAAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGAATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCGTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR723136, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614384 Phaenopsectra sp. water mite diet isolate 8657-BHL101416-GBD11694_6477-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATTCCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGTAGCCCCTGATATAGCATATCCTCGAATAAATAATATAAGATTTTGGCTTTTACCCCCTTCTTTACCTTTAATTCCTTCTAGTTCAATCGAAAAAAATGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614385 Phaenopsectra sp. water mite diet isolate 8727-BHL101416-GBD19574_19301-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGACACCCAGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGAGGGATTTGGGAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTAACCTTACTTCTATCTAGTACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614386 Phaenopsectra sp. water mite diet isolate 8753-BHL101416-GBD24473_17626-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTACTTGGAGATGATCAAATTTATAATGTAATAGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTGATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAACAATATAAGATTTTGACTTTTACCCCCTTCTTTAACTTTACTACTTTCTAGTGCAACCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR293527, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614387 Phaenopsectra sp. water mite diet isolate 8822-BHL101416-GBD21388_24016-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACCTCTACCCCCTTCTTTAACTCTACTACTTTCTAGTACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614388 Phaenopsectra sp. water mite diet isolate 8843-BHL101416-GBD10909_6482-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACTCTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCTGGATCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGGTTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTGGACTTTTACCCCCGTCTTTAACTTTACTACTATCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614389 Phaenopsectra sp. water mite diet isolate 12071-BHL040517-GBD23507_4418-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTTGGAGCTTGATCAGGAATACTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCTGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTATTACCCCCTTCTTTAACTTTACTTCTATCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614390 Phaenopsectra sp. water mite diet isolate 12187-BHL040517-GBD10799_14859-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGAAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCAGTTCCGCGAATAAATAATATAAGTTGTTGACTTTTACCCCCTTCTTGAACTTTACTTCGTGCTAGTTCAATCGTAGAAAATGGAGATGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614391 Phaenopsectra sp. water mite diet isolate 12192-BHL040517-GBD9782_4333-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTATTTCGAGCTGAATTAGGTCACCCAGTTACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCGTCATTAACTTTACTTCTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614392 Phaenopsectra sp. water mite diet isolate 12214-BHL040517-GBD3098_17625-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCTGAATTCGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCCTCTTTAACTTTACTTCTTTCTAGTTCACTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR723136, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614393 Phaenopsectra sp. water mite diet isolate 12271-BHL040517-GBD16986_2528-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACACTGTACTTTATTTTTGGAGCTAGATCAGGAATAGCAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGGCACCCAGGAACTTTAGTTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGTATTTCCTCGAATAAATAATATAATTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR293527, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614394 Phaenopsectra sp. water mite diet isolate 12293-BHL040517-GBD17586_8327-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACCCTTTACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTCTAACTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTAACTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614395 Phaenopsectra sp. water mite diet isolate 12294-BHL040517-GBD18098_27641-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACATTATTTTTGGGGCTTGATCCGAAATAGTGGGAACTTCTTTAAGTATATTAATTCGAGCTAAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGAATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCGTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR723136, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614396 Phaenopsectra sp. water mite diet isolate 12296-BHL040517-GBD11694_6477-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATTCCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGTAGCCCCTGATATAGCATATCCTCGAATAAATAATATAAGATTTTGGCTTTTACCCCCTTCTTTACCTTTAATTCCTTCTAGTTCAATCGAAAAAAATGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614397 Phaenopsectra sp. water mite diet isolate 12366-BHL040517-GBD19574_19301-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGACACCCAGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGAGGGATTTGGGAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTAACCTTACTTCTATCTAGTACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614398 Phaenopsectra sp. water mite diet isolate 12392-BHL040517-GBD24473_17626-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTACTTGGAGATGATCAAATTTATAATGTAATAGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTGATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAACAATATAAGATTTTGACTTTTACCCCCTTCTTTAACTTTACTACTTTCTAGTGCAACCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR293527, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614399 Phaenopsectra sp. water mite diet isolate 12461-BHL040517-GBD21388_24016-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACCTCTACCCCCTTCTTTAACTCTACTACTTTCTAGTACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614400 Phaenopsectra sp. water mite diet isolate 12482-BHL040517-GBD10909_6482-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACTCTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCTGGATCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGGTTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTGGACTTTTACCCCCGTCTTTAACTTTACTACTATCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614401 Podocopida sp. water mite diet isolate 592-BHL072216-GBD22912_16602-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGTACCCTGATTGGGAATGATCAAATTTATAACACGATTGTGACTACCAATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATCGGAGGATATGGAAAATGATTAGTACCTTTAATACTAGAGACACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAATTGGAATACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614402 Podocopida sp. water mite diet isolate 594-BHL072216-GBD14051_28001-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTAATTTTTGGAGCTTGATCTGCTATGCTAGGAACTGCCTTAAGAGTATTTATTCGAGCTGAGCTCGGGCAACCTGGGGCCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACATCTGGTACACTAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614403 Podocopida sp. water mite diet isolate 596-BHL072216-GBD26260_10848-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTTATTTTTGGTGCTTGATCTGCTATGCTAGGAACTGCCTTAAGAGTACTTATTCGAGCTGATCTCGGGCAACCTGGGGCTCTGATTGGAAATGATCAAATTTATAACACAATTGTGACTGCCCATGCTTTTATTATAATTTTTTTTATGGTAATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAACTGGAACACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614404 Podocopida sp. water mite diet isolate 597-BHL072216-GBD10321_27860-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTTATTTTTGGTGCTTGATCTGCTATGCTAGGAACTGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGGCAGTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATTGGAGGGTTTGGAAACTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCATCCTTAACCTTATTAACAACTGGAATACTCGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614405 Podocopida sp. water mite diet isolate 601-BHL072216-GBD24039_21611-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTATTTATTCGAGCGGAGCTCGGGCAACCTGGAGCTCTGATTGGGAATGATCAAATTTATAACACAATTGTTACTGCCCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTATAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAACTGGAACACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614406 Podocopida sp. water mite diet isolate 602-BHL072216-GBD26906_11010-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTACTTATTCGAGCTGAACTCGGGCAACCTGGGACCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTACCAACTGGAGCACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614407 Podocopida sp. water mite diet isolate 603-BHL072216-GBD26855_7504-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTATTTATTCGAGCTGAGCTCGGGCAACCTGGGGCCTTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCTCATGCATTTATTATAATTTTTTTATAGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTTCCTTTAATACTAGGGGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTATCCTTATTAACAACTAGAATACTAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614408 Podocopida sp. water mite diet isolate 605-BHL072216-GBD16609_24960-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATACTAGGAACAGCCTTTAGAATACTTATTCGAGCTGAGTTCGGGCAACCTGGGACCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTATGGTAATACCAATTATAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAAAAATTGGAAGACTTACAGAAAAAGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614409 Podocopida sp. water mite diet isolate 607-BHL072216-GBD13153_10856-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTAATTTTTGGTGCTTGATCTGCTATACTAGGAACAGCCTTAAGAGTAATTATTCGAGTTGAGTTCGGGCAACCAGGGGCACTGATTGGAAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTATGGTAATACCAATTATAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCATCCTTAACCTTATTAACAACTGGAATACTAACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614410 Podocopida sp. water mite diet isolate 609-BHL072216-GBD24291_7289-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGACTCTTATTGGAGATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTATAGTAATACCAATTATAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATACTAGGAGCCCCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAACTGGAAGACTAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614411 Podocopida sp. water mite diet isolate 610-BHL072216-GBD29164_18946-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGAGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTACTTATTCGAGCTGAGCTCGGTCAACCTGGGACCTTGATTGGAAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAAAAACTGGAACACTAACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614412 Podocopida sp. water mite diet isolate 611-BHL072216-GBD25039_20630-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTTATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTACTTATTCGAGCTGAGCTCGGGCAACCTGGGTCATTGATTGGGAATGATCAAATTTATAATACAATTGTGACTGCTCATGCTTTTATTATAATTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGACTAGTACCTTTAATACTAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAACTGGAACACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614413 Podocopida sp. water mite diet isolate 612-BHL072216-GBD23030_9746-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTTATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTATTTATTCGAGCTGAGCTCGGGCACCCTGGTGCCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCTTTTATTATAATTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAACATAAGATTTTGATTACTTCCCCCATCCTTAACCTTACTAACAACTGGAATACTAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614414 Podocopida sp. water mite diet isolate 613-BHL072216-GBD9288_5069-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTTATTTTTGGTGCTTGATCTGCTATGCTAGGAACTGCCTTAAGATTAATTATTCGAGCTGAGCTCGGTCAACCTGGGGCCCTGATTGGAAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTATGGTAATACCAATTATAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATACTAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGAATACTTCCCCCATCCTTAACCTTATTAACAACTGGAATACTAACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614415 Podocopida sp. water mite diet isolate 614-BHL072216-GBD26414_11765-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTTATTTTTGGTGCTTGATCTGCTATGCTAGGAACATCCTTAAGAGTATTTATTCGAGCTGAGCTCGGTCACCCTGGGGCAGTGATTGGAAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTATAGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAATTGGAATACTAACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614416 Podocopida sp. water mite diet isolate 615-BHL072216-GBD24068_9830-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGGCCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCAACAGATATTACGTTTCCCCGAATAAAAAAAAAAAAAATTTGAATACCTCCCCCATCCCTATCCTTATTAACAATTGGAATACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614417 Podocopida sp. water mite diet isolate 617-BHL072216-GBD21529_21140-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTATTTATTCGAGCTGAGCTCGGGCAACCTGGTGCCCTGATTGGGAATGATCAAATTTATAACATAATTGTGACTGCCCATGCATTTATTATAATTTTTTTATAGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGTGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCATTAACCTTATTAACAACTGGCACACTAACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614418 Podocopida sp. water mite diet isolate 620-BHL072216-GBD27539_11173-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTATTTATTCGAGCTGAGCTCGGTCAACCTGGGTCTCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCTCATGCAGTTATTATAATTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAACTAGAACACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614419 Podocopida sp. water mite diet isolate 623-BHL072216-GBD20464_21791-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACTGCCTTAAGAGTGCTTATTCGAGCTGAGCTCGGGCAACCTGGGACACTGATTGGGGATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTATGGTAATACCAATTATAATAGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCATCCTTAACCTTATTAACAATTGGAACACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614420 Podocopida sp. water mite diet isolate 624-BHL072216-GBD10894_22502-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGTCAACCTGGGGCCCTGATTGGAAATGCTCAAATTTATAACACAATTGTGACTGACCATGCATTTATTATAATTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGACACCAGATATAGCGTTTCCTCGAATAAAAAATAAAAGATTTTGATTACGTCCCCCAGCCTTATCCTGATTAACAATTGGAATACTTACAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614421 Podocopida sp. water mite diet isolate 628-BHL072216-GBD20263_21573-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTAATTTTTGGTGCTTGATCTGGTATGCTAGGAACAGCCTTTAGAGTATTTATTCGAGCTGAGCTCGGGCAACCTGGGGCATTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCTCATGCATTTATTATAATTTTTTTATGGTAATACCAATTATAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCATCCTTAACCTTATTAACAATTGGAACACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614422 Podocopida sp. water mite diet isolate 629-BHL072216-GBD21355_4661-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGTGCTTGATCTGCTATGCTAGGAACATCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGACTATGATTGGGAATGATCAAATTTATAATATAATTGTGACTGCCCATGCATTTATTATAATTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTACCAACTGGAATACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614423 Podocopida sp. water mite diet isolate 630-BHL072216-GBD12972_17005-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGGCCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGACTAGTACCTTTAATAATAGGGGCACCAGAAATAGCGTTTCCTCCAATAAAAAAAAAAAGATTTTGATTACCTCCCCCATCCTTAACCTTACTAACAATTGGAATACTAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614424 Podocopida sp. water mite diet isolate 632-BHL072216-GBD20415_14332-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACATCCTTAAGAGTACTTATTCGAGCTGAGCTCGAGCAACCTGAGACCTTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTAAGGTAATACCAATTATAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGACACCAGATATAGCGTTTCCTCGAATAAATAATAAAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAATTGGAATACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614425 Podocopida sp. water mite diet isolate 634-BHL072216-GBD7482_5616-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTACTTATTCGAGCTGAGTTCGCGCAACCTGGATCCCTGATTGGAAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTCATTATAATTTTTTTATGGTAATACCAATTATAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATACTAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAACTGGAATACTAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614426 Podocopida sp. water mite diet isolate 635-BHL072216-GBD11763_23971-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTCATTTTTGGTGCTTGATCTGCTATGCTAGGAACTTCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGACAATGATTGGGAATGATCAAATTTATAACACAATTGTTACTGCCCATGCATTTATTATAATTTTTTTATGGTAATACCAATTATAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATACTAGGGGCATCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAATTGGAATACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614427 Podocopida sp. water mite diet isolate 636-BHL072216-GBD2977_20512-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGCAACAGCCTTGAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGGCCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATACTATAAGACTTTGATCACTTCCCCCATCCTTAACATTATTAAAAAATGGAATACTAACAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614428 Podocopida sp. water mite diet isolate 637-BHL072216-GBD3024_20301-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGACAACCTGGGACCATGATTGGGAATGATCAAATTTATAACACAATTGTTACTGCCCATGCATTTATTATAATTTTTTTATGGTAATACCAATTATAATAGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCCCGAATAAATAATATAAGATTTTGACTACTTCCCCCATCATTAACCTTATTACCAACTGGAATAATTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614429 Podocopida sp. water mite diet isolate 638-BHL072216-GBD6586_22135-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACTTCCTTAAGAGTATTTATTCGAGCTGAGCTCGGGCAACCTGGGGCCATGATTGGGAATGATCAAATTTATAACATAATTGTTACTGCCCATGCATTTGTTATAATTTTTTTATGGTGATACCAATTATAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTATCCTTATTAACAACTGGAATACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614430 Podocopida sp. water mite diet isolate 640-BHL072216-GBD18572_21404-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTTATTTTTGGTGCTTGATCTGCTATGCTAGGAACTGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCAGGGACCCTGATTGGAAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGACTAGTACCTTTAATACTAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCCTCCTTAACCTTATTAACAAGTGGAATACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614431 Podocopida sp. water mite diet isolate 641-BHL072216-GBD14661_8967-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACTTCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGACCCTGATTGGAGATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTATAGTAATACCAATTATAATTGGAGGGTTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTTCTTCCCCCATCCTTAACCTTATTAACAATTAGAATAATTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614432 Podocopida sp. water mite diet isolate 642-BHL072216-GBD11969_5356-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTCATTTTTGGTGCTTGATCTGCTATGCTAGGAACTGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGACCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTATGGTAATACCAATTATAATGGGAGGGTTTGGAAATTGATTAGTACCCTTAATACTAGGGGCCCCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCATCCTTAACCTTATTAACAACAGGAATACTAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614433 Podocopida sp. water mite diet isolate 643-BHL072216-GBD10660_3954-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTATGAACGGCCTTAAGAGTATTTATTCGAGCTGAGCTCGGGCAACCTGGGACTATGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAACTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAACTGGAAGACTAACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614434 Podocopida sp. water mite diet isolate 644-BHL072216-GBD7201_5710-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGTCCCTGATTGGAAATGATCAAATTTATAATACAATTGTGACTGCCCATGCTTTTATTATAATTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTACTAACAACTGGAATACTAACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614435 Podocopida sp. water mite diet isolate 646-BHL072216-GBD24301_11344-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTACTTATTCGAGTTGAGCTCGGACAACCTGGGTCCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGAGCACCAGATATAGCGTTTCCGCGAATAAATAATATAAGATTTTGACTACTACCCCCATCCTTAACCTTATTAACAACTGGAACACTAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614436 Podocopida sp. water mite diet isolate 647-BHL072216-GBD27672_8574-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTTATTTTTGGAGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTACTTATTCGAGCTGAGCTCGGGCAACCTGGGGCGTTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCTCATGCATTTATTATAATTTTTTTATGGTAATACCAATTATAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCATTAACCTTATTAACAACTGGAACACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614437 Podocopida sp. water mite diet isolate 648-BHL072216-GBD22711_22883-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGACAACCTGGGGCCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGACACCGGATATAGCTTTTCCTCAAATAAAAAAAAAAAAATTTTGATTACTTCCCCCATCCTTATCCTTATTAACAAATGGAATACTAACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614438 Podocopida sp. water mite diet isolate 651-BHL072216-GBD24877_19609-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGTGCTTGATCTGCTATGTTAGGAACAGCCTTAAGAGTATTTATTCGAGCTGAGCTCGGGCAACCAGGGACCCTGATTGGGGATGATCAAATTTATAACACAATTGTGACTGCTCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAATAGGAATACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614439 Podocopida sp. water mite diet isolate 652-BHL072216-GBD4335_8075-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTATTTATTCGAGCTGAGCTCGGGCACCCTGGGTCCTTGATTGGAGATGATCAAATTTATAACACAATTGTTACTGCCCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTTCCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAACTGGAACACTAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614440 Podocopida sp. water mite diet isolate 654-BHL072216-GBD14375_4706-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATGATTCGAGCTGAGCGCGGGCAACCTGGTGCCCTGATTGTTAATGATCAAATTTATAACACAATTTTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATAGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTATCCTTATTAACAGTTGGAATACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614441 Podocopida sp. water mite diet isolate 655-BHL072216-GBD18659_6422-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGTGCCATGATTGAGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATAAAAGATATTGAATACGTCCCCCATCCTTAACCTTAATAACAATTGGAATACGTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614442 Podocopida sp. water mite diet isolate 656-BHL072216-GBD7139_10456-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTTAGAGTATTTATTCGAGTTGAGCTCTGTCAACCTGGGGCCTTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAGTTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCATCCTTAACCTTATTAGCAATTGGAATACTTGCAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614443 Podocopida sp. water mite diet isolate 657-BHL072216-GBD20227_10966-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCTTGATCTGCTATGCTAGGAACTTCCTTAAGAGTATTTATTCGAGCTGAGCTCGGGCAACCTGGGGCTCTGATTGGGGATGATCAAATTTATAATATAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATACTAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAACTAGAATACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614444 Podocopida sp. water mite diet isolate 658-BHL072216-GBD21798_10099-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGGCCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCAACAGAAAAAGCCGTTCCCCCAAAAAAAAAAAAAAGAATTTGATTAACTCCCCCATCCTTATCCTTATTAACAATTGGAATACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614445 Podocopida sp. water mite diet isolate 659-BHL072216-GBD20901_26186-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTTATTTTTGGTGCTTGATCTGCTATGCTAGGAACTGCCTTAAGAGTAATTATTCGAGCTGAGTTCGGGCAACCTGGGACCCTGATTGGGGATGATCAAATTTATAATATAATTGTGACTGCTCATGCATTTATTATAATTTTTTTTATAGTAGTACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAATTGGAATACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614446 Podocopida sp. water mite diet isolate 660-BHL072216-GBD28433_10246-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACTGCCTTAAGAGTATTTATTCGAGCTGAACTAGGACAACCTGGGACCTTGATTGGGAATGATCAAATTTATAACATAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTATAATCGGAGGGTTTGGAAATTGATTATTACCTTTAATACTAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAACTAGAAGACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614447 Podocopida sp. water mite diet isolate 661-BHL072216-GBD21360_27482-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGGCCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGAGCACCGGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACCTTATTATCAACTAGAACACTAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614448 Podocopida sp. water mite diet isolate 662-BHL072216-GBD19713_19680-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACTGCCTTAAGTGTAATTATTCGAGCTAAGCTCGGGCGACCTGGGGCCCTGATTGGAGATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAATTAGAATACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614449 Podocopida sp. water mite diet isolate 663-BHL072216-GBD16364_14682-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGCGCAACCTGGGGCCCTGATTGGGAATGATCAAATTTATAACACTATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATAATAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATACTAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCATCCTTAACCTTATTAGCAACTGGAATACTCACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614450 Podocopida sp. water mite diet isolate 664-BHL072216-GBD24705_19953-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTTATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAATATTTATTCGAGCTGAACTCGGTCAACCTGGGTCCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATAATAGGGACACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAATTGGAACACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614451 Podocopida sp. water mite diet isolate 665-BHL072216-GBD27702_15206-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTATTTATTCGAGCTGAGTTCGGGCAACCTGGGGCCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGACCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGAGCACCAGATATAGCGTTTCCTCGAATAAACAATATAAGATTTTGATTACTACCCCCATCCTTAACCTTATTAACAACAGGAAGACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614452 Podocopida sp. water mite diet isolate 666-BHL072216-GBD27207_18732-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGAGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTATTTATTCGAGTTGAGCTCGGGCAACCTGGGGCCCTGATAGGAAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTTGGGGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCATCCTTAACCTTATTAGCAACTGGAACACTAACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614453 Podocopida sp. water mite diet isolate 667-BHL072216-GBD8505_23682-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACATCCTTAAGAGTAATTATTCGAGCTGAACTCGGGCAACCTGGGGCAGTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACGACTGGAATACTAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614454 Podocopida sp. water mite diet isolate 668-BHL072216-GBD10394_4649-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGTTCCCTGATTGGAGATGATCAAATTTATAACACAATTGTTACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCATTAACCTTATTAACAACTGGAATACTAACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614455 Podocopida sp. water mite diet isolate 669-BHL072216-GBD5325_13508-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACTTCCTTAAGAGTAATTATTCGAGCTGAACTCGGGCAACCTGGGGCCTTGATTGGGAATGATCAAATTTATAACATAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTATAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCCTCCTTAACCTTATTAACAACTGGAAGACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614456 Podocopida sp. water mite diet isolate 670-BHL072216-GBD28911_13782-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTTATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTACTTATTCGAGCTGAGCTCGGGCAACCTGGGACCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCTTTTATTATAATTTTTTTTATGGTAATACCAATTATAATTGGAGGGTTTGGAAATTGATTTGTACCTTTAATACTAGGAGCAACAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTCCCCCCATCCTTATCCTTATTAACAACTGGAACACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614457 Podocopida sp. water mite diet isolate 672-BHL072216-GBD14347_28139-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGAGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTATTTATTCGAGCTGAGCTCGGTCAACCTGGGGCCTTGATTGGGAATGATCAAATTTATAATACAATTGTGACTGCTCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAATTGGAATACTAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614458 Podocopida sp. water mite diet isolate 673-BHL072216-GBD16852_15641-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTAATTTTTGGAGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAATAATTATTCGAGCTGAGCTCGGGCAACCTGGGACGTTGATTGGGAAAGATCAAATTTATAACACAATTGTGACTGCACATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAACTGGAAGACTAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614459 Podocopida sp. water mite diet isolate 674-BHL072216-GBD23560_9401-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTTATTTTTGGTGCTTGATCTGCTATGCTAGGAACATCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGGCCCTGATTGGTCATGACCAAATTTATAACACAATTGTGACTGCCCATGCTTTTATTATAATTTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCATCCTTAACCTTATTAACAACTGGAAGACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614460 Podocopida sp. water mite diet isolate 675-BHL072216-GBD16507_26642-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTTATTTTTGGTGCTTGATCAGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGTCAAACAGGGGCCATGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAACTGGAATACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614461 Podocopida sp. water mite diet isolate 677-BHL072216-GBD24974_25426-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGGCACTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTACCTTTAATACTAGGAGCACCAGATATAGCGTTTCCACGAATAAATAATATAAGATTTTGATTACTACCCCCACCCCTAACCTTATTAACAATTAGAAGACTAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614462 Podocopida sp. water mite diet isolate 678-BHL072216-GBD21151_26130-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTTTATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACTGCCTTAAGAGTATTTATTCGAGCTGAGCTCGGGCAACCTGGTGCACTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCGGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCATCCTTAACCTTATTAACAATTGGAATACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614463 Podocopida sp. water mite diet isolate 679-BHL072216-GBD21510_24947-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTTATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTACTTATTCGAGCTGAGCTCGGGCAACCTGGAGCCCTGATTGGGAATGATCAAATTTATAACACTATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTATAATCGGAGGATTAGGAAATTGATTAGTACCTTTAATACTAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCATCCTTAACCTTATTAACAACTAGAATACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614464 Podocopida sp. water mite diet isolate 680-BHL072216-GBD26937_17489-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTACTTATTCGAGCTGAGCTAGGGCAACCTGGGACTCTGATTGGGAATGATCAAATTTATAACACTATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTATAATTGGAGGGTTTGGAAAATGACTAGTACCTTTAATACTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTATCCTTATTAACAACTGGAACACTCACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614465 Podocopida sp. water mite diet isolate 681-BHL072216-GBD11590_16178-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGGCCCTGATTGGGAATGATCAGATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAAATAAAGCCTTTCCCCGAATAAAAAAAATAAGAATTTGAATACCACCCCCATCCTTATCCTTATTAACAATTGGAATACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614466 Podocopida sp. water mite diet isolate 682-BHL072216-GBD8341_13485-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGGCGTTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTATAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAACATAAGATTTTGATTACTACCCCCTTCCTTAACCTTATTAACAATAGGAATACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614467 Podocopida sp. water mite diet isolate 684-BHL072216-GBD22749_8235-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGATTAATTATTCGAGCTGAGCTCGGGCAACCTGGGACACTGATTGGGAATGACCAAATTTATAACACAATTGTGACTGCCCATGCTTTTATTATAATTTTTTTTATGGTAATACCAATTATAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAACAGGAATAATTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614468 Podocopida sp. water mite diet isolate 686-BHL072216-GBD23954_18912-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACTGCCTTTAGAGTATTTATTCGAGCTGAGCTCGGACAACCTGGGGCCCTGATTGGTAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATCGGAGGGTCTGGAAATTGATTAGTACCTTTAATACTAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGAATACTTCCCCCATCCTTAACCTTATTAACAACTAGAATACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614469 Podocopida sp. water mite diet isolate 687-BHL072216-GBD28466_13340-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACTTCCTTAAGTGTACTTATTCGAGCTGAGCTCGGTCAACCTGGGGCACTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCTTTTATTATAATTTTTTTTATGGTAATACCAATTATAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGAGCGCCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCATCCTTATCCTTATTAACAATTGGAATACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614470 Podocopida sp. water mite diet isolate 688-BHL072216-GBD24783_21827-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGAGCAACCTGGGTCTCTGATTGGGAATGATCAACTTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTAGGGGCACCAGATATAGCGTTTCCTCGAATAAACAATATAAGATTTTGATTATTTCCCCCATCCTTAACCTTATTAACAACTGGAACACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614471 Podocopida sp. water mite diet isolate 689-BHL072216-GBD22364_16512-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCGGGGGCACTAATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTGTTATAATTTTTTTTATGGTAATACCAATTATAATGGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCCTTTCCGCGAATAAATAAAATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAACTGGAATACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614472 Podocopida sp. water mite diet isolate 690-BHL072216-GBD8794_26757-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTTATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCTTTAAGAGTAATTATTCGAGCTGAGTTCGGGCAACCTGGGGCACTGATTGGGAATGATCAAATTTATAAAAGAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTATAATCGGTGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTATCCTTATTAACAACTGGAATACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614473 Podocopida sp. water mite diet isolate 691-BHL072216-GBD9943_24029-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTTATTTTTGGTGCTTGATCTGCTATGCTCGGAACAGCCTTAAGAGTACTTATTCGAGCTGAGCTCGGGCAACCTGGAACCTTGATTGGAAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTATCCTTATTACCAACTGGAATACTAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614474 Podocopida sp. water mite diet isolate 692-BHL072216-GBD20686_28036-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGACCTTGATTGGGAATGATCAAATTTATAACACAATTGTTACTGCCCACGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAGCCTTATTAACAAATGGAAGACTAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614475 Podocopida sp. water mite diet isolate 693-BHL072216-GBD17838_18795-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGAAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGTACAACCTGGGGCCCTGATTGGGAATGATCAAATTTATAACACAATTTTGACTGCCCATGCATTTATTATAATTTTTTTGATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAATACCTTTAATACTAGTGGCAACAGATATAGCGTTTCCTCGAATAAACAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAATTGGAATACTTACAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614476 Podocopida sp. water mite diet isolate 694-BHL072216-GBD14032_16896-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGGCCTTTATTGGAGATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTTATACCAATTATAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAACATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTACCAATTGGAATACTAACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614477 Podocopida sp. water mite diet isolate 695-BHL072216-GBD11379_13230-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGTGCTTGATCTGCTATGCTAGGAACTTCCTTAAGAGTATTTATTCGAGCTGAGCTCGGGCAACCTGGGTCCTTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTGTTATAATTTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCATTAACCTTATTAATAACTGGAATACTAACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614478 Podocopida sp. water mite diet isolate 697-BHL072216-GBD26777_7434-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAATAATTATTCGAGCTGAACTCGGACAACCTGGGACATTGATTGGAAATGATCAAATTTATAACACAATTGTTACTGCCCATGCATTTATTATAATTTTTTTCATGGTAATACCAATTATAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCCCCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAACTGGAACACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614479 Podocopida sp. water mite diet isolate 1790-BHL101516-GBD23883_26640-Ldc85 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGATCTCGGGCAACCTGGGGCCCTGTTTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGTGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTATCCTTATTAACAATTGGAAGACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614480 Podocopida sp. water mite diet isolate 1795-BHL101516-GBD2654_13449-Ldc86 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGGCCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTAGATTACTTCCCCCATCCTTAACCTTATTAACAATTGGAATACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614481 Podocopida sp. water mite diet isolate 1827-BHL022317-GBD10308_22320-Ldc88 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGGCCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCAACAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTAGAGTACTTCCCCCATCCATAACCTTATTAACAAATGGAATACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614482 Podocopida sp. water mite diet isolate 1871-BHL022317-GBD6380_8108-Ldc89 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATACTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGGCCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTATCCTTATTAACAATTGGAATACTGACAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614483 Podocopida sp. water mite diet isolate 1876-BHL022317-GBD5360_14007-Ldc89 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGGCCCTGATTGGGAATGATCAAATTTATAACACAATCGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATACTAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTATCCTTACTAACAACTGGAACACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614484 Podocopida sp. water mite diet isolate 1877-BHL022317-GBD5781_24916-Ldc89 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTAGGGCAACCTGGGGCCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCACATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAACCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGTAGCACCAGATATAGCGTTTCCGCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTCATTATCAACTGGAATACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614485 Podocopida sp. water mite diet isolate 1878-BHL022317-GBD15073_21497-Ldc89 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGACAACCTGGGGCCCTGATTGGTAATGATCAAATTTATAACACAATCGTGACTGCCCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTACCTTTAATACTAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCCTCCATAACCTTATTAACAACTGGAATACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614486 Podocopida sp. water mite diet isolate 1879-BHL022317-GBD8637_19772-Ldc89 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTATTTATTCGAGCTGAGCTAGGGCAACCTGGGACCTTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCTATTTTAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTGATTAACAACTGGAATACTAACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614487 Podocopida sp. water mite diet isolate 1880-BHL022317-GBD26784_23179-Ldc89 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTATTTATTCGAGCTGAGCTCGGGCAACCTGGGGCCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAACTGATTAGTACCTTTAATAATAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGAATTTGATTACTACCCCCATCCTGAACCTTATTAACAACTGGAACACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614488 Podocopida sp. water mite diet isolate 1899-BHL022317-GBD9970_11883-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGGCCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTATCCTTATTAACAATTGGAATACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614489 Podocopida sp. water mite diet isolate 1945-BHL022317-GBD8701_4398-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTACTTATTCGAGCTGAGCTCGGGCAACCTGGGGCCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTTCTTCCCCCATCCTTAACCTTATTAACAACTAGAACAATTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614490 Polypedilum sp. water mite diet isolate 2295-BHL072216-GBD8817_10530-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGAACTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTGCCACCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KU497130, identified in GenBank as Polypedilum sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614491 Polypedilum sp. water mite diet isolate 9253-BHL032417-GBD15498_27959-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGGGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTATTTGGAGGGTTTGGAAATTGACTAGTTCCTTTAATATTGGGGGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTTTACCTCCTTCTTTAACTCTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR693297, identified in GenBank as Polypedilum sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614492 Polyphemus sp. water mite diet isolate 589-BHL072216-GBD9597_6799-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAAGAATTCTCATTCGTGCTGAATTAGGACAAGCAGGAAGATTAATTGGTGATGATCAAATTTATAACGTAATTGTTACTGCCCATGCTTTTGTTATAATTTTTTTTATAGTGATGCCTATTATAATTGGGGGGTTTGGTAATTGACTTGTTCCTTTAATGTTAGGAGCTCCTGATATGGCTTTTCCTCGGTTAAATAATTTAAGTTTCTGATTCCTTCCTCCTGCTTTAACTCTTCTCTTAGTTGGGGGGGCTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.0% identical to accession ID GQ406859, identified in GenBank as Polyphemus pediculus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614493 Polyphemus sp. water mite diet isolate 702-BHL072216-GBD11903_12913-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAAGAATTCTCATTCGTGCTGAATTAGGACAAGCAGGAAGATTAATTGGTGATGATCAAATTTATGACGTAATTGTAACTGCCCATGCTTTTGTTATATTTTTTTTTTTTATAGTGATGCCTATTATAATTGGGGGGTTTGGTAATTGACTTGTTCTTCTAATGTTAGGAGCTCCTGATATGGCTTTGCCTCGGTTAAATAATTTAAGTTTCTGATTCCTTCCTCCTGCTTTAACTCTTCTCTTAGTTGGGGGGGCTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID GQ406859, identified in GenBank as Polyphemus pediculus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614494 Polyphemus sp. water mite diet isolate 717-BHL072216-GBD12268_17630-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAAGAATTCTCATTCGTGCTGAATTAGGACAAGCAGGAAGATTAATTGGTGATGATCAAATTTATAACGTAATTGTAACTGCCCATGCTTTTGTTATAATTTTTTTTATAGTGATGCCTATTATAATTGGAGGGTTTGGTAATTGACTTGTTCCTCTAATGTTAGGAGCTCCTGATATGGCTTTTCCTCGGATAAATAATATAAGATTCTGATTCCTTCCCCCTGCTTTAACCCTTCTCTTAGTTGGGGGAGCTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID GQ406859, identified in GenBank as Polyphemus pediculus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614495 Polyphemus sp. water mite diet isolate 726-BHL072216-GBD23718_4881-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAAGAATTCTAATTCGTGTTGAATTAGGACAAGCAGGAAGATTAATTGGTGATGATCAAATGTATAACGTAATTGTAACTGCCCATGCTTTTGTTATAATTTTTTTTATAGTGATGCCTATTATAATTGGGGGGTTTGGTAATTGACTTGTTCCTCTAATGTTAGGAGCTCCTGATATGGCTTTTCCTCGGTTAAATAATTTAAGTTTCTGATTCCTTCCTCCTGCTTTAACCCTTCTCTTAGCTGGGGCAGCTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID GQ406859, identified in GenBank as Polyphemus pediculus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614496 Polyphemus sp. water mite diet isolate 728-BHL072216-GBD20559_18169-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAAGAATTCTCATTCGTGCTGAATTAGGACAAGCAGGAAGATTAATTGGTGATGATCAAATTTTTAACGTAATTGTAACTGCCCATGCTTTTGTTATAATTTTTTTTATAGTGATGCCTATTATAATTGGGGGGTTTGGTAATTGACTTGTTCCTCTAATGTTGGGAGCTCCTGATATAGCATTCCCTCGGATAAATAATATAAGTTTCTGATTCCTTCCTCCTGCTTTAACTCTACTCTTAGTTGGGGGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID GQ406859, identified in GenBank as Polyphemus pediculus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614497 Polyphemus sp. water mite diet isolate 729-BHL072216-GBD8988_9762-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAAGAATTCTCATTCGTGCTGAATTAGGACAAGCAGGAAGATTAATTGGTGATGATCAAATTTATAACTTAATTGTAACTGCCCATGCTTTTGTTATAATTTTTTTTATAGTGATGCCTATTATAATTGGGGGGTTTGGTAATTGACTTGTTCCTTTAATGTTAGGAGCTCCTGATATGGCTTTTCCTCGGTTAAATAATATAAGGGTCTGATTCCTTCCTCCTGCTTTAACCCTTCTCTTAGTGGGGGGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID GQ406859, identified in GenBank as Polyphemus pediculus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614498 Polyphemus sp. water mite diet isolate 740-BHL072216-GBD22349_13630-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAAGAATTCTCATTCGTGCTGAATTAGGACAAGCAGGAAGATTAATTGGTGATGATCAAATTTATAACGTACTTGTAACTGCCCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTATAATTGGGGGGTTTGGTAATTGACTTGCTCCTCTAATGTTCGGAGCTCCTGATATGGCTTTTCCTCGGTTAAATAATTTAAGTTTCTGATTCCTTCCTCCTGCTTTAACTCTACTCTTAGTTGGGGCGGCTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID GQ406859, identified in GenBank as Polyphemus pediculus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614499 Polyphemus sp. water mite diet isolate 741-BHL072216-GBD23758_24969-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAAGAATTCTCATTCGTGCTGAATTAGGACAAGCAGGAAGATTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCCCATGCTTTTGTTATAATTTTTTTTATAGTGATGCCTATTATAATTGGGGGGTTTGGTAATTGACTTGTTCCTCTAATGTTAGGAGCTCCTGATATGGCATTTCCTCGGATAAATAATTTAAGTTTCTGATTCCTTCCTCCTGCTTTAACTCTTCTCTTAGTTGGGGGGACTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID GQ406859, identified in GenBank as Polyphemus pediculus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614500 Polyphemus sp. water mite diet isolate 1804-BHL101516-GBD21323_15664-Ldc86 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAAGAATTCTCATTCGTGCTGAATTAGGACAAGCAGGAAGATTAATTGGTGATGATCAAATTTATAACGTAATTGTAACTGCCCATGCTTTTGTTATAATTTTTTTTATAGTGATGCCTATTATAATTGGGGGGTTTGGTAATTGACTTGTTCCTCTAATGTTAGGAGCTCCTGATATGGCTTTTCCTCGGTTAAATAATTTAAGTTTCTGATTCCTTCCTCCTGCTTTAACTCTTCTCTTAGTTGGGGGGGCTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID GQ406859, identified in GenBank as Polyphemus pediculus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614501 Prochyliza sp. water mite diet isolate 14568-BHL040517-GBD27315_20316-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATACGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.4% identical to accession ID KR262659, identified in GenBank as Prochyliza xanthostoma. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614502 Prochyliza sp. water mite diet isolate 15160-BHL040517-GBD21633_19032-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTTGGAAATTGATTAATTCCTTTAATATTAGGAGCTCCAGATATAGCCTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTAACACTATTACTAGCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.0% identical to accession ID KR262659, identified in GenBank as Prochyliza xanthostoma. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614503 Psectrocladius sp. water mite diet isolate 812-BHL100916-GBD3115_11194-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTAAAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614504 Psectrocladius sp. water mite diet isolate 855-BHL100916-GBD11118_21024-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGATTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614505 Psectrocladius sp. water mite diet isolate 963-BHL100916-GBD21612_18845-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGGGCTTGGTCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGTCATGCCGGCTCATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGGATAAAAAAAATAAGTTTCTGATTACTTCCCCCGTCATTAATTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614506 Psectrocladius sp. water mite diet isolate 964-BHL100916-GBD22539_27002-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTACTTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATAACTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAAAATAAGTTTTTGATTAATTCCCCCGTCATTAAATTTACTATTAACTAGCTCCCTAGTTGAAAAGGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614507 Psectrocladius sp. water mite diet isolate 990-BHL100916-GBD22299_13478-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTATATTTTATTTTCGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACACTGGTTCCTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACTTTACTATTATCTAGCACACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614508 Psectrocladius sp. water mite diet isolate 1028-BHL100916-GBD18732_12385-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAGCTCGGTCACGCCGGTACCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614509 Psectrocladius sp. water mite diet isolate 1054-BHL100916-GBD14853_12880-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGTAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCACACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACCTTACTATCATCTAGCACACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614510 Psectrocladius sp. water mite diet isolate 2571-BHL072216-GBD17038_22017-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACCCCGGGTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTTATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACCTTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614511 Psectrocladius sp. water mite diet isolate 2709-BHL032417-GBD16104_11082-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCACTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614512 Psectrocladius sp. water mite diet isolate 2711-BHL032417-GBD8960_9826-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAATATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614513 Psectrocladius sp. water mite diet isolate 2964-BHL032417-GBD15846_20514-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTATGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAAAGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAGTATTAGGAGCCCCCGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614514 Psectrocladius sp. water mite diet isolate 3005-BHL032417-GBD13804_2406-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGATCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATAATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGAAATACCTTTTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614515 Psectrocladius sp. water mite diet isolate 3119-BHL032417-GBD25833_19678-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTTATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCCATTTTAATTGGAGGATTTGGACATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614516 Psectrocladius sp. water mite diet isolate 4062-BHL032417-GBD25876_23101-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGTGCAGAACTCGGTCACGCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTTGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTCTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614517 Psectrocladius sp. water mite diet isolate 4218-BHL032417-GBD12435_13032-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACACTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCGTCATTAACTTTACTAATATCTAGCGCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614518 Psectrocladius sp. water mite diet isolate 4219-BHL032417-GBD24356_13814-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCCCACGATTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGAATACTTCCCCCGTCATTAACTTTACTATTAGCTAGCACGCCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614519 Psectrocladius sp. water mite diet isolate 4281-BHL032417-GBD8002_14244-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGGTCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATCGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAACATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614520 Psectrocladius sp. water mite diet isolate 4333-BHL032417-GBD25003_12151-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAATGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAACAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614521 Psectrocladius sp. water mite diet isolate 4438-BHL032417-GBD20921_13656-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCAGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTACTATTATCTAGATCACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR288763, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614522 Psectrocladius sp. water mite diet isolate 5422-BHL032417-GBD6889_19075-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACACTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCAGGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCTCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCAAGCAGACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614523 Psectrocladius sp. water mite diet isolate 5613-BHL032417-GBD14261_21405-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAACTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTTGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614524 Psectrocladius sp. water mite diet isolate 5630-BHL032417-GBD15443_8700-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCTGGAACTTTTATTGGAGATGATCAAATGTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614525 Psectrocladius sp. water mite diet isolate 5657-BHL032417-GBD2375_11815-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGCTCAGGCATAGTAGGCAATTCTTTAAGAATTTTAATTCGAGCAGAGCTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTCATTGTTACCGCTCACTTTTTTGTAATACTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTATCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614526 Psectrocladius sp. water mite diet isolate 5662-BHL032417-GBD23827_10164-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGATTTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614527 Psectrocladius sp. water mite diet isolate 5704-BHL032417-GBD12243_8907-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGTATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTTATTGGAGATGATCAAATTTATAGTGTTATTGTTACCGCTCACGCTTATGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCATTAATATTAGGAGCCCCCGACATAGCATTCCCACGAATAAATAATATAAGTTTTTGATTACTTCCACCGTCATTAACTTTACTATTTTCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614528 Psectrocladius sp. water mite diet isolate 5710-BHL032417-GBD4317_9085-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTTGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCTTTAACTCTTCTTTTATCAAGCTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614529 Psectrocladius sp. water mite diet isolate 5822-BHL032417-GBD29217_16623-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCAGGAACGGGAGGAGGAGCGAGCGCGCGAGGGGAAAAGGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614530 Psectrocladius sp. water mite diet isolate 5864-BHL032417-GBD24971_18220-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGTACTTCTTTAAGTATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614531 Psectrocladius sp. water mite diet isolate 5867-BHL032417-GBD29215_17074-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCATGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGTAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCAGTAACGGGAGGAGTAGCTAACTCTCTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614532 Psectrocladius sp. water mite diet isolate 5879-BHL032417-GBD29433_15141-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCATCCTGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTAATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614533 Psectrocladius sp. water mite diet isolate 5899-BHL032417-GBD21796_21749-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCATGCTGGTTCTTTTATCGGTGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCCATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614534 Psectrocladius sp. water mite diet isolate 5901-BHL032417-GBD20105_4594-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGTTACCTATTTTAATTGGAGAGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614535 Psectrocladius sp. water mite diet isolate 5921-BHL032417-GBD5494_13671-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTCGGAGCCTGGTCAGGAATAGTCGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCCCGAATAAATAACATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGCACACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614536 Psectrocladius sp. water mite diet isolate 5923-BHL032417-GBD17419_28372-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCGGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGTAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAAATCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614537 Psectrocladius sp. water mite diet isolate 6069-BHL032417-GBD12533_14448-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATCCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTCCTTCCCCCTTCATGAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614538 Psectrocladius sp. water mite diet isolate 6501-BHL032417-GBD15604_26441-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCTGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCGTCATTAACTCTACTACTATCTAGTTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR776852, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614539 Psectrocladius sp. water mite diet isolate 6977-BHL032417-GBD7527_17591-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATATTGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCGTCATTAACTTTACTATTATCTAGATCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614540 Psectrocladius sp. water mite diet isolate 7455-BHL032417-GBD20752_10415-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGAAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614541 Psectrocladius sp. water mite diet isolate 8554-BHL101416-GBD7500_11805-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGCTGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTTCTACCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614542 Psectrocladius sp. water mite diet isolate 10957-BHL101516-GBD24296_12233-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCTCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTCCCCCCGTCATTAACTTTACTATGATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614543 Psectrocladius sp. water mite diet isolate 11087-BHL110116-GBD22874_6676-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR751697, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614544 Psectrocladius sp. water mite diet isolate 11160-BHL110116-GBD6810_9173-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614545 Psectrocladius sp. water mite diet isolate 11162-BHL110116-GBD19490_9223-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGAAATAGCATTCCCACGAATAAATAATATAAGATTTTGATTACTACCCCCGTCACTAACTTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614546 Psectrocladius sp. water mite diet isolate 11217-BHL110116-GBD10992_4555-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATGGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTGACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.4% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614547 Psectrocladius sp. water mite diet isolate 11270-BHL110116-GBD12625_21196-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAGTTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCCCCAATAAAAAAAATAAGGTTTTGAATACCTCCCCCGTCATTAACCTTACCATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614548 Psectrocladius sp. water mite diet isolate 11316-BHL110116-GBD28345_17678-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTAGTCCCATTAATATTAGGAGCCCCCGATATGGCATTCCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCATCATTAACTTTACTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614549 Psectrocladius sp. water mite diet isolate 11337-BHL110116-GBD16319_27277-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACCCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCTGACATGGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCATCATTAACTTTACTATTATCTAGCAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614550 Psectrocladius sp. water mite diet isolate 11367-BHL110116-GBD4550_14624-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGCTGGCTCCTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCACACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTGATATTAGGAGCCCCCGACATAGCATTCCCGCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACCTTACTATTATCAAACTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614551 Psectrocladius sp. water mite diet isolate 11385-BHL110116-GBD11629_14872-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGACCAGAACTCGGTCACACTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCATTCCCGCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614552 Psectrocladius sp. water mite diet isolate 12193-BHL040517-GBD7500_11805-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGCTGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTTCTACCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614553 Psectrocladius sp. water mite diet isolate 12496-BHL040517-GBD23752_19035-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGTATTTTAATTCGAACAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGTGGTTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCAGACTAGTGGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614554 Psectrocladius sp. water mite diet isolate 12501-BHL040517-GBD27670_10208-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCCGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGGTCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAACCCCTGATATAACATTCCCTCGAATAAAAAAAAATAATTTTTGATTTCTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614555 Psectrocladius sp. water mite diet isolate 12507-BHL040517-GBD12549_6304-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAAAACTCTGTCACGCTGGTTATTTCATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTCTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCTTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCGAGTTGGAAATGGAACTGGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614556 Psectrocladius sp. water mite diet isolate 12509-BHL040517-GBD11127_12608-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGATCCGGTATAGTAGGTACATCTTTAAGATTTTTATTTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTAAAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCACCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCATTAACTTTACTATTATCTAACTCTCTAGTAGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614557 Psectrocladius sp. water mite diet isolate 12511-BHL040517-GBD16303_4231-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCGTGAGCAGGTATAGTAGGGACATCTTTAAGAATTTTAATGCGAGCAGAACTCGGTCACGCTTGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCTCTCACGCTTTTGTAAGAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGCAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614558 Psectrocladius sp. water mite diet isolate 12517-BHL040517-GBD12957_3575-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCTTGTCCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGCTACGCTGGTTCTTTAATGGGAGAAGATCAAATTTATAATGTAATTGTTACCGCACACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAGATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614559 Psectrocladius sp. water mite diet isolate 12525-BHL040517-GBD3663_15541-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTTTTTAATCGGAAACGATCAAATTTATAATGTACTTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCCGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATCAAAGTTACTATTATCCAGCGCTCTAGTTGAAAATGGAGATGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614560 Psectrocladius sp. water mite diet isolate 12531-BHL040517-GBD26074_22092-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTTGGAGCCTGATCAGGTATAGTAGGTACCTCTTTAAGCATTTTAATTCGATCAGAACTCGGTCACGCTGGTTCTTTTATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATACTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGGTTTTGATTATTTCCCCCGTCAGTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614561 Psectrocladius sp. water mite diet isolate 12537-BHL040517-GBD16748_21765-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTACTTCGAGCAGAACTCGGTCACGCTGTGTCTTTAATCGGAGACGATCAAATTTATAATGTTATTGTTACCGCTCACGCTTTTGTAATCATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGATATTGATTAGTTACTTTAAGATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATGATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614562 Psectrocladius sp. water mite diet isolate 12551-BHL040517-GBD20933_28093-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGCTCGGGTATATTAGGTACATCTTTAAGATTTTTAATTCGATCGGAACTCGGTCACGCTGGTTCTTTAATGGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614563 Psectrocladius sp. water mite diet isolate 12553-BHL040517-GBD16993_28765-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGATCAGGTTTAGTAGGAACATCTTTAATATTTTTATTTCGAGCAGAACTCGTTCACGCTGGTTCTTTAATCGGAGACGATCAATTTTATAATGTAATTGTTACCGCTCTCTCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614564 Psectrocladius sp. water mite diet isolate 12555-BHL040517-GBD21323_20613-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGAGGATCAAATTTATAATGTAATTGTTACCGCTCACGCATTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCTCCGTCATTAACTTTACTATTATCAAGCTCACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614565 Psectrocladius sp. water mite diet isolate 12563-BHL040517-GBD14786_20600-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTTGGAGCCTGATCAGGAATAGTAGGAACATCTTTAAGAATTTGAATTCTAGCAGAACGCGGTCACGCAGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGTTTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCGCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614566 Psectrocladius sp. water mite diet isolate 12568-BHL040517-GBD29049_13061-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGATCGGGTATAGTAGGTCCGTCTTTAAGATTTTTAATACGATCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGTGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTGACTATTATCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614567 Psectrocladius sp. water mite diet isolate 12570-BHL040517-GBD20677_3498-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCATGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATCATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAAATGATTAGTACCGGTAATATTAGGAGCCCCCGACCTTGCGTTCCCTCCAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614568 Psectrocladius sp. water mite diet isolate 12571-BHL040517-GBD24307_25448-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGCTCAGGTTTAGTGGGTACTTCTTTAATATTTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGACACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTTTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614569 Psectrocladius sp. water mite diet isolate 12582-BHL040517-GBD21975_20282-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTATTTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAATTTTATAATGTATTTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCTCCTGATATAGCATTCCCGCGAATAAATAATATAAGATTTGGATTACTTGCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614570 Psectrocladius sp. water mite diet isolate 12585-BHL040517-GBD28385_11991-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCGGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGACCAGAACTCGGACACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCTTCATTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614571 Psectrocladius sp. water mite diet isolate 12591-BHL040517-GBD25720_9237-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGATCAGATATATTAGATACATCTTTAAGAATTTTATTTCGATCAGATCTCGGTCACGCTGGTTATTTAATCGGAGACGATCAATTTTATAATGTATTTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614572 Psectrocladius sp. water mite diet isolate 12595-BHL040517-GBD29595_13923-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTTGGACAAGCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGACTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTCTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614573 Psectrocladius sp. water mite diet isolate 12596-BHL040517-GBD13473_1747-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTACAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACATTACTATTATCAAGCACACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614574 Psectrocladius sp. water mite diet isolate 12599-BHL040517-GBD23177_22509-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTATAGTAGTACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614575 Psectrocladius sp. water mite diet isolate 12600-BHL040517-GBD28070_17973-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCTGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614576 Psectrocladius sp. water mite diet isolate 12606-BHL040517-GBD6458_8322-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACCCTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCGTCATTAACTTTACTACTATCAAGCACTCTAGTGGAAAATGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614577 Psectrocladius sp. water mite diet isolate 12608-BHL040517-GBD28862_12741-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCACGCTGGTTCTTTAATAGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCATTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTTGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614578 Psectrocladius sp. water mite diet isolate 12616-BHL040517-GBD5927_9777-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGTTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATACCTTCCCCTCAAAAAAAAAATATAATTTTTTTATTCCTCCCCCCGCCATTAACTTTACTATTATCTAGCTCTCTAGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614579 Psectrocladius sp. water mite diet isolate 12617-BHL040517-GBD27877_13760-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGATCGGGTATAGTAGGTCCATCTTTAAGATTTTTATTTTGAGCAGATCTCGGTCACGCTGGTTCTTTAATCGGAGACGTTCAAATTTATAATGTAATTGTTCCCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGAGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614580 Psectrocladius sp. water mite diet isolate 12619-BHL040517-GBD28301_19967-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATATTAGTTACATCTTTAAGAATTTTAATTCGAGCAGAACTCTGTCACGCTGGTTCTGTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATCGTGATACCTATTTTAATTGGAAGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCACTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTCCCCCCGGCATTAACTTTACTATTATCTAGGTCTCTAGTTGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614581 Psectrocladius sp. water mite diet isolate 12620-BHL040517-GBD26079_23087-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAAAATTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTGGGAGCCACTGATATAGCATTCCCTCGAATAAATAATATAAGATTTCGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614582 Psectrocladius sp. water mite diet isolate 12624-BHL040517-GBD22897_13050-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGACACACTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCATCATTAACCTTACTATTATCTAGCAGACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614583 Psectrocladius sp. water mite diet isolate 12625-BHL040517-GBD28500_13957-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTGTCGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCGCACGCCTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATGGTTTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATGCCCTCGAATAAATAATATAAGTTTTTGATTAATTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAACGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614584 Psectrocladius sp. water mite diet isolate 12626-BHL040517-GBD16216_12247-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAACTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGCTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCTCCCGTCATTAACTTTACTATTATCTAGCTCTCTAATTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614585 Psectrocladius sp. water mite diet isolate 12627-BHL040517-GBD9855_20852-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAAAAATATAAGTTTTTGATTACTTCCCTTGTCATTAACTTTACTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614586 Psectrocladius sp. water mite diet isolate 12629-BHL040517-GBD12654_27425-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAATTAGGACACGCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614587 Psectrocladius sp. water mite diet isolate 12630-BHL040517-GBD6101_14297-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGTCACCCTGGATCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTTCTTCCCCCCTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614588 Psectrocladius sp. water mite diet isolate 12637-BHL040517-GBD24911_17072-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGGACTTCTTTAAGAATCTTAATTCGAGCAGAACTCGGTCATGCTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR751697, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614589 Psectrocladius sp. water mite diet isolate 12639-BHL040517-GBD23190_9966-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAACAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCGCGAATAAATAATATAAGATTTCGATTACTACCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614590 Psectrocladius sp. water mite diet isolate 12642-BHL040517-GBD16725_2738-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGTTCACTCTGTTGCTTTAATCGTTTACGATCAAATTTATAATTTAATTGTTACCGCGCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614591 Psectrocladius sp. water mite diet isolate 12644-BHL040517-GBD17755_14824-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCAGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGGATAAATAATATAAGATTTTGATTATTTCCCCCGTCATTAACCTTACTATTATCTAGATCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614592 Psectrocladius sp. water mite diet isolate 12645-BHL040517-GBD6904_11614-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTTATTCGAGCAGAACTCGGTCACGCTGGTTCTTTTATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTCATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCTCCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614593 Psectrocladius sp. water mite diet isolate 12646-BHL040517-GBD27122_17335-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGACAAGCTGGTACTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTTCTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614594 Psectrocladius sp. water mite diet isolate 12652-BHL040517-GBD8296_6993-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACCCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCACACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGGGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACTGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614595 Psectrocladius sp. water mite diet isolate 12654-BHL040517-GBD16763_16337-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCAAGCTGGTTCTTTAATCGGAGACGATCAACTTTATAATGTACTTGTTACCGCTCACGCTTTTTTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCGTCATTAACTTTACTATTATCTAGCGCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614596 Psectrocladius sp. water mite diet isolate 12656-BHL040517-GBD24926_8417-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACTTTATTTTTGGAGCCTGATCAGGTATAGTTGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGACACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCCCCTGATATAGCATTCCCGCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614597 Psectrocladius sp. water mite diet isolate 12658-BHL040517-GBD12395_7276-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCTGGAATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACCATTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614598 Psectrocladius sp. water mite diet isolate 12662-BHL040517-GBD23232_11165-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAGTAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCACCCTGGTTCTTTAATCGGAGACGATCAAAATTATAATGTAATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614599 Psectrocladius sp. water mite diet isolate 12664-BHL040517-GBD26925_18264-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGCACATCTTTAAGAATTTTAATTCGAGTAGAACTCGGTCACACTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGGGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614600 Psectrocladius sp. water mite diet isolate 12665-BHL040517-GBD16702_21762-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGCACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTTACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATGTAGCATTCCCTCGAATAAAAAATATAAGTTATGGATTACTTCCCCCGTCATTAACAGGACTATTATCTAGCGCTCGAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614601 Psectrocladius sp. water mite diet isolate 12669-BHL040517-GBD19632_23421-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGATACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTTACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614602 Psectrocladius sp. water mite diet isolate 12674-BHL040517-GBD13390_6990-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCCGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGGCCCGCTGGTTCTTTAATCGGAGACGAGCAAATTTATAATGTACTTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTATAATAGTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGGTTACTGCCCCCGTCAGTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614603 Psectrocladius sp. water mite diet isolate 12678-BHL040517-GBD5274_11348-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGAAGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTTGGAGCCCCTGATATAGCATTCCCGCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACCTTACCATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614604 Psectrocladius sp. water mite diet isolate 12680-BHL040517-GBD28448_19152-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATAGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614605 Psectrocladius sp. water mite diet isolate 12682-BHL040517-GBD4116_13629-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGATCTTTAATCGGAGACGATCAAATTTATAATGTAACTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTACTATCTAGCAGACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614606 Psectrocladius sp. water mite diet isolate 12683-BHL040517-GBD23021_18365-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAATAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGACACGCTGGTTCTTTCATCGGAGACGATCAAATTTATAATGTCATTGTTACCGCTCACGCATTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614607 Psectrocladius sp. water mite diet isolate 12684-BHL040517-GBD28058_16067-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGCTGGATCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCACTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614608 Psectrocladius sp. water mite diet isolate 12687-BHL040517-GBD21202_10956-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGGTTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCATTAACCTTACTATCATCAAGAACACTAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614609 Psectrocladius sp. water mite diet isolate 12688-BHL040517-GBD24230_12054-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGTATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCATTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTTTACTATTATCTGGCTCACTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614610 Psectrocladius sp. water mite diet isolate 12689-BHL040517-GBD23174_8911-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGACACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATCTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCACCTGATATAGCATTCCCACGAATAAATAATATAAGTTTTTGATTGCTTCCCCCGTCATTAACTTTACTATTATCTAGCTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614611 Psectrocladius sp. water mite diet isolate 12690-BHL040517-GBD24961_24190-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTTGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCACGCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614612 Psectrocladius sp. water mite diet isolate 12692-BHL040517-GBD15857_9284-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCTGGTATAGTAGGTACCTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTATTCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTACTTCCCCCGTCATTAACATGACTATTATCAAGCTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614613 Psectrocladius sp. water mite diet isolate 12695-BHL040517-GBD19072_20001-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTACGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAACATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCAAGAAGACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614614 Psectrocladius sp. water mite diet isolate 12696-BHL040517-GBD5306_13749-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAAAAATATAAGATTTTGATTACTTCCCCCGTCATTAACATTACAAAAATCTAGCGCTCTAGTTGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614615 Psectrocladius sp. water mite diet isolate 12697-BHL040517-GBD11220_18683-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCCGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTTATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTTGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR751697, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614616 Psectrocladius sp. water mite diet isolate 12698-BHL040517-GBD12765_16242-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGAGCAGGTATAGTAGGTACATCTTTAAGAATTTTAATGCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAACTTTATAATGTCATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGCGCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614617 Psectrocladius sp. water mite diet isolate 12699-BHL040517-GBD24087_21699-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACATCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGCTGGATCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCCTCTTTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614618 Psectrocladius sp. water mite diet isolate 12701-BHL040517-GBD5256_11336-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCGGGTATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAACTCGGTCACGCTGGTTCTTTAATCGGAGAAGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTGATATTGGGAGCCCCTGATATAGCATTCCCTTGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGATCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614619 Psectrocladius sp. water mite diet isolate 12703-BHL040517-GBD2389_18225-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCTGAATTAGGTCACGCTGGATCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTCTGATTACTTCCCCCGTCATTAACTTTTCTATTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614620 Psectrocladius sp. water mite diet isolate 12705-BHL040517-GBD24835_12897-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTCGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTGTTGCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR761745, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614621 Psectrocladius sp. water mite diet isolate 12706-BHL040517-GBD22141_17191-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGTATTTTAATTCGAGCAGAATTCGGTCACCCTGGTTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCAAGATCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614622 Psectrocladius sp. water mite diet isolate 12707-BHL040517-GBD25970_15753-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTATTTTCGGAGCTTGATCAGGTATAGTTGGTACTTCTTTAAGAATTCTAATTCGAGCAGAATTCGGTCATGCTGGCTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR761745, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614623 Psectrocladius sp. water mite diet isolate 12709-BHL040517-GBD2131_17202-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCATGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAATTAGGTCATGCTGGTTCTTTAATCGGAGACGATCAATTTTATAATGTAATTGTTACCACTCACGCTTTTGTAATAATTTTTTTGATAGTTATTCCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614624 Psectrocladius sp. water mite diet isolate 12710-BHL040517-GBD26505_7014-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCCGGTATAGTAGGTATATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTCATCGGAGACGATCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTGTAATATTGGGAGCACCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTACCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614625 Psectrocladius sp. water mite diet isolate 12714-BHL040517-GBD18910_24057-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCTGGTATAGTAGGTACTTCTTTAAGTATTTTAATTCGAGCAGAACTCGGACAACCTGGTTCTTTTATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTATAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGACTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTACTATCAAGCTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614626 Psectrocladius sp. water mite diet isolate 12715-BHL040517-GBD29005_11992-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCTGAACTAGGTCACCCTGGTTCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGAATACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614627 Psectrocladius sp. water mite diet isolate 12717-BHL040517-GBD7771_23395-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCCGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGCTGGTTCTTTAATCGGAGAGGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614628 Psectrocladius sp. water mite diet isolate 12718-BHL040517-GBD14700_27249-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGTACATCTTTTATAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGAATACTTCCCCCTTCATTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614629 Psectrocladius sp. water mite diet isolate 12720-BHL040517-GBD27083_7512-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTAACATTACTATTATCTAGCTCTCTTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614630 Psectrocladius sp. water mite diet isolate 12722-BHL040517-GBD3172_18705-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGATCAGGTTTAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTATTCGGAGACGATCAAATTTATAATGTAATTGTTACCAATCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAATTCCTTTAATATTGGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGGTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614631 Psectrocladius sp. water mite diet isolate 12726-BHL040517-GBD21412_11087-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGCCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCACACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCGTTAACTTTACTATTATCTAGCGCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614632 Psectrocladius sp. water mite diet isolate 12727-BHL040517-GBD12355_12551-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCGGGTTTAGTAGGTACTTCTTTAAGAATTTTAATTCGAGTAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGGTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACCTTACTATTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614633 Psectrocladius sp. water mite diet isolate 12730-BHL040517-GBD6832_6395-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGTACTTCTTTAAGAATATTAATTCGAGCTGAACTAGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGTTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR776852, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614634 Psectrocladius sp. water mite diet isolate 12731-BHL040517-GBD18630_15353-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACACTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTATTATTGGGAGCCCCTGACATGGCATTCCCACGAATAAATAATATAAGATTTTGATTACTACCACCGTCATTAACTTTACTATTATCTAGCACACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614635 Psectrocladius sp. water mite diet isolate 12732-BHL040517-GBD8134_14074-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGTATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGTAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCAATAGTGGAAAATGGAGCTGGGACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614636 Psectrocladius sp. water mite diet isolate 12734-BHL040517-GBD19828_25322-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCATGCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTACTATCTAGTTCTATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR776852, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614637 Psectrocladius sp. water mite diet isolate 12735-BHL040517-GBD16189_12213-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTCGGAGCCTGATCAGGTATAGTCGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACCCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGGTTACTTCCCCCGTCATTAACCTTAATATTATCTAGCACTCTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR761745, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614638 Psectrocladius sp. water mite diet isolate 12736-BHL040517-GBD9723_17186-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATTTTTGGAGCTTGATCCGGAATAGTAGGAACATCTTTAAGAATATTAATTCGAGTAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGGTTACTTCCCCCGTCATTAACTTTACTATTATCTAACTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614639 Psectrocladius sp. water mite diet isolate 12738-BHL040517-GBD24367_6357-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCATGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTTGGAGCCCCGGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614640 Psectrocladius sp. water mite diet isolate 12739-BHL040517-GBD18271_16146-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGATTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTTTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614641 Psectrocladius sp. water mite diet isolate 12742-BHL040517-GBD6785_22371-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACATCTTTAAGAATTTTAATTCGAGCAGAATTCGGACACGCTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614642 Psectrocladius sp. water mite diet isolate 12743-BHL040517-GBD28405_18024-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGTACATCTTTTAGTATTTTAATCCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTTATTGTTACCGCTCACGCTTTTGTGATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614643 Psectrocladius sp. water mite diet isolate 12749-BHL040517-GBD17505_2792-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAGTTTTAATTCGAGCAGAACTCGGTCACGCTTTTTCTTTAATCTGAGACGATCTAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCTCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAACTCTCTAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614644 Psectrocladius sp. water mite diet isolate 12751-BHL040517-GBD21430_16557-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTTGGTACTTCTTTAAGAATTTTTATTCGAGCAGAACTCGGTCACCCTGGTTCTTTAATCGGAGACGATCAAATTTATAACGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAAAAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614645 Psectrocladius sp. water mite diet isolate 12757-BHL040517-GBD12969_14397-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTTTAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGATCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTAGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614646 Psectrocladius sp. water mite diet isolate 12758-BHL040517-GBD9219_24893-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATGGTGATACCTATTTTAATTGGAGGATTTGAAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCTCCCGTCATTAACTTTACTACTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614647 Psectrocladius sp. water mite diet isolate 12760-BHL040517-GBD3562_13752-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGGTCAGGAATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAACTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCTTTCCCTCGAATAAATAACATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614648 Psectrocladius sp. water mite diet isolate 12762-BHL040517-GBD9199_4391-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCTGGTATAGTAGGAACATCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCACGCTGGTTCTTTACTCGGAGACGATCAACTTTATAATGTTATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAACAATATAAGATTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614649 Psectrocladius sp. water mite diet isolate 12763-BHL040517-GBD16172_28049-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGGACTCGGTCACCCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCACATGCATTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTATTTCCTTTAATATTGGGGGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614650 Psectrocladius sp. water mite diet isolate 12768-BHL040517-GBD13754_6652-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACACTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTTATAATTTTTTTTATAGTGATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614651 Psectrocladius sp. water mite diet isolate 12770-BHL040517-GBD7798_17872-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTGGGAACTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATCTTGATTACTACCCCCGTCATTAACCTTACTATTATCTAGCTCTATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614652 Psectrocladius sp. water mite diet isolate 12773-BHL040517-GBD5564_8877-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTGGGTACCTCTTTTAGAATTTTAATTCGAGCAGAATTCGGTCACGCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGAGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCTTCATTAACATTACTATTATCAAGATCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614653 Psectrocladius sp. water mite diet isolate 12774-BHL040517-GBD1794_15123-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTCTAATATTGGGAGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTACTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614654 Psectrocladius sp. water mite diet isolate 12775-BHL040517-GBD25762_21072-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGTATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTAACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCGTCATTAACTCTACTATTATCAAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614655 Psectrocladius sp. water mite diet isolate 12777-BHL040517-GBD5568_13765-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCATGATCAGGAATAGTAGGAACATCTTTAAGAATTTTAATTCGAGTAGAATTAGGACACACTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCGCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614656 Psectrocladius sp. water mite diet isolate 12783-BHL040517-GBD8076_20000-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAAGTATAGTAGGTACTTCTTTAAGTATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTCTTTATAGTGATACCTATTTTAATTGGAGGGTTCGGAAATTGATTAGTTCCTTTAATATTGGGTGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614657 Psectrocladius sp. water mite diet isolate 12784-BHL040517-GBD15432_3800-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTGCATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGTCTACGATCTAATTTATAATGTAATTTTTACCTCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTACCTTTACTATTATCTAGCTCTCTAGTTGAAACTGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614658 Psectrocladius sp. water mite diet isolate 12785-BHL040517-GBD27829_18367-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCACCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614659 Psectrocladius sp. water mite diet isolate 12786-BHL040517-GBD24280_15874-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTTATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGACTACTTCCTTTAATATTAGGAGCCCCCGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614660 Psectrocladius sp. water mite diet isolate 12787-BHL040517-GBD20970_17112-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTCATAGGAGAAGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATGGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCACCGTCATTAACCTTACTAATATCTAGCGCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614661 Psectrocladius sp. water mite diet isolate 12794-BHL040517-GBD12320_28699-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCTGAACTCGGACACCCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614662 Psectrocladius sp. water mite diet isolate 12796-BHL040517-GBD24205_21009-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCATGATCAGGTATAGTAGGTATATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGATCTTTAATCGGAGCCGATCAAATTTATAATATAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCGCTGATATAGCATTCCCACGACTAAACAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614663 Psectrocladius sp. water mite diet isolate 12798-BHL040517-GBD21133_19163-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTTAGTATGCTAATTCGAGCAGAACTCTGTCACGCTAGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTATCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614664 Psectrocladius sp. water mite diet isolate 12799-BHL040517-GBD5095_20880-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGTATTTTTATTCGAGCCGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTCGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCCGATATAGCATTCCCTCGAATAAATAATATAAGTTTCTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614665 Psectrocladius sp. water mite diet isolate 12803-BHL040517-GBD20436_28387-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATTAGGTATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGCTGGTTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGAGTTTGGAAATTGATTAGTTCCTTTAATATTATGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614666 Psectrocladius sp. water mite diet isolate 12804-BHL040517-GBD4837_13650-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGCTGGTACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTTATAATTTTTTTATAATGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCAAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614667 Psectrocladius sp. water mite diet isolate 12805-BHL040517-GBD6099_10060-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATGTTTATTCGAGCAGAACTAGGACAAGCTGGTTCTTTCATCGGAGATGATCAAATTTATAATGTAGTTGTTACCGCTCACGCTTTTATAATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614668 Psectrocladius sp. water mite diet isolate 12806-BHL040517-GBD21338_12010-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTGTAGTAGGTACCTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGACCCTGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTACTTCCCCCGTCATTAACATTACTATTATCTAGCTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614669 Psectrocladius sp. water mite diet isolate 12807-BHL040517-GBD15310_4531-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACATCTTTAAGAATTTTAATTCGAGCAGAACTCGCTCACTCTGTTTCTTTAATCGGAGACGATCAAATTTATAATGAAATGGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTACCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614670 Psectrocladius sp. water mite diet isolate 12809-BHL040517-GBD14362_4435-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACTCCGTATCTTTAATCAGAGACGATCAAATTTATAATGTAATTGTTACCGCACACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAAATGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTTACTTTACTATTATCTAGCTCTCTCGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614671 Psectrocladius sp. water mite diet isolate 12810-BHL040517-GBD24319_14399-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGGGGGTTTGGAAATTGATTAGTGCCTTTAATATTTGGGGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCGTCATTAACATTACTATTATCTAGAACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR776852, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614672 Psectrocladius sp. water mite diet isolate 12811-BHL040517-GBD22123_5107-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAACCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAATAGAACTCTGTCACGCTGGTTCTTTAATCGGAGACGATCAACTTTATAATGTAATTGTTACTGCTCACGCATTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTCTGATTACTTCCACCGTCATTAACTTTACTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614673 Psectrocladius sp. water mite diet isolate 12813-BHL040517-GBD24425_5150-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAAACTGATCAGGAATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614674 Psectrocladius sp. water mite diet isolate 12814-BHL040517-GBD14354_5230-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCGGATCAGGTATAGTAGGGACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACTCTGTTTCTTTAATCGGTGTCGATCTAATTTATAATGGAATTGTTACCGCGCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614675 Psectrocladius sp. water mite diet isolate 12815-BHL040517-GBD4384_15664-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGATCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATATTAATTCGAGCTGAACTCGGTCACACTGGTTCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGGTTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR751697, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614676 Psectrocladius sp. water mite diet isolate 12817-BHL040517-GBD27790_10562-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCCTTAAGTATTCTAATTCGAGCAGAACTTGGACGCACTGGTTCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTTATAATTTTTTTATAGTTATCCCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCCCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614677 Psectrocladius sp. water mite diet isolate 12820-BHL040517-GBD7071_24750-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAACTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGTAGCTCCCGATATAGCATTCCCCCGAATAAATAACATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGAACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614678 Psectrocladius sp. water mite diet isolate 12822-BHL040517-GBD27049_12021-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGACATGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTGCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAATAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614679 Psectrocladius sp. water mite diet isolate 12824-BHL040517-GBD25758_8892-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTAGGATACGCTGGTACTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTATTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCAAGCACACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614680 Psectrocladius sp. water mite diet isolate 12827-BHL040517-GBD21581_7930-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGTGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTTATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGACTAGTTCCTGTAATATTGGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTCCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614681 Psectrocladius sp. water mite diet isolate 12828-BHL040517-GBD17282_15379-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTCATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCACCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTTCTACCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614682 Psectrocladius sp. water mite diet isolate 12830-BHL040517-GBD14716_22925-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGAGGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAACAATATAAGGTTTTGATTTCTTCCCCCGTCATTAACTTTACTATTAGCGAGCACGCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614683 Psectrocladius sp. water mite diet isolate 12831-BHL040517-GBD5757_22687-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCTCTCACGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGAGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGGTTTTGATTACTTCCCCCATCATTAACTTTGCTATTATCTAACACGCTAGTTGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614684 Psectrocladius sp. water mite diet isolate 12834-BHL040517-GBD4002_22395-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGGACTTCTTTAAGTATTTTAATTCGAGCAGAACTCGGTCAAGCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGATCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614685 Psectrocladius sp. water mite diet isolate 12839-BHL040517-GBD18152_27420-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAAAACTCGGACACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACATCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCGTCATTAACTTTACTACTATCTAGCACTATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614686 Psectrocladius sp. water mite diet isolate 12842-BHL040517-GBD9687_20840-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTGTTTTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGTTGGTTCTTTAATCGGGGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTCTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATACTAGAAGTTATTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCGCTCCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614687 Psectrocladius sp. water mite diet isolate 12843-BHL040517-GBD14621_25219-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGACATGCTGGCTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATGGCATTCCCTCGAATAAATAATATAAGTTTTTGATTGCTGCCCCCGTCATTAACTTTACTATTATCTAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614688 Psectrocladius sp. water mite diet isolate 12846-BHL040517-GBD16558_11862-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGTAGAACTCGGTTACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAATTCCTTTAATATTGGGAGCCTCTGATATAGCAGTCCCTCGAAAAAATAATATAAGGTTTTGATTACTTCCCCCGTCATTAACTTTGCTATTATCTAACACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614689 Psectrocladius sp. water mite diet isolate 12847-BHL040517-GBD4052_14753-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCTGGTATAGTAGGTACATCTTTTAGAATTTTAATTCGAGCAGAACTCGGTCATGCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTATTAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACATTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614690 Psectrocladius sp. water mite diet isolate 12848-BHL040517-GBD4287_14804-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCTGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTTGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCGTCTTTAACTTTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614691 Psectrocladius sp. water mite diet isolate 12850-BHL040517-GBD7166_12473-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACACTGGTACTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTGACTTTACTATTATCTAGCACACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614692 Psectrocladius sp. water mite diet isolate 12851-BHL040517-GBD28566_16415-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCATGCTGGTACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCATTAACTTTACTATTATCTAGTTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR776852, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614693 Psectrocladius sp. water mite diet isolate 12856-BHL040517-GBD4968_15239-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCATGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCCTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCACGAATAAATAATATAAGTTTTTGATTACTGCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614694 Psectrocladius sp. water mite diet isolate 12858-BHL040517-GBD27080_13841-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCATGATCAGGTATAGTAGGAACATCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCAAGCTGGTTCTTTCATCGGAGACGATCAAATTTATAATGTACTTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTTGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614695 Psectrocladius sp. water mite diet isolate 12859-BHL040517-GBD17148_4189-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGACACGCTGGATCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCACACGCTTTTTTAATAATTTTTTTTATAGTGATACCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTTGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCTTTAACTTTACTATTATCTATCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614696 Psectrocladius sp. water mite diet isolate 12860-BHL040517-GBD27586_21852-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTCGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGTAGAACTAGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTTGTACCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTAGTAGCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR761745, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614697 Psectrocladius sp. water mite diet isolate 12862-BHL040517-GBD16645_23233-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTTATTTTATTTTTGGAACCTGATCAGGTATAGTGGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCAGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGGCATTAACTTTACTATTATCTAGCTCGCTAGGTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614698 Psectrocladius sp. water mite diet isolate 12865-BHL040517-GBD21863_27825-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATGGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGATCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAAATTTACTATTATCTAGCAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614699 Psectrocladius sp. water mite diet isolate 12867-BHL040517-GBD25522_21545-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAATTAGGTCAAGCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTTGTTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTTGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614700 Psectrocladius sp. water mite diet isolate 12872-BHL040517-GBD23101_16795-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGTACATCTTTAAGTATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTTATCGGAGAGGATCAAATTTATAATGTTATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCTCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTCTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614701 Psectrocladius sp. water mite diet isolate 12876-BHL040517-GBD14905_18054-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGACACGCTGGTTCCTTAATCGGAGACGATCAGATTTATAATGTAATTGTTACCGCTCACGCCTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGTAAATTGATTAGTTCCTTTAATATTTGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGATCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614702 Psectrocladius sp. water mite diet isolate 12877-BHL040517-GBD23899_25355-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGTGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCATGCTGGTTCTTTTATCGGAGACGAACAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGTAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCAAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614703 Psectrocladius sp. water mite diet isolate 12878-BHL040517-GBD9340_17151-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCCGGAATAGTAGGTACTTCTTTAAGAATTTTTATTCGAGCAGAACTCGGTCACGCTGATTCTTTAATCGGAGACGATCAAATTTATAATGTTATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACATATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCACCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614704 Psectrocladius sp. water mite diet isolate 12881-BHL040517-GBD26732_19686-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGTAGAACTAGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTGATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCGGCATTAACTTTACTATTATCTAGCTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614705 Psectrocladius sp. water mite diet isolate 12885-BHL040517-GBD24558_21035-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGCTATAGTAGCTACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCATGCTGGTTCTTTAATTGGAGACGATCAAATTTATTATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614706 Psectrocladius sp. water mite diet isolate 12890-BHL040517-GBD9076_24228-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTCGGAGCCTGATCAGGAATAGTCGGTACATCCTTAAGAATTTTAATTCGAGCAGAATTAGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGTATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR761745, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614707 Psectrocladius sp. water mite diet isolate 12892-BHL040517-GBD20066_19276-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCATGCTGGTTCTTTAATCGGTGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAAGGTTTGGAAATTGATTATTACCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTTACTTTACTACTATCTAGCACACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614708 Psectrocladius sp. water mite diet isolate 12893-BHL040517-GBD13738_18497-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGATCTTTAATCGGTGACGATCAAATTTATAATGTAATTGTTACCGCACATGCTTTTGTAATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATGGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614709 Psectrocladius sp. water mite diet isolate 12894-BHL040517-GBD4776_7452-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTTTTTTTGGAGCCTGATCAGGTATAGTAGGAACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACTCTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTGGGAGCCCCTGATATGGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCACCGTCATTAACTTTACTATTATCTAGCACACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614710 Psectrocladius sp. water mite diet isolate 12896-BHL040517-GBD20664_17993-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGATATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACCCTGGTTCTTTAATCGGTGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTTGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACTTTACTATTATCTAGCGCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614711 Psectrocladius sp. water mite diet isolate 12897-BHL040517-GBD29471_12961-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTCGGAGCTTGATCAGGTATAGTAGGTACTTCCTTAAGAATCTTAATTCGAGCAGAACTAGGTCATGCCGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614712 Psectrocladius sp. water mite diet isolate 12898-BHL040517-GBD15179_8133-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGTGCCTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAACTCGGTCATGCTGGTTCTTTTATAGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614713 Psectrocladius sp. water mite diet isolate 12900-BHL040517-GBD19224_14068-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACATCTTTAAGAATTTTAATTCGAGCAGAATTCGGACACGCTGGTTCTTTAATCGGAGACGATCAACTTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCAATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGCGCTCCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR751697, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614714 Psectrocladius sp. water mite diet isolate 12901-BHL040517-GBD9875_8822-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCTGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTATAGTGATACCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACCTTACTATCAACTAGCACTCTAGCTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614715 Psectrocladius sp. water mite diet isolate 13260-BHL040517-GBD16594_13834-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCTCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614716 Psectrocladius sp. water mite diet isolate 13282-BHL040517-GBD5029_14358-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATCTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAGGAATTTTAATTCGAGCAGAACTCAGTCACGCTGGTTCTTTAATCGGATACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGGGATACCTATTTTAATTGGAGGGTTTGGAAATCGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAGATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR761745, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614717 Psectrocladius sp. water mite diet isolate 13317-BHL040517-GBD17199_14846-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTCATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCTCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTCTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614718 Psectrocladius sp. water mite diet isolate 13321-BHL040517-GBD23796_20893-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCTCCCGACATAGCATTCCCTCGAATAAATAATATAAGCTTTTGATTACTTCCCCCATCTTTAACCCGTCTGCTATCAAGAAGATGAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614719 Psectrocladius sp. water mite diet isolate 13352-BHL040517-GBD13178_23142-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTCGGAGCTTGGTCAGGAATATTCGGAACATCCTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCTCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614720 Psectrocladius sp. water mite diet isolate 13364-BHL040517-GBD10547_17612-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATCTTAATTCGAGCAGGACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTATTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCTCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAACTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614721 Psectrocladius sp. water mite diet isolate 13419-BHL040517-GBD4234_8787-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATACTTTATTTTCGGAGCTTGGTCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGATTGGAAATTGATTAGTTCCTTTAATATTGTGAGACCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCGCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR761745, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614722 Psectrocladius sp. water mite diet isolate 13421-BHL040517-GBD20158_24852-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCAAGCAGAACTCGGTCACGCTGGTTCTTTAATCTGAGACAATCAAATTTATAATGTAATTGTTACCGCTCAAGCTTTTGTAATAATTTTTTTATAGTGATACCCATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAACATTCCCTCGAATAAATAATATAAATTTTTGATTACTTCCCCCGTCATTAACTTTAGTAATAACTAGCTCTCTAGTTGAAAAAGGAGCTGGAACAGGA	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614723 Psectrocladius sp. water mite diet isolate 13454-BHL040517-GBD18881_24601-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCTTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTACTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCTCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTTCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614724 Psectrocladius sp. water mite diet isolate 13607-BHL040517-GBD14704_10818-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGTAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614725 Psectrocladius sp. water mite diet isolate 13655-BHL040517-GBD26202_13254-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAAAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATATAATTGTTACCGCTCACGCTTTTGTTATAATTTTTTTATAGTAATACCTATTTTAATTTGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGTAGCCCCCGACATAGCATTCCCTCGAATAAATAATAAAAGTATTTGATTACTACCCCCGTCAGTAACATTACAATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614726 Psectrocladius sp. water mite diet isolate 13659-BHL040517-GBD13638_9964-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACCCTGGTTCCTTAATTGTAGATGATCAAATTTATAATGTAATTGTTACCGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTACTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614727 Psectrocladius sp. water mite diet isolate 13660-BHL040517-GBD28452_16314-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCCTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCAAGCTGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACTCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614728 Psectrocladius sp. water mite diet isolate 13682-BHL040517-GBD22549_14431-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACCCTGGTTCCTTAATTGGAGATGATCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAACATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614729 Psectrocladius sp. water mite diet isolate 13751-BHL040517-GBD27816_16642-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACCCTGGTACATTTATTGGAGATGATCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCGTTAATATTAGGAGCCCCAGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614730 Psectrocladius sp. water mite diet isolate 13756-BHL040517-GBD27992_11244-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCCTGATCAGGAATAGTAGGCACTTCTTTAAGTATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGTGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614731 Psectrocladius sp. water mite diet isolate 13763-BHL040517-GBD10452_25334-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCCCTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTTTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCTCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAATTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614732 Psectrocladius sp. water mite diet isolate 13765-BHL040517-GBD21102_23741-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCTGTCACACTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTACTTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCAGACATAGCATTCCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGCGCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614733 Psectrocladius sp. water mite diet isolate 13773-BHL040517-GBD26171_10168-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCCGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTCATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTACTAATTTTTTTATAGTAATACCTATTTTAATTGAAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATGGCATTCCCCCGAATAAAAAAAAAAAGTTTTGGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614734 Psectrocladius sp. water mite diet isolate 13803-BHL040517-GBD4086_11003-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCCTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCTGAATTCGGTCACCCAGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGCTAATATTAGGAGCCCCTGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614735 Psectrocladius sp. water mite diet isolate 13806-BHL040517-GBD22716_24210-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGTCACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGTCACGCTGGTTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCTGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614736 Psectrocladius sp. water mite diet isolate 13823-BHL040517-GBD27674_15160-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACCTCTTTTAGAATTTTAATTCGAGCAGAACTAGGTCATGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCATTAACATTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614737 Psectrocladius sp. water mite diet isolate 13825-BHL040517-GBD9299_22195-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTCGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTTATTCGAGCTGAACTCGGTCACGCTGGTACCTTAATTGGTGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614738 Psectrocladius sp. water mite diet isolate 13846-BHL040517-GBD20012_3978-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGCAATTGTTACCGCCCACGCTTTTGTAATAATTTTTTTATAGTAATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTCTCGTTAATATTAGGAGCCCCCGACACAGCATTCCCTCGAATAAATAATATAAGGTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATTTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614739 Psectrocladius sp. water mite diet isolate 13860-BHL040517-GBD21137_24450-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTATTTTTGGAGCCTGATCAGGCATAGTTGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCAGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTGCCCCCGTCATTAACGTTACTATTATCTAGATCACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614740 Psectrocladius sp. water mite diet isolate 13871-BHL040517-GBD4117_11569-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTCTAATTCGAGCAGAATTCGGTCACGCTGGATCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTTTAATAATTTTTTTATAGTAATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAACTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614741 Psectrocladius sp. water mite diet isolate 13877-BHL040517-GBD5747_11088-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACCCTGGTACCTTAATTGGAGATGATCAAATTTGTAATGTAATTGTTACCGCTCATGCTTTTATAATAATTTTTTTATGGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614742 Psectrocladius sp. water mite diet isolate 13918-BHL040517-GBD4900_16071-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTCGGACACCCTGGCTCCTTGATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACCTTACTATTATCAAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614743 Psectrocladius sp. water mite diet isolate 13920-BHL040517-GBD28126_18145-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCAGGCATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGACACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCTGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTTCTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614744 Psectrocladius sp. water mite diet isolate 13934-BHL040517-GBD16728_16160-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTTGGAGCTTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGAAGAATTCGGTCACGCTGGTTCCTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614745 Psectrocladius sp. water mite diet isolate 13935-BHL040517-GBD24249_20134-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGATTCATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATCTTAATTGGAGGATTTGGAAATTGATTACTTCCTTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614746 Psectrocladius sp. water mite diet isolate 13941-BHL040517-GBD24812_8474-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCTGAACTCGGACACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTACCGTTAATATTAGGAGCCCCCGACATAGTATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR751697, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614747 Psectrocladius sp. water mite diet isolate 13948-BHL040517-GBD9329_23056-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATCTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGTGCTCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCAAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614748 Psectrocladius sp. water mite diet isolate 13953-BHL040517-GBD18001_13764-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACACTGGTTCCTTAATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCGTTAATATTAGGAGCCCCCGACATAGCATTCCCACGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACTTTACTATTATCTAGCACTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614749 Psectrocladius sp. water mite diet isolate 13954-BHL040517-GBD29498_17763-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTCCCCCCGTCAGGAACGGGACGAGGAGCGAGCGCGCGAGGGGAAAAGGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614750 Psectrocladius sp. water mite diet isolate 13963-BHL040517-GBD6270_11585-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCATGATCAGGCATAGTAGGCACTTCTTTAAGAATTCTAATACGAGCAGCAGGCGGTCACGCTAGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTGGGAGCCCCCGACATAGCATTCCCTCGAATAAATGATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614751 Psectrocladius sp. water mite diet isolate 13965-BHL040517-GBD26613_11412-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCACGCTGGTTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCAGTAACCTTACTATTATCAAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614752 Psectrocladius sp. water mite diet isolate 14578-BHL040517-GBD21423_6709-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCTCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614753 Psectrocladius sp. water mite diet isolate 14607-BHL040517-GBD22967_11781-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCTCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614754 Psectrocladius sp. water mite diet isolate 14636-BHL040517-GBD26021_22376-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTACTTTAAGATTTTTAATTCGACTAGAATTAGGACACCCAAGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCATATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTAATTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614755 Psectrocladius sp. water mite diet isolate 14661-BHL040517-GBD22362_15129-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGACACCCAGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCTGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCAAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614756 Psectrocladius sp. water mite diet isolate 14662-BHL040517-GBD19272_13068-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTCGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCTGAACTCGGTCATGCCGGTTCCTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTCCCGTTAATATTAGGAGCCCCAGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614757 Psectrocladius sp. water mite diet isolate 14679-BHL040517-GBD16315_24413-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGAAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGAAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614758 Psectrocladius sp. water mite diet isolate 14714-BHL040517-GBD23554_6920-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTCGGGGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACCCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCACATGCTTTTGTAATAATTTTTTTGATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614759 Psectrocladius sp. water mite diet isolate 14716-BHL040517-GBD14553_29020-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCTTGATCAGGCATAGTAGGCACTTCTTTAAGATTTTTAATTCGAGCAGAACTCGGACACGCAGGATCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614760 Psectrocladius sp. water mite diet isolate 14719-BHL040517-GBD9959_2908-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGTCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGCCGGTACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTACTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614761 Psectrocladius sp. water mite diet isolate 14737-BHL040517-GBD13419_6765-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTCATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCCCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTACCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614762 Psectrocladius sp. water mite diet isolate 14739-BHL040517-GBD7042_20437-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCCGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACCCCGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCACATGCTTTTGTAATAATTTTTTTATACTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614763 Psectrocladius sp. water mite diet isolate 14741-BHL040517-GBD13391_5934-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCATGAGCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATGCGAGCAGAGCTCGGTCACGCCGTTTCCTTAATGGGAGATGATCAAATTGATAATGTAATTGTTACCGCGCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGACTAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGCGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614764 Psectrocladius sp. water mite diet isolate 14766-BHL040517-GBD28588_10073-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTGCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCCCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCCTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAAAAAAAAGTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614765 Psectrocladius sp. water mite diet isolate 14809-BHL040517-GBD27188_11088-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCACCCCGGTTCCTTAATTGGTGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614766 Psectrocladius sp. water mite diet isolate 14812-BHL040517-GBD2270_14764-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614767 Psectrocladius sp. water mite diet isolate 14816-BHL040517-GBD17002_15733-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGGATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCACGACATAGCATTCCCTCGAATAAATAATATAATTTTTTGATTACATCCCCCGTCATTAACTTGACGATTAACTAGCTCTCTAGGTGAAAATGCAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614768 Psectrocladius sp. water mite diet isolate 14823-BHL040517-GBD25097_12035-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCCGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTACCTTCATTGGAGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTCTGATTTCTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614769 Psectrocladius sp. water mite diet isolate 14844-BHL040517-GBD4486_16045-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTTATTCGAGCTGAATTCGGTCACACCGGTTCCTTAATTGGTGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGTGCTCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614770 Psectrocladius sp. water mite diet isolate 14859-BHL040517-GBD6297_6129-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACCCGGGTACCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTGATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCCCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCAAGCACTCTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614771 Psectrocladius sp. water mite diet isolate 14874-BHL040517-GBD5526_22324-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTACCTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGAAATTGATTAGTTCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCAGACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614772 Psectrocladius sp. water mite diet isolate 14888-BHL040517-GBD29205_14187-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGCATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGACACACAGGTTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCACGTCATTAACTTTACTATTATCTAGCTCTCGAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614773 Psectrocladius sp. water mite diet isolate 14901-BHL040517-GBD5119_14638-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTTGAGCAGAACTCGGTCACCCCGGATCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGAACACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614774 Psectrocladius sp. water mite diet isolate 14912-BHL040517-GBD27165_12304-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTTAGAATTTTAATTCGAGCAGAACTCGGTCATGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCATTAACATTACTATTATCAAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614775 Psectrocladius sp. water mite diet isolate 14923-BHL040517-GBD14894_3879-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGCAACTTTCATTGGAGATGACCAAAGTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACCTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614776 Psectrocladius sp. water mite diet isolate 14926-BHL040517-GBD2192_12090-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTACCTTAATTGGTGATGATCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTAATAATTTTTTCATAGTAATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCGTTAATATTAGGAGCCCCAGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614777 Psectrocladius sp. water mite diet isolate 14928-BHL040517-GBD16975_4761-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGACACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCACCCGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCATTAACTTTACTTTTATCTAGCTCTCTCGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614778 Psectrocladius sp. water mite diet isolate 14929-BHL040517-GBD26012_15569-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGTTTTTTAATTCGAGCAGAACTCGGTCACACCGGTTCCTTAATTGGAGATGATCATATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGAATACTTCCCCCGTCATTAACTTTACTATTATCTAGCACTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614779 Psectrocladius sp. water mite diet isolate 14933-BHL040517-GBD20353_27531-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCACGCCGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCAGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614780 Psectrocladius sp. water mite diet isolate 14936-BHL040517-GBD22141_6852-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCGTTAATATTAGGATCCCCCGATATAGCATTCCCCCGAATAAATAACATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCAAGCACATTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614781 Psectrocladius sp. water mite diet isolate 14956-BHL040517-GBD19386_9046-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGCCGGTTCCTTAATTGGTGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAACATAAGTTTTTGATTACTACCCCCGTCATTAACTTTACTATTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614782 Psectrocladius sp. water mite diet isolate 14959-BHL040517-GBD15520_18596-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACCCCGGTTCCTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCGTTAATATTAGGAGCCCCAGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTCCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614783 Psectrocladius sp. water mite diet isolate 14986-BHL040517-GBD12432_24232-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCTGGCATAGTGGGCACTTCTTTTAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATACTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTACTTCCACCGTCATTAACATTACTATTATCTAGCTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614784 Psectrocladius sp. water mite diet isolate 14987-BHL040517-GBD28925_13339-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCATGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGATCACGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTGCCCCCGTCAGTAACTTTACTATTATCTAGCTCACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614785 Psectrocladius sp. water mite diet isolate 14991-BHL040517-GBD5169_9795-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTTGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTACCTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTGGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCGTCATTAACTTTACTATTATCTAGCGCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614786 Psectrocladius sp. water mite diet isolate 14993-BHL040517-GBD18064_21176-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGTAGAACTCGGTCACGCCGGTTCCTTAATGGGAGATGATAAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGTGCTCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614787 Psectrocladius sp. water mite diet isolate 15007-BHL040517-GBD20056_11103-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGAAATAGCACCCCCAAAAAAAAAAAATATAAGTTTTTGATTCCTCCCCCCGCCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614788 Psectrocladius sp. water mite diet isolate 15022-BHL040517-GBD22171_15733-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCGGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTAATAATTTTTTTACAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCGTTAATATTAGGAGCCCCCGATATAGCATTCCCGCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACCTTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614789 Psectrocladius sp. water mite diet isolate 15033-BHL040517-GBD17186_8355-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGTCTGATCAGGCATAGTAGGCACTTCTTTTAGAATTTTAATTCGAGTTGAATTCGCTCACGCCGGTTCCTTACTTGGAGATGATCAACTTTATAATGCAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTCTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614790 Psectrocladius sp. water mite diet isolate 15042-BHL040517-GBD17284_28942-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCGGAACTCGGTCACGCCGGTTCCTTAATTGGTGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCACTAACTTTACTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614791 Psectrocladius sp. water mite diet isolate 15052-BHL040517-GBD7544_25796-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCACACAGGTTCCTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCTTTAACTTTACTATTATCTAGCACAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614792 Psectrocladius sp. water mite diet isolate 15054-BHL040517-GBD17400_4385-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATGTTAATTCGAGCAGAACTCGGACACTCCGTTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCACACGCTTTTGTAATAATTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTTCTATTGTCTAGCTCTCTCGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614793 Psectrocladius sp. water mite diet isolate 15056-BHL040517-GBD2378_16165-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACACAGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCAAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614794 Psectrocladius sp. water mite diet isolate 15059-BHL040517-GBD7210_5309-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAACCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGCTGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTTTTTTAATTGGAGGGTTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACCTAGCATTTCCCCCAATAAAAAAAAAAGGTTTTGATTACCTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614795 Psectrocladius sp. water mite diet isolate 15066-BHL040517-GBD12791_3669-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCGTGAGCAGGCATAGTAGGCACTGCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACTCCGGTTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCGCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAAATTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614796 Psectrocladius sp. water mite diet isolate 15072-BHL040517-GBD23620_17686-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614797 Psectrocladius sp. water mite diet isolate 15074-BHL040517-GBD17652_10186-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAACAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCGCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACCTTAAGATTATCAAGCTCTATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614798 Psectrocladius sp. water mite diet isolate 15086-BHL040517-GBD21487_25381-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGTAGAATTAGGTCACCCCGGTTCCTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCACACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTCGGAAATTGATTAGTCCCGTTCATATTAGGAGCCCCCGACATAGCATTCCCGCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614799 Psectrocladius sp. water mite diet isolate 15087-BHL040517-GBD25021_20128-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCTTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCATGCTGGTTCCTTAATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCAAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614800 Psectrocladius sp. water mite diet isolate 15089-BHL040517-GBD15481_16025-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATATTAATTCGAGCAGAACTCGGTCATCCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTGCCGTTAATATTAGGAGCCCCCGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614801 Psectrocladius sp. water mite diet isolate 15096-BHL040517-GBD18170_26723-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCATGCAGGTTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTATTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614802 Psectrocladius sp. water mite diet isolate 15101-BHL040517-GBD27892_10800-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGTATTTTAATTCGAGCAGAACTAGGTCAAGCCGGATCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614803 Psectrocladius sp. water mite diet isolate 15103-BHL040517-GBD20328_14781-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACCCCGGTTCATTAATTGGAGATGATCAAATTTATAATGTAATCGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCAGTCATTAACTTTACTATTATCTAGCTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614804 Psectrocladius sp. water mite diet isolate 15122-BHL040517-GBD15679_27127-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTCCCTTTGATATTAGGAGCTCCTGACATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTATTTCCCCCGTCATTAACCTTACTATTATCTAGATCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614805 Psectrocladius sp. water mite diet isolate 15123-BHL040517-GBD22158_26122-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTTAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCGTCATTAACATTACTATTATCTAGATCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614806 Psectrocladius sp. water mite diet isolate 15127-BHL040517-GBD10227_18273-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGACACGCCGGTTCCTTCATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCACATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCGTCATTAACTTTACTACTATCTAGCTCTCTAGTAGGAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614807 Psectrocladius sp. water mite diet isolate 15130-BHL040517-GBD24000_19023-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAATAGGCACTCCTTTTAGAATTTTAATTCGAGCAGAACTCGGTCACCCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTCCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614808 Psectrocladius sp. water mite diet isolate 15131-BHL040517-GBD17224_27930-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCCGGAATAGTAGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTCGGTCACCCCGGTTCCTTCATTGGAGATGACCAAATTTATAGTGTTATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614809 Psectrocladius sp. water mite diet isolate 15135-BHL040517-GBD18493_14059-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACCCCGGTTCCTTAATTGGAGATGACCAAATTTATGATGTAATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCCTCGTCATTAACTTTACTATTATCTAACACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614810 Psectrocladius sp. water mite diet isolate 15140-BHL040517-GBD22547_23031-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCGGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCATGCTGGTTCCTTAATTGGAGATAATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCATTAATATTAGGAGCCCCCGACATAGCATTCCCACGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACTTTACTATTATCAAGCACTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614811 Psectrocladius sp. water mite diet isolate 15143-BHL040517-GBD28280_10705-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCTTGATCAGGCATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGAACCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTCCCTTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCAAGCACACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614812 Psectrocladius sp. water mite diet isolate 15150-BHL040517-GBD18407_22674-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAACAATATAAGATTTTGACTACTACCCCCGTCATTAACCTTACTATTATCTAGCGCTCCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614813 Psectrocladius sp. water mite diet isolate 15154-BHL040517-GBD18937_26841-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGACACCCAGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCACGCATTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTCCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614814 Psectrocladius sp. water mite diet isolate 15163-BHL040517-GBD3547_17335-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTCTAATTCGAGCAGAACTCGGTCAAGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCTTTCCCTCGTATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTACTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614815 Psectrocladius sp. water mite diet isolate 15172-BHL040517-GBD7478_19715-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCGAACCGGTTCCTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614816 Psectrocladius sp. water mite diet isolate 15174-BHL040517-GBD16618_14315-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGTAGAATTAGGTCACCCCGGTTCCTTAATTGGAGAAGATCAAATTTATAATGTAATTGTTACCGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACCTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614817 Psectrocladius sp. water mite diet isolate 15183-BHL040517-GBD28442_11018-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGCATAGTAGGCACTTCTTTAAGTATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCGATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGAACTTTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614818 Psectrocladius sp. water mite diet isolate 15189-BHL040517-GBD26682_12713-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCAGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCACATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCACGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGATCAATAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614819 Psectrocladius sp. water mite diet isolate 15191-BHL040517-GBD23923_8902-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGATTTTTTCTTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGATCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTACTATCTGGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614820 Psectrocladius sp. water mite diet isolate 15194-BHL040517-GBD12225_10633-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGATGTAGCATTCCCACGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614821 Psectrocladius sp. water mite diet isolate 15201-BHL040517-GBD16813_15792-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCTGTTCCTTCATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGATATTGATTAGTCCCGTTAATATTAGGAGCCCCCGAAATAGCATTCCCTCGAATAAAAAATAAAAGTTTTTGATTACTTCCCCCGTCATTAACTTTGCTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614822 Psectrocladius sp. water mite diet isolate 15211-BHL040517-GBD20602_22882-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCATGCCGGTTCCTTAATTGGAGATGATCAAATTTCTAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGTGCCCCCGACATAGCATTCCCTCGAATAAAAAATATAAGTTTTTGATTACTTCCCCCGTCATTAACATTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614823 Psectrocladius sp. water mite diet isolate 15217-BHL040517-GBD15407_21202-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGTCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCATCATTAACTTTACTATTATCTAGAAGACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614824 Psectrocladius sp. water mite diet isolate 15219-BHL040517-GBD27077_21481-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTGTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCAAGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTAGCGCTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTCCCCCTAATATTAGGAGCCCCTGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614825 Psectrocladius sp. water mite diet isolate 15227-BHL040517-GBD5907_23643-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCGTCATTAACTTTACTACTATCTAGTACAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614826 Psectrocladius sp. water mite diet isolate 15241-BHL040517-GBD4113_13412-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACCCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGTAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAAAAATAAAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATCATCTAGCACGCTAGTTGAAAAAGGAGCCGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614827 Psectrocladius sp. water mite diet isolate 15262-BHL040517-GBD18197_6629-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCCGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCGCCCCGGTTCCTTCATTGGAGATGATCAAATTTATAATGTTATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATCGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACAACTTCCCCCGTCACTAACTTTACTACTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614828 Psectrocladius sp. water mite diet isolate 15264-BHL040517-GBD27989_17328-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGCCGGTTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCACCTGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614829 Psectrocladius sp. water mite diet isolate 15270-BHL040517-GBD27506_20095-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTTAGAATTTTAATTCGAGCAGAATTCGGTCATGCCGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCAGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCTCGTCATTAACATTACTATTATCTAGATCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614830 Psectrocladius sp. water mite diet isolate 15276-BHL040517-GBD23188_11889-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGGCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATACTGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGTCATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTACCCCCGTCACTAACTTTACTACTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614831 Psectrocladius sp. water mite diet isolate 15284-BHL040517-GBD1771_14568-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACCCCGGTTCCTTAATTGGTGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCTGACATAGCATTCCCTCGAATAAATAATATAAGTTTCTGATTACTCCCCCCGTCACTAACTTTACTAATATCTAGTTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614832 Psectrocladius sp. water mite diet isolate 15286-BHL040517-GBD26057_8546-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTAATTTTGGAGCCTGATCATGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCCTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCGTTAATATTAGGAGCCCCCGACATAGCATTCCCACGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACTTTACTATTATCTAGCACACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614833 Psectrocladius sp. water mite diet isolate 15289-BHL040517-GBD17434_28029-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGAGCCTGATCGGGCATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATCTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCACCCGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGATCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614834 Psectrocladius sp. water mite diet isolate 15292-BHL040517-GBD22368_27440-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGCATAGTAGGCACTTCTTTAAGAATTCTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTGACTTTACTATTATCTAGCGCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614835 Psectrocladius sp. water mite diet isolate 518-BHL040517-GBD13387_19805-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGTCTGATCAGGCATAGTAGGCACTTCATTAAGAATTTTAATTCGAGCAGAACTTGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATAGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTATTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614836 Psectrocladius sp. water mite diet isolate 999-BHL100916-GBD22965_18860-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACCCAGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCATTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614837 Psectrocladius sp. water mite diet isolate 2698-BHL032417-GBD6091_17524-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTTTTTTTTTGGAGCTTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.1% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614838 Psectrocladius sp. water mite diet isolate 2973-BHL032417-GBD10015_14219-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGTTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCCTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614839 Psectrocladius sp. water mite diet isolate 3037-BHL032417-GBD23563_10102-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTCAAGAAATTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTCTTTACAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTCTTGATTACTTCCCTCGTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614840 Psectrocladius sp. water mite diet isolate 3113-BHL032417-GBD24619_14004-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAAAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTCGGAAATTGATTAGTCCCGTTAGTATTAGGAGCCCCTGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTCCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614841 Psectrocladius sp. water mite diet isolate 3259-BHL032417-GBD5238_6492-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTCTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAGCTCGGTCACGCCGGTTCCTTAATTGGAGATGGTCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATACTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614842 Psectrocladius sp. water mite diet isolate 3266-BHL032417-GBD15786_5030-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTGTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGAACTTCTTTAAGAATTTTAATACGAGCAGAACTCGGTCACGCCGTTTCCTTAATTGGAGATGATCAAATTTATAATGGAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614843 Psectrocladius sp. water mite diet isolate 3320-BHL032417-GBD24748_20921-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAGTTCGAGCAGAACTCGTTTACTCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGACTACATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614844 Psectrocladius sp. water mite diet isolate 3424-BHL032417-GBD15298_15059-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTTGGCGCTTCTTTAAGAATTTTAATTCGAGTTGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGACATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTAGCTAACTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614845 Psectrocladius sp. water mite diet isolate 4780-BHL032417-GBD18546_7302-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTCAAGAATTTTAATTCGAGCGGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614846 Psectrocladius sp. water mite diet isolate 5566-BHL032417-GBD15684_5671-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCTTGACCAGGCATAGAAGGCACTTCTTTAAGAATTTTAATCCGAGCAGAACCCGGTCACGCGGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCCCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614847 Psectrocladius sp. water mite diet isolate 5831-BHL032417-GBD25559_19010-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATGGGAGATGATCAAATTTATAATGTAATTTTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614848 Psectrocladius sp. water mite diet isolate 10947-BHL101516-GBD16594_14480-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAAAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACGTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614849 Psectrocladius sp. water mite diet isolate 11018-BHL110116-GBD22476_11707-Lq75 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614850 Psectrocladius sp. water mite diet isolate 11035-BHL110116-GBD25671_8897-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATCAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614851 Psectrocladius sp. water mite diet isolate 11489-BHL101516-GBD21270_12985-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATGGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACATTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614852 Psectrocladius sp. water mite diet isolate 11498-BHL101516-GBD11119_3282-Lq80 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATGCCCTCGAATAAACAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614853 Psectrocladius sp. water mite diet isolate 11617-BHL101516-GBD7694_12871-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGTAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACATTACTATTATCAAGCTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614854 Psectrocladius sp. water mite diet isolate 11821-BHL101516-GBD9608_22179-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGTTCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614855 Psectrocladius sp. water mite diet isolate 12638-BHL040517-GBD21556_18780-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGCACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCGTATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAAAATAAGTTCTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGGTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614856 Psectrocladius sp. water mite diet isolate 12667-BHL040517-GBD11284_22233-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTACAGTAATACCTATTTTAAATGGAGGGTTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGAAATAACATTCCCTCGAATAAAAAATAAAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614857 Psectrocladius sp. water mite diet isolate 12970-BHL040517-GBD24864_21508-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614858 Psectrocladius sp. water mite diet isolate 13571-BHL040517-GBD11679_14492-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGCTGGTTCCTTAATTGGTGATGAACAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTTATAATTTTTTTATAGTAATACCTATTTTAATTGGAAGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAAAAAATAATATAAGGTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614859 Psectrocladius sp. water mite diet isolate 13610-BHL040517-GBD13539_16803-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGATCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCAGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614860 Psectrocladius sp. water mite diet isolate 13657-BHL040517-GBD20180_6162-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGCATAGTCGGCACTTCTTTAAGTATTTTAATTCGAGCAGAACTCGGTCACCCTGGTACCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGATCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614861 Psectrocladius sp. water mite diet isolate 13670-BHL040517-GBD27187_22588-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCATTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTCCCGTTAATATTAGGAGCCCCCGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614862 Psectrocladius sp. water mite diet isolate 13675-BHL040517-GBD22034_25251-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGAAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGATCACGCTGATTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATCTTAATTGGAGGATTTGGAAATTGATTAGTTCAGTTAATATTAGGAGCCCCCGACATACCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTACTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614863 Psectrocladius sp. water mite diet isolate 13690-BHL040517-GBD17498_11100-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACTTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGATATAGCTTTCCCGCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614864 Psectrocladius sp. water mite diet isolate 13695-BHL040517-GBD22644_14378-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACTCTGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614865 Psectrocladius sp. water mite diet isolate 13706-BHL040517-GBD23185_25403-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCTGGTATAGTAGGCACTTCTTTTAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACTTAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614866 Psectrocladius sp. water mite diet isolate 13716-BHL040517-GBD10197_11581-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGATCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTGATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTTCCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGGTTTTGATTGCTTCCCCCGTCATTAACTTTACTATTATCTAGCACGCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614867 Psectrocladius sp. water mite diet isolate 13721-BHL040517-GBD26410_13359-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTATCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCGCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACATTACTATTATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614868 Psectrocladius sp. water mite diet isolate 13734-BHL040517-GBD14585_2741-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAAGTCGAGCAGAACTCGGTCACGCTGGTCCCTTAATTGGAGATGATCAAATTTATAATGGAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGGCACGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614869 Psectrocladius sp. water mite diet isolate 13738-BHL040517-GBD24146_24644-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGCACTTCTTTTAGAATTTTAATTCGAGCAGAACTCGGTCACCCTGGTTCCTTCATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614870 Psectrocladius sp. water mite diet isolate 13746-BHL040517-GBD9050_18776-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCAGACATAGCATTCCCTCGAATAAATAACATAAGATTCTGATTACTTCCCCCGTCATTAACATTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614871 Psectrocladius sp. water mite diet isolate 13747-BHL040517-GBD9670_7323-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTCGGAGCTTGATCAGGCATAGTAGGCACTTCCTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACAAAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614872 Psectrocladius sp. water mite diet isolate 13777-BHL040517-GBD13070_4341-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACCCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAACTGTTACCGCTCATGCTTTTGTTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTTGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614873 Psectrocladius sp. water mite diet isolate 13810-BHL040517-GBD3849_11310-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTACTTGGAGATGATCAAATTTATAATGTACTTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTGCCCCGTCATTAACTTTACTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614874 Psectrocladius sp. water mite diet isolate 13813-BHL040517-GBD15031_20602-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACACAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.4% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614875 Psectrocladius sp. water mite diet isolate 13814-BHL040517-GBD23055_11455-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTTGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGCTGGTTCCTTACTTGGAGATGATCAAATTTATAATGTAATTGCTACTGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCAGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614876 Psectrocladius sp. water mite diet isolate 13815-BHL040517-GBD11900_22388-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTGTTATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAAGATTTGTAAACTGATTATTCCCGTTAATATTAGGAGCCCCCGACAAAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCACTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR751697, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614877 Psectrocladius sp. water mite diet isolate 13821-BHL040517-GBD8886_6502-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACCCTGGTTCCTTCATTGGAGATGATCAAATTTATAATGTCATTGTTACCGCTCACGCTTTCGTAATAATTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAACTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR751697, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614878 Psectrocladius sp. water mite diet isolate 13826-BHL040517-GBD13208_22882-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTCTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTTAGAATATTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGTGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCATTTGTAATAATTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCAGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614879 Psectrocladius sp. water mite diet isolate 13856-BHL040517-GBD13172_26899-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCAGGCATAGTCGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTCGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614880 Psectrocladius sp. water mite diet isolate 13883-BHL040517-GBD12905_27148-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTCTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCAGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGTAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTATTTCCCCCGTCATTAACCTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614881 Psectrocladius sp. water mite diet isolate 13893-BHL040517-GBD15070_3014-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACCTCTTTAAGAATTTTGATTCGAGCAGAACTCGGTCACTCTGTTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTGATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGACACGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614882 Psectrocladius sp. water mite diet isolate 13942-BHL040517-GBD11845_23087-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCAGTCACGCTGGTTCCTTAATTGGAGATGATCAATTTTATAATGTATTTGTTACCGCTCACGCTTTTGTAATATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCGCTCTAGTTGAAAACGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614883 Psectrocladius sp. water mite diet isolate 13995-BHL040517-GBD5434_7525-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAAATCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614884 Psectrocladius sp. water mite diet isolate 14562-BHL040517-GBD23023_11427-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGCATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATTATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTACTAATTTTTTTATAGTAATACCTATTTTAATTGGAGGAATTTGAAATTGATTAGTCCCGTCAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614885 Psectrocladius sp. water mite diet isolate 14567-BHL040517-GBD26556_21225-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGCGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTCTAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTCATACCTATTTTAATTGGAGGATTTGGAAAATGATTAGTCCCGTTAATATTAGGAGTCACCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTAATATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614886 Psectrocladius sp. water mite diet isolate 14569-BHL040517-GBD10002_25071-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGATCAGGCATATTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCACTCCCTCGAATAAATAATAAAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGAACACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614887 Psectrocladius sp. water mite diet isolate 14605-BHL040517-GBD9481_13692-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCGCGCCGGTTCCTTAATTGGAGATGATCATATTTATAATGTAATTGTTACCGCTCCCGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGAGGTGAAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614888 Psectrocladius sp. water mite diet isolate 14632-BHL040517-GBD6308_5532-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTCATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTATTGTATTAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTATTTGATTACTTCCCCCGTCATTAACTCTACTATTATCTAGCACTCTAGTTAAAAAAGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614889 Psectrocladius sp. water mite diet isolate 14635-BHL040517-GBD24428_21971-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAACCTGATTAGTCCCGCTCATATTAGGAGTCCCCAACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTAACTAGCTCTCTAGGTGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614890 Psectrocladius sp. water mite diet isolate 14671-BHL040517-GBD21831_6840-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGACACGCTGGTTCCTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614891 Psectrocladius sp. water mite diet isolate 14681-BHL040517-GBD24410_9364-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTTGGCACTTCTTTTAGAATTTTAATTCGAGCAGAACTTGGTCACGCAGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATATTAATTGGAGGATTTGGAAATTGATTAGTACCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614892 Psectrocladius sp. water mite diet isolate 14724-BHL040517-GBD14134_16716-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTCGGTGCCTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCTGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614893 Psectrocladius sp. water mite diet isolate 14750-BHL040517-GBD22970_23824-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACCCCGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTTATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCTCGTCATTAACTTTACTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614894 Psectrocladius sp. water mite diet isolate 14751-BHL040517-GBD10575_7531-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGATCACGCCGGTTCCTTCATTGGAGATGATCAAATTTATAATGTAATTGTTACCGTTTACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTCCCGTTAATATTAGGAGCACCCGACATAGCATTCCCTCGAATAAATAATATAAGTTCTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614895 Psectrocladius sp. water mite diet isolate 14770-BHL040517-GBD5332_8211-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTGCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGGTCACGCATTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTAGTATCTAGCGCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614896 Psectrocladius sp. water mite diet isolate 14794-BHL040517-GBD10087_12408-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCTGGCATAGTAGGCACTTCTTTAAGTATTTTAATTCGAGCAGAACTTGGCCAACCTGGTTCCTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614897 Psectrocladius sp. water mite diet isolate 14797-BHL040517-GBD16509_2903-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTGCTTTAAGAATTTTAATTCGAGCAGAACTCGTTCACGCCGTTTCCTTAATTGGAGATGATCAAATTTATAATGGAATTGTTACCGCCCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCCTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTCGTTGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614898 Psectrocladius sp. water mite diet isolate 14798-BHL040517-GBD19684_21419-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGATCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTCCCGTTAATATTAGGAGCTCCCGACATAGCCTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCACTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614899 Psectrocladius sp. water mite diet isolate 14821-BHL040517-GBD26591_10490-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATGTTTATTCGAGCAGAACTCGGTCACACCGGTACCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAGATTGATTAGTCCCGTTAATATTAGGAGCACCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614900 Psectrocladius sp. water mite diet isolate 14843-BHL040517-GBD24005_14730-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCACCAGACATGGCATTCCCTCGAATAAATAATATAAGTTTTTGTTTACTTCCACCGTCATTAACTGTACTATTATCTAGCTCTCTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614901 Psectrocladius sp. water mite diet isolate 14849-BHL040517-GBD25430_5892-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATAGATTAGTCCCATTAATATTAGGAGACCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614902 Psectrocladius sp. water mite diet isolate 14857-BHL040517-GBD17983_3891-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTCTAAGAATTTTAATTCGAGCAGCACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGTTTTGGAAATTGATTAGTCACGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGCGCTGGACCAG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614903 Psectrocladius sp. water mite diet isolate 14860-BHL040517-GBD25794_5698-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGACCAGGCATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACCGTTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTGATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614904 Psectrocladius sp. water mite diet isolate 14877-BHL040517-GBD15815_6982-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTTTAATGTAATTGTTACCACTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTGCCCCCGTGATGAACTTGACGATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614905 Psectrocladius sp. water mite diet isolate 14881-BHL040517-GBD20589_20090-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGACACGCTGGATCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614906 Psectrocladius sp. water mite diet isolate 14884-BHL040517-GBD8688_6175-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCTTAGTAGGCACTTCTTTATGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCTCCGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614907 Psectrocladius sp. water mite diet isolate 14886-BHL040517-GBD26511_15346-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAACTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCTGACATAGCATTCCCTCGAAAAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACTTTACTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614908 Psectrocladius sp. water mite diet isolate 14889-BHL040517-GBD25601_16636-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCTTAGTAGGCTCTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAATTTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTATGAGCCCCCGGCATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCGCCCGTCATTAACTTTACTATTATCTAACTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614909 Psectrocladius sp. water mite diet isolate 14892-BHL040517-GBD24514_17610-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACACCGGTTTCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACATATTTTAATTGGAGGATTTGGAAATTGAATAGTCCCGTTAATATTAGGAGACCCCTACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614910 Psectrocladius sp. water mite diet isolate 14894-BHL040517-GBD18723_15513-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGATCAGGCATAGTATACACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACACCGTTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTTACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614911 Psectrocladius sp. water mite diet isolate 14896-BHL040517-GBD14674_3763-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGAGCAGGCATAGTAGGCACTTCTTTAAGATTTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCCCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAGTTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614912 Psectrocladius sp. water mite diet isolate 14903-BHL040517-GBD19831_5822-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCCCACGCTTTTGTAATAATTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGACCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTGCTTCCCCCGTCATTAACTTTACTATTATCTAGCTCGCGAGTTGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR288763, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614913 Psectrocladius sp. water mite diet isolate 14919-BHL040517-GBD22732_9476-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACTCCTGTTCCTTAATTGGAGATGATCAATTTTATACTGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCCTTAATATTAGGAGCCACCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614914 Psectrocladius sp. water mite diet isolate 14921-BHL040517-GBD5126_16244-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCCGGCATAGTAGGCGCTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTAGAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGTAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACGTCCCCCGTCATTAACGTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614915 Psectrocladius sp. water mite diet isolate 14925-BHL040517-GBD19206_12547-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTTAGAATCTTAATTCGAACAGAACTCGGTCACGCCGGATCCTTAATTGGAGATGATCAAATTTATAATGTTATAGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614916 Psectrocladius sp. water mite diet isolate 14930-BHL040517-GBD27094_16491-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTGGGCACTTCTTTAAGAATGTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTACTTGTTACCGCTCACGCTTTTGTAATAATTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTCCCGTTAATATTAGGAGCCCCTGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTTCTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTCGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614917 Psectrocladius sp. water mite diet isolate 14932-BHL040517-GBD8647_4110-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTCTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCCAATAAATAATATAATTTTTTGATTACTTCCCCCGGCATCAACTTTACTATGATCTAGCTCTCTCGTTGAAAATGCAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614918 Psectrocladius sp. water mite diet isolate 14937-BHL040517-GBD28181_12219-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCAGGCATAGAAGGCACTTCTTTAAGAATTTTAATTCGAGTAGAACTCGGTCACGCAGGTTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTCTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614919 Psectrocladius sp. water mite diet isolate 14938-BHL040517-GBD7413_10132-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATATTTATTTTTGGAGCCTGATTAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACAAAGCATTCCCTCTAATAAATAATAAAAGTTTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGCTCTCTACTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614920 Psectrocladius sp. water mite diet isolate 14943-BHL040517-GBD10339_27464-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTCTAATTCGAGCAGAATTCGGTCACCCCGGTACCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTTATAATTTTTTTACAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614921 Psectrocladius sp. water mite diet isolate 14955-BHL040517-GBD5985_11602-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATACTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTTCTTCCCCTGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614922 Psectrocladius sp. water mite diet isolate 14958-BHL040517-GBD27429_21159-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGCTTAATAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTATTTGATTACTTCCCCCGTCAGCAACTTTACAATTATCTAGCTCTCGAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614923 Psectrocladius sp. water mite diet isolate 14968-BHL040517-GBD6260_19230-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGAATAGTAGGCATTTCTTTAAGAATTTTAATTCGAGCTGAACTCGGTCACCCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614924 Psectrocladius sp. water mite diet isolate 14972-BHL040517-GBD25504_7846-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTACTACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGACATAGCATTCCCCCGAATAAATAACATAAGATTTTGAATACTTCCCCCGTCATTAACATTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614925 Psectrocladius sp. water mite diet isolate 14976-BHL040517-GBD5806_9015-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGAACTTATTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGAAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATGGGATGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614926 Psectrocladius sp. water mite diet isolate 14978-BHL040517-GBD29645_14022-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCCGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCACTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCCCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCGTTAACTTTACTATTATCTAGCTCTCTATTTGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614927 Psectrocladius sp. water mite diet isolate 14981-BHL040517-GBD23749_22307-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCTCCCGACATAGCATTCCCTCGAATAAATAATAGAAGTTTTTGATTACTTCCCCCGACATTAACTGTACTATTATCGAGCTCTATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614928 Psectrocladius sp. water mite diet isolate 14984-BHL040517-GBD19271_17515-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGTCTGCTCATGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGTTTCCTTAATTGGAGATGTTCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTTTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATGTAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614929 Psectrocladius sp. water mite diet isolate 14988-BHL040517-GBD20592_21764-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTTTTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCAGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTCGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGAATACTTCCCCCGTCATTAACTTTACTATTATCTAGCACTCTAGTTGAAAATGGAGCTGGAAAAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614930 Psectrocladius sp. water mite diet isolate 14989-BHL040517-GBD16003_3836-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAGTGTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGGAATTGTTACCGCGCTCGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGGCCCGTTAATATTAGGAGCCACCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614931 Psectrocladius sp. water mite diet isolate 14992-BHL040517-GBD17047_2517-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCAAGCCGTTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCGAACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGACCCGTTAATATTAGGAGCCCCTGACATAGCATTCCCTCGAATAAATAATATAATTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614932 Psectrocladius sp. water mite diet isolate 14998-BHL040517-GBD25193_14204-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATATTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCATTAATTGGAGATGATCAACTTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTCCCGTTAATATTAGGAGCCCCAGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614933 Psectrocladius sp. water mite diet isolate 15014-BHL040517-GBD7584_25390-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCACGCCGGGTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCATTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTTCTTCCCCCGTCATTAACTTTACTACTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614934 Psectrocladius sp. water mite diet isolate 15020-BHL040517-GBD10283_10657-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGATCAGGCATAGTAGGCCCTTCTTTAAGAATTTTATTTCGAGCAGAACTCGGTCACGCCGTTTATTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGATCACGATTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614935 Psectrocladius sp. water mite diet isolate 15021-BHL040517-GBD14686_23060-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGATTAAATAATATAAGTTATTGATTACGTCCCCCGTCATTAAATTTACAATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614936 Psectrocladius sp. water mite diet isolate 15023-BHL040517-GBD27255_21948-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATGGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACACCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTCCCGTTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTAGATTACTTCCCCCGTCATTAACGTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614937 Psectrocladius sp. water mite diet isolate 15029-BHL040517-GBD25952_7393-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTATAATAATTTTTTTTATAGTAATACCTATTTTAATTGAAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCAACATAGCATTCCCTCGAATAAATAATATAATTTTTATATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614938 Psectrocladius sp. water mite diet isolate 15032-BHL040517-GBD16943_4617-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACGCGTTCACGCCGTTGCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGGTAATATTAGGAGCCCACGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614939 Psectrocladius sp. water mite diet isolate 15035-BHL040517-GBD12808_4463-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATGTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAAAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCACTCGAATAAATAATATAAGTTTTTGATCATTTCCCCCGTCATTAACTTTACTATTATTTAGCTCTCTAGTTGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614940 Psectrocladius sp. water mite diet isolate 15038-BHL040517-GBD24498_20138-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGACACGCCGGTACCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTATAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTTGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTCTGACTACTTCCCCCCTCACTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614941 Psectrocladius sp. water mite diet isolate 15043-BHL040517-GBD10662_8803-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGTCACTGACATAGCATTCCCTCTAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAAGGGAGCTCGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614942 Psectrocladius sp. water mite diet isolate 15044-BHL040517-GBD11496_27008-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATATTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTTCTTAATTGGATATGATCAAATTTATAATGTAATTGTTACCACTCACGCTTTTGTAATAATTTTTTTTATATTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATAGTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614943 Psectrocladius sp. water mite diet isolate 15060-BHL040517-GBD11213_22888-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCCGATCAGGCATAGTAGGCACTTCTCTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTCCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATCTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGTGTCCCCGACATAGCATTCCCCCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614944 Psectrocladius sp. water mite diet isolate 15068-BHL040517-GBD14082_5425-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCGGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGGGCAGAACTCGGTCACGCCGGATCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCGTTAATATTAGGAGCCCCCGACATAGCTTTCCCTCGACTAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTCCTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614945 Psectrocladius sp. water mite diet isolate 15069-BHL040517-GBD19183_22374-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTAGGAGCCTGATCAGGCACAGTAGGCACTTCTTTAAGAATTTTGATTCGACCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCTTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAAATTTACTATCATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614946 Psectrocladius sp. water mite diet isolate 15077-BHL040517-GBD29659_14045-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTTATTGTTACCCCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTTGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCGTCGTTAACTTTACTATTATCTAGCTCTCTTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614947 Psectrocladius sp. water mite diet isolate 15078-BHL040517-GBD5151_9219-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCAACGACATAGCATTCCCTCGAATAAATAATATAAGTTCTTGATTACATCCCCCTTCATTAACTTTACTATGAACTAGCTCTCTAGTTGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614948 Psectrocladius sp. water mite diet isolate 15088-BHL040517-GBD24756_13385-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATAGGAGATGATCACATTTATACTGTAATTGTTACCGCTCACTCTTTTGTAATAATTTTTTTATAGTAATACATATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCTCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614949 Psectrocladius sp. water mite diet isolate 15090-BHL040517-GBD8734_9848-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTGCTTAATTGGTGATGATCAAATTTATAATATAATTGTAACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATCCCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGTTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614950 Psectrocladius sp. water mite diet isolate 15095-BHL040517-GBD27981_12395-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCATGATCAGGCATAGTAGGAACTTCTTTAAGAATTTTAATTCAAGCAGAACTAGGTCAAGCCGGTTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAACCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614951 Psectrocladius sp. water mite diet isolate 15097-BHL040517-GBD18189_26539-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGTCACGCAGGTACCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGCGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614952 Psectrocladius sp. water mite diet isolate 15100-BHL040517-GBD25789_5952-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATCTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAACTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTGGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAACATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACGTTACTATTATCTAACTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614953 Psectrocladius sp. water mite diet isolate 15106-BHL040517-GBD24741_12575-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCATGCATAGTAGGCACTTCTTTAAGAATTTTAATTCAAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTGTTAGATTACTTCCCCCGACATTAACTTTGCTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614954 Psectrocladius sp. water mite diet isolate 15107-BHL040517-GBD11977_8444-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCCGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGTCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTATGATTACTTCCCCCGTCATTAACTTTACTATTAGCTAACCCTCTAGCTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614955 Psectrocladius sp. water mite diet isolate 15109-BHL040517-GBD20354_11769-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAACCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAACTTTATAATGTTATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTCTTCCCGTTAATATTAGGAGCATCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614956 Psectrocladius sp. water mite diet isolate 15111-BHL040517-GBD23971_14948-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTATGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTACTTAATTGGAGATGATCAAATTTCTAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGAACCCGACATAGCATTCCCTCGAATAAATAACATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614957 Psectrocladius sp. water mite diet isolate 15116-BHL040517-GBD19395_4931-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACACCGGTTGCTTAATTGTAGATGATCAAATTTATAGTGTCATTGTTACCGATCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAAGAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614958 Psectrocladius sp. water mite diet isolate 15118-BHL040517-GBD24570_16812-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGTTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTATAGTAATCCCTATTTTAATCAGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCTCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCAGTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614959 Psectrocladius sp. water mite diet isolate 15119-BHL040517-GBD20515_6518-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCGTAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTAATTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCTCGACATAGCATCCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAACTCGCTAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614960 Psectrocladius sp. water mite diet isolate 15125-BHL040517-GBD20518_4918-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGCACTTCTTTAAGAATATTAATTCGAGCAGAATTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGACATAGCATTCCCACGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTAATATCTAGCTCATTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614961 Psectrocladius sp. water mite diet isolate 15128-BHL040517-GBD15677_6189-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACTCAGTTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTCAATATTAGGAGCCCCTGTCATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCCCCGTCATTAACTTTACTATTATCTAGCTCCCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614962 Psectrocladius sp. water mite diet isolate 15132-BHL040517-GBD11983_9583-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATAAAATTTATAATGTAATTGTTACCGCCCACGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATGGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614963 Psectrocladius sp. water mite diet isolate 15137-BHL040517-GBD27721_16953-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTTAGAATTTTAATTCGAGCAGAACTCGGTTACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTATGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614964 Psectrocladius sp. water mite diet isolate 15139-BHL040517-GBD12666_22992-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGATCTCGGTCACTCCGGTTCCTTAATTGGAGTTGATCAAAGTTATAATGTAATCGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614965 Psectrocladius sp. water mite diet isolate 15141-BHL040517-GBD27563_15714-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCATTAATTGGAGATGATCAAATTTCTAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGAATTGGAAATTGATTAGTCCCGTTAATATTAGTAGCTCCAGACATAGCATTCCCTCAAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614966 Psectrocladius sp. water mite diet isolate 15145-BHL040517-GBD25985_22072-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTCAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAACTGGAGATGATCAAATTTATAATGTAATTGTTACCGATCACACTTTTGTAATAATTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCGTGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614967 Psectrocladius sp. water mite diet isolate 15149-BHL040517-GBD20908_7025-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGACCTCTATCACGCCGGTTCCTTAATTGGAGATGATCAAATTTCTAATGTAATTGTTACCGATCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGAAAATTGATTAGTCCCGTTAATATTAGGAGTCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614968 Psectrocladius sp. water mite diet isolate 15152-BHL040517-GBD25515_11781-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTAACGCCGTATCCTTAATTGGAGATGATCAAATTTATAATGCAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAAAAAATAATATAAGTGTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614969 Psectrocladius sp. water mite diet isolate 15162-BHL040517-GBD13301_1934-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCAATAAATATAAAAATATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614970 Psectrocladius sp. water mite diet isolate 15164-BHL040517-GBD21111_10187-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGTCATAGTAGTCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTATTTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTAATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCACGTTAATAGTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCGAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614971 Psectrocladius sp. water mite diet isolate 15166-BHL040517-GBD12431_10214-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCGCCCCAGTTCTTTAATTGGAGATGATCAAATTTATAATGTTATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATATTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCACCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614972 Psectrocladius sp. water mite diet isolate 15169-BHL040517-GBD26490_18265-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCCGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTCCTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCCAATAAATAATATAAGTTATGGATTACTTCCCCCGTCATTAACTGTACTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614973 Psectrocladius sp. water mite diet isolate 15171-BHL040517-GBD5713_23351-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGGATAGTAGGAACTTCTTTAAGTATTTTAATTCGAGCAGAACTCGGTCACGCCGGTACCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTGCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATCATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614974 Psectrocladius sp. water mite diet isolate 15175-BHL040517-GBD25461_12559-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGCTCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAAAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTTATTGTTACCGCACACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGTGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614975 Psectrocladius sp. water mite diet isolate 15176-BHL040517-GBD27412_17282-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCATTAATTGGAGATGATCAAATTTATAATGTAATAGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCATTAACTTTACTATTATCTAGCTCTCTTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614976 Psectrocladius sp. water mite diet isolate 15178-BHL040517-GBD2344_12218-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGGAGGCACTTCTTTAAGAATTTTAATTCGAGTAGAACGCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTCATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATGTGGAAATTGATTAGTCCCGTTAATAGTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACCATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614977 Psectrocladius sp. water mite diet isolate 15179-BHL040517-GBD14244_2545-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCTGTTCCTTAATTGAAGATGATCAAATTTATAATGGAATTGTTACCGCTCACGCCTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGACCCGTTAATATTAGGATCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAACTCTCTAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614978 Psectrocladius sp. water mite diet isolate 15185-BHL040517-GBD7167_10187-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGACGGTTCTTTAATTGGAGAGGATCAAATTTATAATGTAATTGTTACCCCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTACCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614979 Psectrocladius sp. water mite diet isolate 15186-BHL040517-GBD11804_24536-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTAGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACACCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGGTTTTGATTACTTCCCCCGTCAATAACTTTACCATTATCTAGCTCTCTAGGTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614980 Psectrocladius sp. water mite diet isolate 15188-BHL040517-GBD11461_24046-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTACTTCGAGTAGAACTCGATCACGCCGGTTCCTTAATTGGAGATGATCAACTTTATAATGTAATTGTTACCGCTCACGCTTTTGTACTAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGTAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614981 Psectrocladius sp. water mite diet isolate 15195-BHL040517-GBD6761_12338-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTTTATTTTATTTTTGGAGTCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACACCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCCATTTTAATTGGAGGATTTGGAAACTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614982 Psectrocladius sp. water mite diet isolate 15197-BHL040517-GBD20975_11224-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATGTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTTATTACATCCCCCGTCATTAAAATTACTATGATCTAGCTCTCTAGTTGAAAATGGCGCTCGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614983 Psectrocladius sp. water mite diet isolate 15204-BHL040517-GBD13997_25166-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCCTTAAGAATTTTAAATCGAGCAGAACTCGGTCACGCCGGTTCCTTAATGGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTGGGAAATTGATTAGTCCCGTTAGTATTAGGAGCCCCAGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTATCGTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614984 Psectrocladius sp. water mite diet isolate 15206-BHL040517-GBD12927_15440-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAATATGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGATATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACACAACATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCTCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614985 Psectrocladius sp. water mite diet isolate 15207-BHL040517-GBD3289_10129-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTTTAATAATTTTTTTATAGCAATTCCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCTCCTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614986 Psectrocladius sp. water mite diet isolate 15213-BHL040517-GBD5674_22065-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGAAACTTCTTTAAGAATTTTAATTCGATCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTATTACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614987 Psectrocladius sp. water mite diet isolate 15216-BHL040517-GBD26253_7135-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATCTTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACACCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTATTTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAACAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACGATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614988 Psectrocladius sp. water mite diet isolate 15222-BHL040517-GBD6494_13161-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGACTTTTAATTCGAGCAAAACTCGGTCACGCCAGTTCCTTAATTGGAGATGCTCAAATTTATAATGTAATTGTTACCGCTCATCCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTATCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614989 Psectrocladius sp. water mite diet isolate 15228-BHL040517-GBD3737_9532-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTCTATTTTTGGAGCCTGATCAGGTATAGTAGGCACTTCTTTAAGAATTTTTATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTCTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCAGTAACTTTACTATTATCTAGCTCGCTAGTTGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614990 Psectrocladius sp. water mite diet isolate 15229-BHL040517-GBD14539_4751-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTTTTTAAGAATTTTAATTCGAGCAGAACTCGTTCACGCCTTTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCACGTTAATATTAGGAGCCACCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTCACTCTCTAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614991 Psectrocladius sp. water mite diet isolate 15230-BHL040517-GBD29281_17924-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCAGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGATATTGATTAGTCTCGTTAATATTAGGAGCCGCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTTCTTCCCCCGGCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614992 Psectrocladius sp. water mite diet isolate 15231-BHL040517-GBD6943_23419-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGACATAGCATTCCCCCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTGTACTATTATCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614993 Psectrocladius sp. water mite diet isolate 15233-BHL040517-GBD2588_14045-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTCTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAAGACTCGGTCACGCCGTTTCCTTAATTGGAGATGATCACATTTATAATGTAATTGGTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614994 Psectrocladius sp. water mite diet isolate 15235-BHL040517-GBD26643_11037-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCAAGCAGAACTCGGTCACGCCGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTTGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTGATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614995 Psectrocladius sp. water mite diet isolate 15237-BHL040517-GBD11134_5474-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGATATTTTATGTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGGATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGCTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAACACAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATCGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614996 Psectrocladius sp. water mite diet isolate 15244-BHL040517-GBD18740_27951-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAACTTTATAATGTAATTGTTACCGCTCACGCTTTTGCAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCATTAATATTAGGAGCCCCCGACATAGCATTCCCACGAATAAATAATAGAAGATTTTGATTACTTCCCCCGCCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW614997 Psectrocladius sp. water mite diet isolate 15245-BHL040517-GBD17945_18278-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTTGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGTATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTATTTGGAGATGATCAAATTTATAATGTAATTATTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTAGTTTATTTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGGTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614998 Psectrocladius sp. water mite diet isolate 15246-BHL040517-GBD21951_17574-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACCCCGGTTCCTTAATTGGAGATGATCAAATATATAATGTAATTGTTACCGCACACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCATCATTAACTTTACTATTATCTAGCTATCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW614999 Psectrocladius sp. water mite diet isolate 15249-BHL040517-GBD15271_17969-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGCATAGTAGGCACTTCTTTAAGAGTTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATCATCTAGCCCTCTAGCTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615000 Psectrocladius sp. water mite diet isolate 15250-BHL040517-GBD13862_7495-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCGTTAATATTAGGTGCCCCCGATTTAGCATTCCCTCGAATAAATAATATAAGGTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGATCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615001 Psectrocladius sp. water mite diet isolate 15254-BHL040517-GBD28882_15179-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTCTAAGAATTTTACTTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTAGTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACTCTGGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615002 Psectrocladius sp. water mite diet isolate 15261-BHL040517-GBD5743_9152-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCATTAAGAATGTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAATCTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCACTAACTTTACTACTATCTAGCTCTCTCGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615003 Psectrocladius sp. water mite diet isolate 15263-BHL040517-GBD27105_21426-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTCATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACCCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGTTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCTTTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615004 Psectrocladius sp. water mite diet isolate 15265-BHL040517-GBD14023_4162-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCGGTTTCCTTAATTGTAGATGATCAAATTTATAATGTAATTGTTACCTCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTCCTTCCCCCGTCATTAACTTTACTATTATCCAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615005 Psectrocladius sp. water mite diet isolate 15267-BHL040517-GBD27495_18508-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTCTTGTAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGACCTCGATCACGCCGGTTTCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCTCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615006 Psectrocladius sp. water mite diet isolate 15268-BHL040517-GBD14199_26214-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGACACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCTGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTGATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCTCTCGCCATTAACTATACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW615007 Psectrocladius sp. water mite diet isolate 15269-BHL040517-GBD5218_20441-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAATAGGCACTTCTTTAAGAATTTTAATTCGAGTAGAACTCGGTCAAGCCGGATCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTCATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615008 Psectrocladius sp. water mite diet isolate 15273-BHL040517-GBD6834_9683-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTGTATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGCACTCGGCCACGCCGGTTACTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAAAAATATAAGTTTATGATTACTTCCGCCGTCATTAACTTTACTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615009 Psectrocladius sp. water mite diet isolate 15275-BHL040517-GBD25993_8086-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTACATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAAGTCGAGCAAAACTCGGTCACGCCGGTACCTTAACTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTTACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGAATTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615010 Psectrocladius sp. water mite diet isolate 15277-BHL040517-GBD19397_11577-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGATCCTGATCAGGCATAGTAGGCACCTCTTTAAGAATTTTAATTCGAGCAGCACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCTCTGTCATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615011 Psectrocladius sp. water mite diet isolate 15281-BHL040517-GBD7467_11186-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTCATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAACAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGACCACGACATAGCATTCACTCGAATAAATAATATAAGTTTTTTATTACTTCCCCCGTCATTAACTTTACGATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615012 Psectrocladius sp. water mite diet isolate 15288-BHL040517-GBD23079_8151-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGTCTGTTCAGACATAGTAGTCACTTCTTTAAGATTTTTATTTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATGGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615013 Psectrocladius sp. water mite diet isolate 15290-BHL040517-GBD17507_28886-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCATGATCAGGCATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCACGCCGGATCCTTCATTGGAGCTGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCTGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615014 Psectrocladius sp. water mite diet isolate 15294-BHL040517-GBD8571_24552-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATTAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCAGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGATGATTTGGAAATTGATTAGTCCAGTTAATATTAGGAGCCCCCGACATAGCATTCCCCCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615015 Psectrocladius sp. water mite diet isolate 15296-BHL040517-GBD4720_13560-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCTCTTCTTTAAGAATTTTAATTCGAGCAGACCTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTATTTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCTGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTGGATTACTGCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615016 Psectrocladius sp. water mite diet isolate 15297-BHL040517-GBD26848_7768-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTACCGCTTTTGTAATCATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCTCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATGTAAGGTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW615017 Rheotanytarsus sp. water mite diet isolate 5789-BHL032417-GBD7944_7767-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGTGCATGATCAGGAATAATTGGAACTTCTTTAAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACT-TTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR271819, identified in GenBank as Rheotanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615018 Rheotanytarsus sp. water mite diet isolate 5806-BHL032417-GBD15194_20677-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTATTTCTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGACGTCCTGGAACTTTTATTGGAGATGACCAAATTTATAATATAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGACTTTTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCTCGAATAAATAACATAAGTTTCTGATTACTTCCTCCCTCTCTTTCTCTTCTTCTTTCAAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR271819, identified in GenBank as Rheotanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615019 Rheotanytarsus sp. water mite diet isolate 5824-BHL032417-GBD6843_12624-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGACTTTTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCTCGAATAAATAACATAAGTTTCTGATTACGTCCTCCCTCTCTTTCTCTTCTCCTTTCAAGTTCAATCGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR655191, identified in GenBank as Rheotanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615020 Rheotanytarsus sp. water mite diet isolate 5981-BHL032417-GBD18045_11073-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGACTTTTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCTCGAATAAATAACATAAGTTTCTGATTACTTCCTCCCTCTCTTTCTCTTCTTCTTTCAAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR271819, identified in GenBank as Rheotanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615021 Scaptomyza sp. water mite diet isolate 14934-BHL040517-GBD28268_10813-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGATCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTATAATTGGTGAATTCGGGAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTACTTCCTCCTTCACTAACACTACTATTAGCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID EU493679, identified in GenBank as Scaptomyza frustulifera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615022 Sididae sp. water mite diet isolate 2096-BHL072216-GBD7841_7479-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTCTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615023 Sididae sp. water mite diet isolate 2099-BHL072216-GBD18266_9474-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACCTATTCGAGCAGAATTAGGTCGACCTGGAGCTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.0% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615024 Sididae sp. water mite diet isolate 2109-BHL072216-GBD20472_9906-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACGCCCAGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.7% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615025 Sididae sp. water mite diet isolate 2134-BHL072216-GBD7533_14066-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGCATTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTGTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.7% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615026 Sididae sp. water mite diet isolate 2225-BHL072216-GBD22125_3679-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATATTATTTTTGGAGCTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGACAGTGCGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGAGGCTTTGGTAATTGGCTGGTGTCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTTCTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.3% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW615027 Sididae sp. water mite diet isolate 2242-BHL072216-GBD22677_22510-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGGGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTCTCCTCGTTTAAACAATTTAAGGTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.4% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615028 Sididae sp. water mite diet isolate 2318-BHL072216-GBD17856_26018-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTTTATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACATCTTTAAGTATACTTATTCGTGCAGAATTAGGTCATCCAGGCACTTTTATTGGAGACGACCAAATTTACAATGTAATTGTTACAGCCCATGCTTTTATCATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGGTATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.7% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615029 Sididae sp. water mite diet isolate 2393-BHL072216-GBD15075_9866-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACATCTTTAAGAATACTTATCCGAGCAGAATTAGGTCATCCAGGTACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCTCTTGCTTTTATTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615030 Sididae sp. water mite diet isolate 2427-BHL072216-GBD16815_7409-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAGCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTCTTTATGGTTATACCTATTCTTATTGGTGGGTTTGGAAATTGGTTGGTTCCTTTAATGTTAGGGGCTCCTGATATGGCCTTCCCTCGTTTAAATAATTTAAGATTTTGATTACTTCCTCCTTCTTTAACTTTACTTTTAGTTGGTAGGGCTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.8% identical to accession ID MG449947, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615031 Sididae sp. water mite diet isolate 2498-BHL072216-GBD18873_13304-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTATACTTTATTTTCGGAGCTTGATCTGGAATAGTCGGAACTTCCTTAAGTATATTAATTCGTGCAGAATTAGGACACCCGGGAACTTTAATCGGAGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTACTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.3% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615032 Simocephalus serrulatus water mite diet isolate 2126-BHL072216-GBD22421_10385-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGGGTCTGATCTGGAATAGTAGGAACTGCCCTAAGTATACTTATTCGTGCAGAACTTGGACAATCAGGAGGCTTAATTGGTGACGATCAAATTTACAATGTAATTGTAACTGCTCATGCTTTTGTTATGATTTTTTTTATAGTTATGCCAATTATGATTGGGGGGTTTGGAAATTGACTTGTCCCCTTAATGTTGGGGGCCCCAGATATGGCATTCCCACGTTTAAACAACTTAAGTTTTTGACTTTTACCCCCTGCACTAACTCTTCTTTTGGTTGGGGGTGCTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.1% identical to accession ID MF747258, identified in GenBank as Simocephalus serrulatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615033 Simocephalus serrulatus water mite diet isolate 2691-BHL072216-GBD18555_13113-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGACTTTGTACTTTATTTTTGGGGTCTGATCTGGAATAGTAGGAACTGCCCTAAGTATACTTATTCGTGCAGAACTTGGACAATCAGGAAGCTTAATTGGTGACGATCAAATTTACAATGTAATTGTAACTGCTCATGCTTTTGTTATGATTTTTTTTATAGTTATGCCAATTATGATTGGGGGATTTGGAAATTGACTTGTCCCCTTAATGTTGGGTGCCCCAGATATGGCATTCCCACGTTTAAACAACTTAAGTTTTTGACTTTTACCCCCTGCACTAACTCGTCTTTTGGTTGGGGGTGCTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID MF747258, identified in GenBank as Simocephalus serrulatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615034 Stylaria lacustris water mite diet isolate 11410-BHL101516-GBD4059_22892-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTAGGAGTATGAGCAGGAATAATTGGAACAGGTCCAAGAATACTAATTCGAATTGAATTATCTCAACCAGGAGCATTTCTAGGTAGAGATCAATTTTATAACACTTTAGTAACAGCTCATGCATTTTTAATAATTTTTTTCTTAGTAATGCCTGTATTAATTGGTGGATTTGGAAATTGATTACTTCCATTAATACTAGGGGCACCAGACATAGCTTTTCCACGACTAAATAACATGAGATTTTGACTTCTACCTCCATCACTAATTCTATTAATTTCATCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID AF534860, identified in GenBank as Stylaria lacustris. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW615035 Stylaria lacustris water mite diet isolate 11969-BHL101516-GBD4714_8537-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTAGGAGTATGAGCAGGAATAATTGGAACAGGTACAAGAATACTAATTCGAATTGAATTATCTCAACCAGGAGCATTTCTAGGTAGAGATCAATTATATAACACTTTAGTAACAGCACATGCATTTTTAATAATTTTCTTCTTAGTAATGCCTGTATTTATTGGTGGATTCGGAAATTGATTACTTCCATTAATACTAGGGGCACCAGACATAGCTTTTCCACGACTAAATAACATGAGATTTTGACTTCTACCTCCATCACTAATTCTATTAATTTCATCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.1% identical to accession ID AF534860, identified in GenBank as Stylaria lacustris. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>MW615036 Tanypodinae sp. water mite diet isolate 2265-BHL072216-GBD22630_6027-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGAGTTTGGTCCGGTATAGTTGGAACAGCTCTAAGTATACTTATTCGAGCTGAATTCGGGCAGTGTGGCTGTCTTATTGGTGATGATCAAATCTATAATGTAATTGTAACGGCACATGCTTTTGTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGTGGATTTGGTAATTGACTAGTACCCCTTATACTAGGAGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTACTACCCCCTTCTTTAACCTTACTATTATCTAGCTCTATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.4% identical to accession ID KR775767, identified in GenBank as Tanypodinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW615037 Tanytarsus mendax water mite diet isolate 2079-BHL072216-GBD12533_3864-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACATCTTTAAGAATACTTATCCGAGCAGAATTAGGTCATCCAGGTACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATGCCTGTCTTAATTGGAGGATTTGGAAATTGATTATTACCATTAATACTTGGAGCTCCAGATATAGCCTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCATCTTTAACTCTTCTTCTTTCTAGTTCCATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR742201, identified in GenBank as Tanytarsus mendax. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615038 Tanytarsus mendax water mite diet isolate 2288-BHL072216-GBD13466_8284-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATGCCTATCTTAATTGGAGGATTTGGAAATTGATTATTACCATTAATACTTGGAGCTCCAGATATAGCCTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCATCTTTAACTCTTCTTCTTTCTAGTTCCATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR742201, identified in GenBank as Tanytarsus mendax. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615039 Tanytarsus sp. water mite diet isolate 2138-BHL072216-GBD23928_10539-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGCATTAGGACATCCTGGAACTTTTATTGGCGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGGGGCTTTGGAAATTGATTATTGCCTCTTATACTCGGGGCTCCCGACATAGCCTTTCCTCGAATAAATAACATGAGATTCTGATTACTTCCCCCATCTATTTCTTTACTTCTCTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KP043761, identified in GenBank as Tanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615040 Tanytarsus sp. water mite diet isolate 2165-BHL072216-GBD29234_15083-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACGCCCAGGTACTTCTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGAATATTGCCTCTTATACTCGGGACTCCCGACATAGCCTTTCCTCGAATAAATAACATGAGATTCTGATTGCTTCCCCCATCTATTTCTTTACTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR289638, identified in GenBank as Tanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615041 Tanytarsus sp. water mite diet isolate 2195-BHL072216-GBD25028_4977-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACTTATTTTAATTGGAGGCTTTGGAAATTGATTATTGCCTCTTATACTCGGGTCTCCCGACATAGCCTTTCCTCGAATAAATAACATGAGATTCTGATTGCTTCCCCCATCTATTTCTTTACTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KR289638, identified in GenBank as Tanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615042 Tanytarsus sp. water mite diet isolate 2201-BHL072216-GBD7309_6753-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTATTGCCTCTTATACTCGGGGCTCCCGACATAGCCTTTCCTCGAATAAATAACATGAGATTCTGATTGCTTCCCCCATCTATTTCTTTACTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR289638, identified in GenBank as Tanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615043 Tanytarsus sp. water mite diet isolate 2232-BHL072216-GBD25330_20019-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTTTATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACATCTTTAAGTATACTTATTCGTGCAGAATTAGGTCATCCAGGCACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCCCATGCTTTTATCATAATTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR762788, identified in GenBank as Tanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615044 Tanytarsus sp. water mite diet isolate 2238-BHL072216-GBD17320_9295-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTATTGCCTCTTATACTCGGGGCTCCCGACATAGCCTTTCCTCGAATAAATAACATGAGATTCTGATTGCTTCCCCCATCTATTTCTTTACTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR289638, identified in GenBank as Tanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615045 Tanytarsus sp. water mite diet isolate 2294-BHL072216-GBD7487_19140-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGCATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTATTATAATTTTTTTATAGTTATGCCTGTCTTAATTGGAGGATTTGGAAATTGATTATTACCATTAATACTTGGAGCTCCAGATATAGCCTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCATCTTTAACTCTTCTTCTTTCTAGTTCCATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR742201, identified in GenBank as Tanytarsus mendax. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615046 Tanytarsus sp. water mite diet isolate 2313-BHL072216-GBD23717_24057-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACCTTATACTTTATTTTCGGAGCTTGATCTGGAATAGTCGGAACTTCTTTAAGTATATTAATCCGTGCAGAATTAGGACACCCGGGAACTTTAATCGGAGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCATTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAATAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KR293770, identified in GenBank as Tanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW615047 Tanytarsus sp. water mite diet isolate 2321-BHL072216-GBD20698_21946-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTACGCCTATCTTAATTGGAGGATTTGGAAATTGATTATTACCATTAATACTTGGAGCTCCAGATATAGCCTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCATCTTTAACTCTTCTTCTTTCTAGTTCCATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR742201, identified in GenBank as Tanytarsus mendax. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615048 Tanytarsus sp. water mite diet isolate 2350-BHL072216-GBD6711_14797-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACATCTTTAAGTATACTTATTCGTGCAGAATTAGGTCATCCAGGCACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCCCATGCTTTTATCATAATTTTTTTATAGTAATACCTATTTTAATTGGGGGCTTTGGAAATTGATTATTGCCTCTTATACTCGGGGCTCCCGACATAGCCTTTCCTCGAATAAATAACATGAGATTCTGATTACTTCCCCCATCTATTTCTTTACTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR764698, identified in GenBank as Tanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615049 Tanytarsus sp. water mite diet isolate 2358-BHL072216-GBD18895_13705-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGAAATTGACTTTTACCATTAATGCTTGGAGCACCAGATATAGCTTTCCCCCGAATGAATAATATAAGTTTTTGACTTCTTCCCCCATCTCTAACCCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR177414, identified in GenBank as Tanytarsus wirthi. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615050 Tanytarsus sp. water mite diet isolate 2391-BHL072216-GBD25110_14139-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGTACCTCCCTTAGTATCCTTATTCGTACAGAATTAGGTCACCCAGGAGCTTTAATTGGAGACGATCAAATCTATAATGTAATTGTAACGGCACATGCTTTTGTTATAAATTTTTTTATAGTAATACCTATTTTAATTGGGGGCTTTGGAAATTGATTATTGCCTCTTATACTCGGGGCTCCCGACATAGCCTTTCCTCAAATAAATAACATGAGATTCTGATTACTTCCCCCATCTATTTCTTTACTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KP043761, identified in GenBank as Tanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615051 Tanytarsus sp. water mite diet isolate 2399-BHL072216-GBD25521_14349-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATGCCTATCTTAATTGGAGGATTTGGAAATTGATTATTACCATTAATACTTGGAGCTCCAGATATAGCCTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCATCTTTAACTCTTCTTCTTTCTAGTTCCATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR742201, identified in GenBank as Tanytarsus mendax. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615052 Tanytarsus sp. water mite diet isolate 2436-BHL072216-GBD9281_14870-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGCTTTGGAAATTGATTATTGCCTCTTATACTCGGGGCTCCCGACATAGCCTTTCCTCGAATAAATAACATGAGATTCTGATTACTTCCCCCATCTATTTCTTTACTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR281137, identified in GenBank as Tanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615053 Tanytarsus sp. water mite diet isolate 2496-BHL072216-GBD24081_25020-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCTGTCTTAATTGGAGGATTTGGAAATTGATTATTACCATTAATACTTGGAGCTCCAGATATAGCCTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCATCTTTAACTCTTCTTCTTTCTAGTTCCATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR742201, identified in GenBank as Tanytarsus mendax. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615054 Tanytarsus sp. water mite diet isolate 2524-BHL072216-GBD9928_24952-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTATACTTTATTTTCGGAGCTTGATCTGGAATAGTCGGAACTTCTTTAAGTATATTAATCCGTGCAGAATTAGGACACCCGGGAACTTTAATCGGAGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATGCCTATCTTAATTGGAGGATTTGGAAATTGATTATTACCATTAATACTTGGAGCTCCAGATATAGCCTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCATCTTTAACTCTTCTTCTTTCTAGTTCCATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR742201, identified in GenBank as Tanytarsus mendax. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615055 Tanytarsus sp. water mite diet isolate 2531-BHL072216-GBD21264_15647-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACCTTATACTTTATTTTCGGAGCTTGATCTGGAATAGTCGGAACTTCCTTAAGTATATTAATTCGTGCAGAATTAGGACACCCGGGAACTTTAATCGGAGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTATTGCCTCTTATATTCGGAGCTCCCGACATAGCCTTTCCTCGAATAAATAACATAAGATTCTGATTGCTTCCCCCATCTATAACTTTACTTCTATCAAGAACAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR289369, identified in GenBank as Tanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615056 Tanytarsus sp. water mite diet isolate 2597-BHL072216-GBD10860_12932-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGAATACTTATCCGAGCAGAATTAGGTCATCCAGGTACTTTTATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATGCCTGTCTTAATTGGAGGATTTGGAAATTGATTATTACCATTAATATTTGGAGCTCCAGATATAGCCTTCCCCCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTAC-CTTATTACTTTCAAATTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR742201, identified in GenBank as Tanytarsus mendax. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW615057 Tanytarsus sp. water mite diet isolate 2601-BHL072216-GBD4028_21679-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACATCTTTAAGAATACTTATCCGAGCAGAATTAGGTCATCCAGGTACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGCTTTGGAAATTGATTATTACCTCTTATATTCGGGGCTCCCGACATAGCCTTTCCTCGAATAAATAACATGAGATTCTGATTACGTCCCCCATCTATTTCTTTACTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KM641507, identified in GenBank as Tanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615058 Tanytarsus sp. water mite diet isolate 2602-BHL072216-GBD6249_12694-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTATACTTTATTTTCGGAGCTTGATCTGGAATAGTCGGAACTTCTTTAAGTATATTAATCCGTGCAGAATTAGGACACCCGGGAACTTTAATTGGAGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGCTTTGGAAATTGATTATTGCCTCTAATACTCGGTGCTCCCGACATAGCCTTTCCTCGAATAAATAACATGAGATTCTGATTACTTCCCCCATCTATTACATTACTTCTATCTAGATCAGTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ165913, identified in GenBank as Tanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615059 Tanytarsus sp. water mite diet isolate 2642-BHL072216-GBD11976_12571-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTATACTTTATTTTCGGAGCTTGATCTGGAATAGTCGGAACTTCTTTAAGTATATTAATCCGTGCAGAATTAGGACACCCGGGAACTTTAATCGGAGATGATCAAATTTATAATGTTATTGGTACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGCTTTGGAAATTGATTATTGCCTCTTATACTCGGGGCTCCCGACATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KP043761, identified in GenBank as Tanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615060 Tanytarsus sp. water mite diet isolate 2452-BHL072216-GBD11775_16427-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCTTGATCAGGTCTAGTAGGAACTTCTTTAAGTATATTAATCCGTGCAGAATTAGGACACCCGGGAACTTTAATCGGAGATGCTCAAATTTATAATGTTATTGTTCCTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGCTGTGGAAATTGATTATTGCCTCTTATACTCGGGGCTCCCGACATAGCCTTTCCTCGAATAAATAACATGAGATTCTGATTGCTTCCCCCATCTATTTCTTTACTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR966081, identified in GenBank as Tanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615061 Tanytarsus sp. water mite diet isolate 2471-BHL072216-GBD20217_10102-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATATTAATCCGTGCAGAGTTAGGACACCCGGGAACTTTAATCGGAGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTATTGCCTCTTATACTCGGGGCTCCCGACATAGCCTTTCCTCGAATAAATAACATGAGATTCTGATTGCTTCCCCCATCTATTTCTTTACTTCTTTCTAGATCAATTGCTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR966081, identified in GenBank as Tanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615062 Toxonevra sp. water mite diet isolate 14680-BHL040517-GBD3945_19667-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATTTTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGTGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTACTACCCCCTTCACTTACCCTACTATTAGCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID KR262683, identified in GenBank as Toxonevra saltuum. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615063 Toxonevra sp. water mite diet isolate 14848-BHL040517-GBD14344_12025-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATTTTTGGAGCATGAGCAGGAATAGTCGGAACTTCTTTAACAATTTTTATTCGTGCTGAATTAGGACATCCTGGAGCATTAATTGGCGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGTGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCACTTACACTATTATTAGCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID KR262681, identified in GenBank as Toxonevra carterosoma. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615064 Toxonevra sp. water mite diet isolate 14883-BHL040517-GBD6492_14994-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATTTTTGGAGCATGATCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAACATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTAGGGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCGTTCCACGAATAAATAATATAAGTTTTTGACTACTTCCTCCTTCACTTACACTATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID KR262683, identified in GenBank as Toxonevra saltuum. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615065 Toxonevra sp. water mite diet isolate 14983-BHL040517-GBD25762_16906-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTTTATTTTATTTTTGGAGCCTGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAACTAGGACACCCTGGTGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGTGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCGTCACTTACACTATTATTATCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID KR262681, identified in GenBank as Toxonevra carterosoma. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615066 Toxonevra sp. water mite diet isolate 14994-BHL040517-GBD23273_9768-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTTTATTTTATTTTTGGAACATGAGCAGGAATAGTCGGAACTTCTTTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAACATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCACATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTATTGACTTCTTCCCCCTTCACTTACACTATTATTAGCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID KR262683, identified in GenBank as Toxonevra saltuum. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>MW615067 Toxonevra sp. water mite diet isolate 15157-BHL040517-GBD7524_18774-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACACTTTATTTTATTTTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTAAATTAGGACACCCTGGAGCATTAATTGGTGACGACCAAATTTATAATGTAATTGCTACCGCCCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACACTATTATTAGTAAGAAGTATAGTAGAAAATGGAGTTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID KR262683, identified in GenBank as Toxonevra saltuum. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615068 Toxonevra sp. water mite diet isolate 15177-BHL040517-GBD4806_11165-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGAAATTGTTACAGCTCATGCATTTATAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTGTGAATACTTCCCCCATCACTTACACTACTATTAGCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.0% identical to accession ID KR262683, identified in GenBank as Toxonevra saltuum. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615069 Uramya sp. water mite diet isolate 14223-BHL040517-GBD26379_17370-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATAAAGATATTGGTACATTATCTTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTCGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTGCTTTAACATGATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KP899675, identified in GenBank as Uramya sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615070 Xenochironomus sp. water mite diet isolate 2374-BHL072216-GBD12855_18662-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCCTGATCTGGAATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTTTTCATAGTTATGCCTATTTTAATTGGTGGCTTTGGGAATTGATTAGTTCCCCTAATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCGAAGATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KR294880, identified in GenBank as Xenochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>MW615071 Zaprionus sp. water mite diet isolate 15092-BHL040517-GBD20109_15863-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AATCATAAAGATATTGGAACACTTTATTTTATTTTTGGAGCACGAGCAGGAATAGTCGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTGTTATAATTTTTTTTATAGTTATACCAATTATAATTGATGGATTCGGAAATTGATTAGTACTTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACACTATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID FJ948772, identified in GenBank as Zaprionus taronus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10000 Oligochaeta sp. water mite diet isolate 10000-BHL040517-GBD8779_14241-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCTTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.1% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10005 Chironomus riparius water mite diet isolate 10005-BHL040517-GBD6884_23334-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCCTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTACTACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCCCTCTTACTCTGCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10006 Dicrotendipes sp. water mite diet isolate 10006-BHL040517-GBD3868_17904-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGTAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGATTATACCTATTCTAATTGGAGGATCCGGAAATTGATTAGTTCCTTTAATATTAGGAGCCACCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCCCTAACCCTTCTTCCTTCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10014 Paratanytarsus sp. water mite diet isolate 10014-BHL040517-GBD8074_15010-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTAATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10017 Culex pipiens water mite diet isolate 10017-BHL040517-GBD14961_17587-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAATTAACCAGGTGTATTTATTGGAAATGATCAAATTTATAGTGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGTCTTTCCTCGAATAAATAATATAAGCTTTTGAATACTACCTCCTTCATTGACACTACTACTTCCAAGTAGTTTAGTAGGAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL10018 Oligochaeta sp. water mite diet isolate 10018-BHL040517-GBD10207_3775-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.5% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10020 Chironomidae sp. water mite diet isolate 10020-BHL040517-GBD17432_20377-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGTTTTTCCTCGAATAATTAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10022 Diptera sp. water mite diet isolate 10022-BHL040517-GBD20457_14475-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGCTTTTGAATACTACCTCCTCCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10023 Chironominae sp. water mite diet isolate 10023-BHL040517-GBD19137_5950-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTTGGGGCTTGAGTTGGAATAGTTGGAACTTCTTTAAGTTTATTATTCCGAGTAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR765094, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10024 Chironomus riparius water mite diet isolate 10024-BHL040517-GBD14067_8742-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAAGAATGCTTATTTGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGC	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10030 Chironomus riparius water mite diet isolate 10030-BHL040517-GBD16227_8014-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCCGAATTTGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCTCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCCTACTCTTCTTCTGTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10037 Chironomus sp. water mite diet isolate 10037-BHL040517-GBD22947_6524-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGCATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCACTGGAGATGACGAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTGTAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAGGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10040 Cryptochironomus sp. water mite diet isolate 10040-BHL040517-GBD25734_21080-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATACTTCATTTTCGGTGCCTAATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTGCCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10042 Oligochaeta sp. water mite diet isolate 10042-BHL040517-GBD20875_9564-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAGTTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10045 Oligochaeta sp. water mite diet isolate 10045-BHL040517-GBD6970_18264-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTTCTTAGTAATACCAGTTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACT-TTACCCCCCTCTCTTACTCTGCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL1005 Chironomidae sp. water mite diet isolate 1005-BHL100916-GBD26999_11816-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTT-GGAGCTTGATCGGGGATTGTAGGCACTTCTTTTAGAATTTTAATTCGACTAGGATTTGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10052 Chironomus sp. water mite diet isolate 10052-BHL040517-GBD23808_16111-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTTCATTATACTTCATTTTCGGTGCCTAATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTAAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCGTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10067 Amphichaeta raptisae water mite diet isolate 10067-BHL040517-GBD24882_5846-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCATTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTTCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGGTATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10092 Cryptochironomus sp. water mite diet isolate 10092-BHL040517-GBD16399_18992-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10096 Amphichaeta raptisae water mite diet isolate 10096-BHL040517-GBD26938_9508-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGAACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTTCTTAGTAATCCCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTTCCCCCCATCACTAATCCTATTAGTTGCATCGGCTGCAGTAGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10098 Amphichaeta sp. water mite diet isolate 10098-BHL040517-GBD23405_4511-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATAAAATAATATAAAATTTTGACTATTCCCCCCATCACAAAATCTATAAGCTGCATCAGCTGCAGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10099 Chironomidae sp. water mite diet isolate 10099-BHL040517-GBD14317_21863-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTAATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAGATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGTA--TCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.6% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10100 Chironomus sp. water mite diet isolate 10100-BHL040517-GBD6357_9542-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTCTCCCCCTAATACTTGGAGCGCCTGACAAAGCTTTTCCTCCAAAAAATAATATAAGTTTCTGGCTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10107 Oligochaeta sp. water mite diet isolate 10107-BHL040517-GBD14047_27881-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTTCCCCCCATCACTAATTCTTCTACT---ATCTAGTTCTTTCACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.5% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10110 Paratanytarsus sp. water mite diet isolate 10110-BHL040517-GBD19312_26284-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGCTCTTTATACTTTATTTTCGGTGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGTAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL10112 Diptera sp. water mite diet isolate 10112-BHL040517-GBD9602_9635-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGTTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTTTTGTAACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCCGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10113 Chironomus riparius water mite diet isolate 10113-BHL040517-GBD16951_6138-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACTACCCTTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCAAATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATAAGGAAACTGACTTATCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10117 Amphichaeta sp. water mite diet isolate 10117-BHL040517-GBD27505_16080-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGAATTGAATTAACCCATCCTGGAGCATTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTTCCCCCATCACTAATTCTATTAGTTGCATCGGCTTCAGTATAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10121 Chironomidae sp. water mite diet isolate 10121-BHL040517-GBD18074_13971-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGACTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTTTTGCCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10122 Oligochaeta sp. water mite diet isolate 10122-BHL040517-GBD22128_9795-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTCGGAGCACCAGATATAGCTTTCCCACGACATAACAATTTAAGATTTTGACTTCTTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10128 Amphichaeta sp. water mite diet isolate 10128-BHL040517-GBD19926_4811-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGAACAGGGACAAGAATATTAATTCGAATTGAATTAACCCAACCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCCTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAAAACCAGTTTTAATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10139 Chironomidae sp. water mite diet isolate 10139-BHL040517-GBD10562_22270-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.1% identical to accession ID KR287302, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10144 Paratanytarsus sp. water mite diet isolate 10144-BHL040517-GBD20098_16418-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTGTACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGTGGATTTGGGAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCCTTTCCTCGAATAAATAATCTAAGATTTTGACTTCTTCCCCCCCTCTTTAACCCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10146 Culex sp. water mite diet isolate 10146-BHL040517-GBD17356_21653-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGTTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATCTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10163 Chironomus sp. water mite diet isolate 10163-BHL040517-GBD10260_19640-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATCCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGTCATAGCTTTTCCTCGAATAAATGATATAAGTTTCTGACTTTCACCCCCCTCTCTTACACGACATCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL1018 Cricotopus sp. water mite diet isolate 1018-BHL100916-GBD28780_15755-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGACTTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGATTTCCCTCGAATAAATAAAATAAGTTTTTGATTATTACCCCCGTCGCTCAACTTACTTCTTTCAAGGTCAATTGTTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10183 Cryptochironomus sp. water mite diet isolate 10183-BHL040517-GBD17447_25163-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTACTTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGATTATTACCTCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10186 Paratanytarsus sp. water mite diet isolate 10186-BHL040517-GBD22428_14068-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTACATTATATTTTATTTTCGGTGCCTGATCAGGCATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCAGAACTAGGACACCCCGGATCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10193 Chironomidae sp. water mite diet isolate 10193-BHL040517-GBD17996_20223-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10195 Paratanytarsus sp. water mite diet isolate 10195-BHL040517-GBD19199_9239-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTGTAGTTCATTTTCGGTGCCTGATCCGGTATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTACTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACACGTTTACTGTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10205 Paratanytarsus sp. water mite diet isolate 10205-BHL040517-GBD28748_16152-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTCCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGGTATAGCTTTTCCCCGAACAAATAAGATAAGAATTTGACTTCTTCCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10212 Paratanytarsus sp. water mite diet isolate 10212-BHL040517-GBD23611_16503-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGTACTTCCCTATGAATATTAATTCGAGCTTAACTAGGACATCCCGGAACTTTTATTGGAGTTGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTGTAACTCATTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10221 Amphichaeta raptisae water mite diet isolate 10221-BHL040517-GBD8449_16060-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGTACAAGACTATAAATTCGTGGTGAATTAGCCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCATAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10252 Amphichaeta sp. water mite diet isolate 10252-BHL040517-GBD10698_21412-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTAGGTACAGGAACAAGACTATTAATTCGAATTGAATTAAGCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCTCATGCATTTTTAATAATTTTTTTTCTTAGCAATACCAATTTTAATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGTGGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.7% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10258 Paratanytarsus sp. water mite diet isolate 10258-BHL040517-GBD3386_16081-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATCATACTTTATTTTCGGTGCCTAATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGACTTAACAATATAAGATTCTGACTACTTCCACCTTCACTAATCCTATTAGTTTCTTCTTCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL10286 Paratanytarsus sp. water mite diet isolate 10286-BHL040517-GBD15846_8710-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTAATCAGGAATAGTCGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTCTCCTCGAATAAATAACATAAGATTTTGACTACTTCCCCCATCTTTAACCCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10293 Chironomus sp. water mite diet isolate 10293-BHL040517-GBD26397_13650-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGTAGAATTATGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTGGGAAACTGACTTGTCCCCCTAATACTTGGAGAACCTGACATAGCTTTTCCTCGAAAAAAAAATATAAGATACTGACATTTACCCCACCCTCTCTTACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10297 Oligochaeta sp. water mite diet isolate 10297-BHL040517-GBD8025_24005-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACGTGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTTTTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATTAAAAAATTAAGATTCTGACTACTACCACCCTCACTAAACCTATTAGTTTCTTCGGCGGCCGTAGAAAAAGGAGCCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10298 Paratanytarsus sp. water mite diet isolate 10298-BHL040517-GBD9830_22656-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATAGTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTGATTGGAGGATTTGGGAACTGATTATTGCCTTTAATGTTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGAAATTGACTTCGCCCCCCCTCTTTAACACTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10299 Paratanytarsus sp. water mite diet isolate 10299-BHL040517-GBD10566_7321-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGTCTGATCAGGAATAGTGGGAACTTCCCCAAGAATATTAATTCGAGTTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCATTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCGCCCTCTGTAACACTATTAATTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10301 Chironomidae sp. water mite diet isolate 10301-BHL040517-GBD21189_19529-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGAACAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATGTAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCGAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10305 Chironomus sp. water mite diet isolate 10305-BHL040517-GBD6892_23318-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGAACAAACCTTTCCCCGGAAAAAAAAAAAAAGTTTCCGACTTTTAACCCCCCCCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10317 Dicrotendipes sp. water mite diet isolate 10317-BHL040517-GBD18778_18988-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGCACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTATGAGCCCCCGATATAGCTTCCCCACGAAAAAATA--ATAAGATTCTGACTATTACCTCCTTTTCTAACCCTACTTCTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10321 Oligochaeta sp. water mite diet isolate 10321-BHL040517-GBD7008_15531-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATACTGGCACTCTATACTTAATCTTTGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTCAAGATTCTGACTACGACCACCTTCATTAACCCTATAAGAATATTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10322 Oligochaeta sp. water mite diet isolate 10322-BHL040517-GBD20092_14153-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAAGGAACAATATAAGATACTGACTACGACCGCCTTCACTAAACCGATAAGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL10329 Amphichaeta sp. water mite diet isolate 10329-BHL040517-GBD24677_10945-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCTTTTTTAGGAAGAGACCAACTATATAATACCTTTGTTACTGCACATGCATTTTTAATTATTTTTTTCATAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTTCCTTTAATACTTTGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCCGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10339 Paratanytarsus sp. water mite diet isolate 10339-BHL040517-GBD24876_9746-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTGTACTTCATTTTCGGTGCCTAATCAGGAATAGTGGGAACTTCCCTAAGTATATTAATTCGAGCTGAACTAGGTCATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGGACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10348 Paratanytarsus sp. water mite diet isolate 10348-BHL040517-GBD12127_14843-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTGTAGTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTTAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGTCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCGTTAACTCTGTTACTTTCAAGTAGAAGAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10350 Paratanytarsus sp. water mite diet isolate 10350-BHL040517-GBD25295_10688-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATAGTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGTCATCCCGGAACGTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAAATGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCACTTTAACTCATTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10357 Chironomus sp. water mite diet isolate 10357-BHL040517-GBD4656_9955-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTCATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGT-CCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10368 Chironomus riparius water mite diet isolate 10368-BHL040517-GBD11210_6401-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCCGAGCAGAATTAGTACGACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTTTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTATTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10382 Paratanytarsus sp. water mite diet isolate 10382-BHL040517-GBD23346_4865-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTAATCAGGAATAGTGGGAACTTCCCTAAGAATTTTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTGATACCTATTTTAATTGGGGGATTTGGGAATTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTCTCCCCGAATAAATAATATAAGATTTTGACTTCTCCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10389 Chironomus riparius water mite diet isolate 10389-BHL040517-GBD22417_16140-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGGCTTGATCGGGAATAGTGGGAACTTCATTAAGATTGTTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCTTTGGAGATGACCAATTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTATTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10393 Chironomidae sp. water mite diet isolate 10393-BHL040517-GBD4764_6627-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATCTTAGGAGTTTGAGCCGGAATAATTGGAACAGGAACTAGAATTTTAATTCGAGTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATTAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10394 Oligochaeta sp. water mite diet isolate 10394-BHL040517-GBD12712_25548-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATATTTTATCTTAGGAGCTTGAGCTGGAATAATTGGAACAGGAATTAGAATATTAATTCGGATTGAATTATCTTAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTTCTAATAATTTTCTTTCTAGTTATACCAATATTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATATTCGGAGCACCAGATATAGCTTTCCCACGACTTAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL10395 Paratanytarsus sp. water mite diet isolate 10395-BHL040517-GBD15447_20579-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTGTCGTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTGATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCATCTTTAACTCTGTCACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10419 Chironomidae sp. water mite diet isolate 10419-BHL040517-GBD17226_4936-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATTAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGACTTCTACCTCTAATACTCGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.1% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10438 Oligochaeta sp. water mite diet isolate 10438-BHL040517-GBD14588_10803-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACGACCCCCTACGCTAATCCAATAAGAAGATTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10456 Paratanytarsus sp. water mite diet isolate 10456-BHL040517-GBD11547_27551-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTCGGAGCCTAATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGTCACCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1046 Chironomidae sp. water mite diet isolate 1046-BHL100916-GBD7349_22931-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATCTTTTATTTT-GGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTTGTATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTCATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGAGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCAGTAACCTTACTATTAGCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10471 Dicrotendipes sp. water mite diet isolate 10471-BHL040517-GBD13513_6332-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATTTTTGGTGCTTTATCCGGAATAGTTGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTAGAATGATGTAGTTACTGCAGATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10477 Paratanytarsus sp. water mite diet isolate 10477-BHL040517-GBD26984_7600-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTCTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGAACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAAAAATAACCTTTCCCCGAATAAAAAATAAAAGAATTTTACCTCTCCCCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10486 Amphichaeta sp. water mite diet isolate 10486-BHL040517-GBD26694_23958-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTGGAGTATGATCAGGAATAGTTGGTACAGGAACAAGAATATTAATTCGAATTGAATTAACCCATCCTGGCGCCTTTTTAGGAAGAGACCAACTTTATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTTCATAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAACTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10490 Paratanytarsus sp. water mite diet isolate 10490-BHL040517-GBD16620_10332-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTAATCTGGAATAGTTGGAACTTCCCTTAGAATATTAATTCGAGCTGAACTATGACATCCCGGAACTTTTATTGGAGATGATCAACTTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTCTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10495 Oligochaeta sp. water mite diet isolate 10495-BHL040517-GBD27084_18288-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTATCTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACATAACAATATAAGATTCTGACTACTACCACCTACGCTAATCCAATAAGTTGCTTCTGCTGCCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL10496 Amphichaeta sp. water mite diet isolate 10496-BHL040517-GBD22047_16713-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGATTTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGTCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTGCCCCCATCACTAATACAATAAGAAGCATCGGCTGCAGTAGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10525 Paratanytarsus sp. water mite diet isolate 10525-BHL040517-GBD5704_8743-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTAATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGAAATAGCCTTTCCTCGAATAAATAATATAAGGTTTTGGCCTCTTCCCCCCTCTTTTACCCCTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10529 Dicrotendipes sp. water mite diet isolate 10529-BHL040517-GBD5257_19455-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTCATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTAGTGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATAGAGCTTTCCCACGAATAA--AAAATAAGGTTCTGACTATTACCTCCTTTTCTAACCCTTCTTCTTTCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10536 Paratanytarsus sp. water mite diet isolate 10536-BHL040517-GBD22109_22024-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTAATCAGGTATAGTGGGTACTTCTCTAAGAATATTAATTCGAGCTGAACTCGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCGTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10538 Paratanytarsus sp. water mite diet isolate 10538-BHL040517-GBD24901_19241-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTAATCAGGAATAGCGGGAACTTCCTTAAGAATATTTATTCGAGCTGAACTAGGACAACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGTAACTGATTATTCCCTTTAATATTCGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1055 Cricotopus sp. water mite diet isolate 1055-BHL100916-GBD5309_18920-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCCCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATGAATAATATAAGTTATTGATTATTACCTCCTTCTCTTACCTTATTACCGTAAAGTTCAATTGTTGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10554 Paratanytarsus sp. water mite diet isolate 10554-BHL040517-GBD20291_22018-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATAGTTCATTTTCGGTGCCTGATCAGGAAGAGTGGGAACTTCCCTAGGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTACTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCGTCCCCCCGCTTTAACACGATAACTGGCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10555 Paratanytarsus sp. water mite diet isolate 10555-BHL040517-GBD27831_20120-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCTTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGTTGAACTAGGATATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGATCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATAAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGGCTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10559 Oligochaeta sp. water mite diet isolate 10559-BHL040517-GBD26829_12785-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTTAACCAGGATCATTCCTAGGAAAAGATCAACTATATAATACTCTAGTAACTGCACATTCATTTCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCCCCTTCACTAACCCTACTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10588 Oligochaeta sp. water mite diet isolate 10588-BHL040517-GBD4890_23291-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGGGCTTGAGCTGGAATAATTGGAACATGATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTTCTAATAATTTTTTTTCTGGTTATACCAGTATTTATTGGGGGATTTGGAAATTGACTTCTACCTCTAATACTCGGAGCACCAGATATAGCTTTCCCACGACTTAACAAATAAAGATTCTGACTACTACCCCCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL10618 Paratanytarsus sp. water mite diet isolate 10618-BHL040517-GBD8549_8676-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTTTACTTCATTTTCGGTGCCTAATCAGGAATAGTGGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCTTCTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCATTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10619 Paratanytarsus sp. water mite diet isolate 10619-BHL040517-GBD11729_4424-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTAATAAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCCGATATTGCTTCTCCTCGAATAAATAATATAAGATTTTGACCTCCTCCCCCCTCTTTAACCTTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10624 Oligochaeta sp. water mite diet isolate 10624-BHL040517-GBD21298_26493-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAACTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATACTGACTACTACCGCCTTCACTAATCCTATAAGTTTCTTCTGCTTCCGTATAAAAGGGAGCTG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10631 Oligochaeta sp. water mite diet isolate 10631-BHL040517-GBD21691_9248-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATATTTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGGGCACCAGATACAGCTTTCCCACGACTTAACAAAATAAGATTCTGACTACTACCACCGGCACTAAACCTATAAGTTTCTACTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10637 Paratanytarsus sp. water mite diet isolate 10637-BHL040517-GBD3719_20937-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTAATCAGGAATCGTGGGTACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCGGCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10646 Dicrotendipes sp. water mite diet isolate 10646-BHL040517-GBD16248_15970-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCCAATTGGAGGATTCGGAAATCGATTAGTCCCTTTAATATTAGGAG-CCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTCCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10652 Paratanytarsus sp. water mite diet isolate 10652-BHL040517-GBD17515_4258-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTATAATTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCTGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTACTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGGATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10656 Chironominae sp. water mite diet isolate 10656-BHL040517-GBD10797_20909-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATATCAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTCGGACGACCTGGTACTTTCATTGTAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTT-ATTATAATTTTTTTTATAGTTATGACAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCTCCGGATATGGCTTTCCCTCGAGTAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10671 Amphichaeta sp. water mite diet isolate 10671-BHL040517-GBD27581_17806-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGACCAAGACTATTAATTCGTATTGAATTAACCCATCCTGAAGCCTTTTTAGGAAGAGACCAACTATATAATACTTTAGTTACTGCAAATGCATTTTTAATAATTTTTTTTCTTAGTAATGCCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAACGCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10672 Chironomus sp. water mite diet isolate 10672-BHL040517-GBD13576_23526-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGTAGGATTCGTAACCTGACTTGTCCCCCTAATACTTGCAGCGCCTGACATAGCTTTTCCCCGAATAAAAAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCACCTTCTTTCTAGTTCTTTCGAAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL10674 Chironomus sp. water mite diet isolate 10674-BHL040517-GBD3172_18551-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATGCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCACAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCCCCTGACATAGCCTTTCCCCGAAAAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCCTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10676 Paratanytarsus sp. water mite diet isolate 10676-BHL040517-GBD24684_9266-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTTATTATATTTCATTTTCGGAGCCTAATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATGCCCGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCATTAACTCTTTTACTTTCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10686 Paratanytarsus sp. water mite diet isolate 10686-BHL040517-GBD16884_4363-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGATATCCCTTAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGGCACAGCTCATGCATTTATTGTAATTTTTTTCATAGGTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCATTTAATATTAGGAGCCCAAGATATAGCTTTTCCTCGCATAAATAATATAAGATTTTGACTTCTTCCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10690 Chironomus sp. water mite diet isolate 10690-BHL040517-GBD27292_18449-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGTATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTCACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGACTCGGAAACTGACTTGTACCCCTAATACTTGGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTATATCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10693 Oligochaeta sp. water mite diet isolate 10693-BHL040517-GBD9961_11607-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGATCTAGAATATTAATTCGGATTGAATTATCTTAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTAATTGGTGGATTTGGAAATTGACTTCTCCCCCTAATACTCGGAGCACCAGATATAGCTTTCCCACGACTAAACAATATAAGATTCTGACTTCTACCCCCTTCTCTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10694 Oligochaeta sp. water mite diet isolate 10694-BHL040517-GBD18406_10228-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATATTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGTATCTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATCGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTAAACAATTTAAGATTCTGACTACTACCACCTACACCAACCCAATAAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10697 Chironomus riparius water mite diet isolate 10697-BHL040517-GBD10507_8853-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGGATTAGTGGGAACTTCATTAGGATTGCTTATTTGGGCGGAATTAGGACGACCCGGAACTTTCATTGAAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10698 Oligochaeta sp. water mite diet isolate 10698-BHL101516-GBD20117_25406-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTTAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCTCTAATACTTGGAGCTCCAGATATGGCTTTCCCGCGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10699 Dicrotendipes sp. water mite diet isolate 10699-BHL101516-GBD22300_19798-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTTAACTCTTCTACTATCTAGTTCTTTCACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10700 Cricotopus sp. water mite diet isolate 10700-BHL101516-GBD24644_11862-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTCCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL10701 Dicrotendipes tritomus water mite diet isolate 10701-BHL101516-GBD8802_3249-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATACTTCATTCCTGGAGCTTGATCAGGAATAGTTGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTACGGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAAGTGGAGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10702 Chironominae sp. water mite diet isolate 10702-BHL101516-GBD10417_8468-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTCATTTTTTTGGGGCTTGATCAGGAATAGTAGGCACTTCCTTAAGTATACTTATTCGAGCAGAGTTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTAACCGCACATGCTTTTATTATAATTTTCTTTATAGTTATACCGATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGGGCCCCTGATATAGCCTTCCCGCGAATAAATAATATAAGATTTTGACTTCTCCCACCGTCTCTTTCTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR751654, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10703 Dicrotendipes tritomus water mite diet isolate 10703-BHL101516-GBD17806_2587-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCTACCTTGAACTTTTATTGGTGACGATCAAAATTTACAATGTAATTGTGACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10704 Lebertia quinquemaculosa water mite diet isolate 10704-BHL101516-GBD17599_2148-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATACTTCGCTTTTGGGGCTTGATCAGGAATGGTGGGAGCAAGACTAAGAACTTTAATCCGGTTAGAATTAGGACAACCAGGAACTCTCCTAGGAAGAGACCAAATTTATAATACTATCGTAACAGCTCACACCTTCGTTATAATTTTCTTTATAGTTATGCCAATAATAATTGGAGGATTAGGAAATTGACTAGTCCCATTGATAATTAGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGACTTTTCCCCCCCCTCTTTAACTCTTCTACTATCTAGTTCTTTCGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID MG773261, identified in GenBank as Lebertia quinquemaculosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10706 Lebertia sp. water mite diet isolate 10706-BHL101516-GBD18127_16040-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATACTTCGCTTTTGGGGCTTGATCAGGAATGGTGGGAGCAAGACTAAGAACTTTAATCCGTTTAAAATTAGGACAACCAGGAACTCTCCTAGGAAGAGACCAAATTTATAATACTATCGTAACAGCTCACGCCTTCGTTATAATTTTCGTTATAGTTATGCCAATAATAATTGGAGGATTCGGAAATTGACTAGTCCCATTGATAATTAGAGCTCCAGATAGAGCATTGCCACGAATAAACAATATAAGATTTTGACTTTTACCCCCCTCTTTAACTCTTCTACAACCTACTTCTTTCTAGAGCAATCGGAG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID MG773261, identified in GenBank as Lebertia quinquemaculosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10707 Dicrotendipes sp. water mite diet isolate 10707-BHL101516-GBD12923_24299-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGACTTCTCTAAGTATACTTATTCGAGCAGGGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCCTTCTCTCACCTTACTTCTCTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1071 Chironomidae sp. water mite diet isolate 1071-BHL100916-GBD28367_19942-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGAATAGTAGGTACTTCCCTGAGAATCTTAATTCGAGCTGAATTAGGCCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATATTTTTTTTTATAGTTATACCTATTTCAATTGGAGG--------------------ATTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.2% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10711 Oligochaeta sp. water mite diet isolate 10711-BHL101516-GBD12838_22220-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.1% identical to accession ID LN810268, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10714 Dicrotendipes sp. water mite diet isolate 10714-BHL101516-GBD17469_11816-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTCTTGGAGCTTGATCAGGAATAGTTGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTAGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGGGCCCCTGATATAGCCTTCCCGCGAATAAATAATATAAGATTTTGACTTCTCCCACCGTCTCTTTCTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10726 Dicrotendipes tritomus water mite diet isolate 10726-BHL101516-GBD10084_2975-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTCTTGGAGCTTGATCAGGAATAGTTGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGTACTATTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGAGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTACCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL10736 Dicrotendipes tritomus water mite diet isolate 10736-BHL101516-GBD13901_2504-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATAAGGAATAGTTGGGACTTCTCTAAGTATACTTATGCGAGCAGAGCTGGGGCTACCTGGAACTTTTATTGGTGACGATCCAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATTATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGCGCTGGATCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10738 Oligochaeta sp. water mite diet isolate 10738-BHL101516-GBD24969_23317-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGCGCAGGAATAATTGGTACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTATCCCACGACAAAATAATTTAAGAGTCTGACTACTACCACCATCTCTAATCTAACTAATTGCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10755 Chironomidae sp. water mite diet isolate 10755-BHL101516-GBD6626_13255-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACTTTAATTGGAGATGATCAAGTTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTGATCGGAGGCTTTGGAAATTGACTATTACCACTTATACTTGGAGCCCCTGATATGGCCTTTCCTCGAATAAATAACATAAGATTCTGGTTACTACCTCCGTCTATTTCTTTGCTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10757 Dicrotendipes tritomus water mite diet isolate 10757-BHL101516-GBD17967_17730-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTACTTTAATATTAGGGGGCTCCAGATATAGCTTGTCCTCGAATAAATAATATAAGTTTGTGATGACTTCCTCCTTCTCTTACTCGACTTCGTTCTAGATCAATCGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10758 Dicrotendipes tritomus water mite diet isolate 10758-BHL101516-GBD19410_27505-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATACAGCTTTTCCTCGAATAAATAAAATAAGTTATTGATTACTTCCTCCTTCTCTTACTCTACATATTTCTAGATCAATTGTATAAAATGGCGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10768 Oligochaeta sp. water mite diet isolate 10768-BHL101516-GBD20899_9708-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAAAATAAGATACTGACTACGACCACCATCTCTAAACTAAATAATTGCTTCTGCAGCAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10782 Oligochaeta sp. water mite diet isolate 10782-BHL101516-GBD13424_9965-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTAAGGAGTATGAGCAGGAATAATTGGAACATGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGGTATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAAGCTTACTGAGTTCTGCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10786 Cricotopus sp. water mite diet isolate 10786-BHL101516-GBD21770_5036-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACGTTATATTTTATTTTCGGAGCCTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTACCTTTAATGTTAGGGGCTCCTGATATAGCATTCCCGCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTGCTATCAAGTACAATTGTTGAAAAGGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10788 Dicrotendipes sp. water mite diet isolate 10788-BHL101516-GBD22288_16371-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTCGGGACTTCTCTAAGTATATTTATTCGAGCAGAGCTGGGACGTCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGACTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTACCTCCTTCACTTACCCTACTTCTATCAAAATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10795 Oligochaeta sp. water mite diet isolate 10795-BHL101516-GBD20889_21355-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAACGATATTGGCACTCTTTACTTAATTTTCGGAGTATGAGCAGGAATAATTGGAACTGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCACCTATATAACACCCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCCGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID KY633410, identified in GenBank as Uncinais uncinata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL10809 Oligochaeta sp. water mite diet isolate 10809-BHL101516-GBD7817_9027-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCAAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTGATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGGTTTGGAAACTGACTAGTTCCATTAATACTCGGAGCCCCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.8% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10813 Chironomidae sp. water mite diet isolate 10813-BHL101516-GBD15094_5895-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGGGACGATCTAAGTTACAATGTAATTGTTACGTCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCGATTTTAATTGGGGGTTTCGGAAATTGATTAGTACATTTAATGTTAGGGGCCCCTGATATAGCCTTCCCGCGAATAAATAATATAATATTTTGACTTCTCCCACCGTCTCTTTCTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KJ208847, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10836 Dicrotendipes tritomus water mite diet isolate 10836-BHL101516-GBD27332_14114-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGAGTCTCCAGATATAGCTATTCCTCGAAAAAATAATAGAAGTTTTTGATTACTTCCTCCTTCTCTTACTCGACTTCTATCTAGATCAATTGTATAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1085 Psectrocladius sp. water mite diet isolate 1085-BHL100916-GBD29328_18616-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCAGTAACGGGACGAGGAGCGAGCGCGCGAGGGGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10893 Dicrotendipes tritomus water mite diet isolate 10893-BHL101516-GBD23119_22957-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGAAGCTTGATCAGGAATAGTTGTTACTTCTCTATGTATACTTATTCGAGCATAGCTGGGTCGACCTGGAACTTTTATTGTTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10901 Dicrotendipes tritomus water mite diet isolate 10901-BHL101516-GBD24827_5493-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTCCTATAAGTATACTTATTCGAGCATAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGTAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCACCTTCACTAACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10903 Chironominae sp. water mite diet isolate 10903-BHL101516-GBD18041_10567-Lq83 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTCATTTTTGGGGCTTGATCAGGAATAGTAGGCACTTCCTTAAGTATACTTATTCGAGCTGAGTTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTAACCGCACATGCTTTTATTATAA-TTTTTTTATAGTTATACCGATTTTAATTGGGGGGTTCGGAAACTGATTAGTACCTTTAATGTTAGGGGCCCCTGATATAGCTTTCCCGCGAATAAATAATATAAGATTTTGACTATTACCACCGTCTCTTACCCTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR751654, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL10919 Oligochaeta sp. water mite diet isolate 10919-BHL101516-GBD28208_14140-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACATGGACTAGTATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCATGTATTACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGAAATGGCCTTCCCACGACTAAATAAATAAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10934 Oligochaeta sp. water mite diet isolate 10934-BHL101516-GBD29220_16223-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATAGTTAATTTTAGGAGTATGAGAAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACACCCAGGAGCATTCTTAGGAAGAGATCAACTATATAAAACCCTAGTTAGTGCACATGCATTCTGAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAACCTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAATATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL1096 Cricotopus sp. water mite diet isolate 1096-BHL100916-GBD3614_19522-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGCTCAGGAATAGTAGGGACTTCCTTGAGAATCGTAATTCGAGCTGAATTAGGTCATGCCGGGTCATTTATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGTCTCCTGATATAGCCTTCCCTCGAAAAAATAATATAAGTTTTTGATTATTACCCCCCTTCTCTCACCTTACTTCTATCAAGTACAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL10970 Chaetogaster diastrophus water mite diet isolate 10970-BHL101516-GBD8368_3738-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTCTTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGAATTCTACCTTTAATAATAGGAGCCCCAGTTACGGCATGCCCACGATAAAACAATCTAAGATTTTGACTTCTACCACCTGCACTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10974 Oligochaeta sp. water mite diet isolate 10974-BHL101516-GBD26170_21217-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACTGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACAAAATAATATAAGATTCAGACTACTACCACCAACTCAAATCTAACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10981 Oligochaeta sp. water mite diet isolate 10981-BHL101516-GBD14171_10652-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGGTTTGGAAACTGACTAGTTCCATTAATACTCGGAGCCCCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.4% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL10991 Oligochaeta sp. water mite diet isolate 10991-BHL101516-GBD22821_7721-Lim84 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGGATTATCACAACCAGGATCATTCTTAGGAAGGGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTCCACACGACTAAATAATTTAAGATTCTGACTACGACCACCATCGCTAACCTAACTAATTGCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11030 Oligochaeta sp. water mite diet isolate 11030-BHL110116-GBD15810_14675-Lq76 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGGTTTGGAAACTGACTAGTTCCATTAATACTCGGAGCCCCAGATATGGCATTCCCACGTCTAAATAATTTAAAATTCTGACTACTACCACCATCTCTAACCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.8% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11032 Chironomidae sp. water mite diet isolate 11032-BHL110116-GBD6021_22873-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11033 Chironomidae sp. water mite diet isolate 11033-BHL110116-GBD25019_8321-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACTTTAATTGGAGATAATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTTTATAGTAATACCTATTTTGATCGGAGGCTTTGGAAATTGACTATTACCACTTATACTTGGAGCCCCTGATATGGCCTTTCCTCGAATAAATAACATAAGATTCTGGTTACTACCTCCGTCTATTTCTTTGCTTCTTTCTAGATCAATTGTTGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11036 Chironomidae sp. water mite diet isolate 11036-BHL110116-GBD13124_10928-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGGCGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11037 Paratanytarsus sp. water mite diet isolate 11037-BHL110116-GBD1738_15773-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTTGGGGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCATTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11038 Paratanytarsus sp. water mite diet isolate 11038-BHL110116-GBD19339_2274-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACCTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGTAACTTTTATTGGAGATGACCAAATTTATAATGTCATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTCTACATATTTTCATTGGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTGCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL11039 Paratanytarsus sp. water mite diet isolate 11039-BHL110116-GBD4537_19572-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTCATAGTTATACCTATTTTAGTTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCGTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGTTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11040 Paratanytarsus sp. water mite diet isolate 11040-BHL110116-GBD28842_19393-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAATTTTTATTGGAGATGACCAAGTTTATAACGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAAACATAGCTTTTCCTCGAATAAATAAGATAAGATTTTGACTTCTTCCCCCCTCGTTAACTCATTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11041 Paratanytarsus sp. water mite diet isolate 11041-BHL110116-GBD21060_11094-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCACTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTACGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCTAATTTCTAATGTAATTGTTACCGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGTGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCTCAAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11042 Chironominae sp. water mite diet isolate 11042-BHL110116-GBD23561_22917-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGACCGGCATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACAAATATTAGGACCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTGTATTACTTGCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11043 Paratanytarsus sp. water mite diet isolate 11043-BHL110116-GBD26621_15399-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGTATATTAATTCGAGCTGAACTAGGACATCCCGGACATTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCATGTACTGTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11045 Chironomidae sp. water mite diet isolate 11045-BHL110116-GBD18775_26358-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11046 Paratanytarsus sp. water mite diet isolate 11046-BHL110116-GBD19810_2661-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGCAGGAACTTCCCTAGGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCGCAAGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAGTAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11055 Chironomidae sp. water mite diet isolate 11055-BHL110116-GBD15883_28832-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACAATCAAATTTATAATTTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGTAACTTGATTATTACCTTTGATACTATGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTCCCCCCCTTCATTAACCTTACTTTTATCAAAATCAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11057 Paratanytarsus sp. water mite diet isolate 11057-BHL110116-GBD22011_24018-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCCCGAAAAAAAAAAAAAGACTTTGAATTCCTACCCCCTTCATTAAC---CTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11061 Paratanytarsus sp. water mite diet isolate 11061-BHL110116-GBD12275_20740-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAACTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAAATGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCCTCTTTAACTCTCTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL11062 Paratanytarsus sp. water mite diet isolate 11062-BHL110116-GBD27524_20320-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGATCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTTGGAACTGATTATTGCCTTTAATATTAGTAACCCCAGATATAGCTTTTCCTCAAATAAATAATATAAGATTTTGACTTCTCCCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11066 Psectrocladius sp. water mite diet isolate 11066-BHL110116-GBD10965_10617-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1107 Chironomidae sp. water mite diet isolate 1107-BHL110116-GBD19328_28648-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAATAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATAAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTGGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCATCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11073 Oligochaeta sp. water mite diet isolate 11073-BHL110116-GBD15645_12819-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATAACAACCAGGATCATTCTTAGGAAGCGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCATTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATATCTTCCGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11076 Paratanytarsus sp. water mite diet isolate 11076-BHL110116-GBD10285_23452-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGTCCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCCCCAAAAAAAAATATAAGAATTTGACTTCTTCCCCCCCTCTTTAACTCTTTTACTTTTAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11079 Chironominae sp. water mite diet isolate 11079-BHL110116-GBD28358_12120-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATGGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGAGATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCACCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11080 Chironomidae sp. water mite diet isolate 11080-BHL110116-GBD3072_13101-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTAGATGTGATTTTTGGAGCTTGATCGGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCATGCTCATTTATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTAGTTTAATTGGATGCTTTGGAAATTGATTAGTACCTTTGATATTAGGTGCTCCTGATATAGCTTTTCCGCTAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11086 Paratanytarsus sp. water mite diet isolate 11086-BHL110116-GBD6636_16633-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCCTTTCCTCGAATAAATAAAATAAGATTTTGACTTCTTCCCCCCTTCATTAAC---CTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1109 Paratanytarsus sp. water mite diet isolate 1109-BHL110116-GBD12466_22851-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11090 Paratanytarsus sp. water mite diet isolate 11090-BHL110116-GBD8744_17647-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCAGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAGCTGATTATTGCATTTAATATTAGGAGCCCCTTATATAGCTGTTCCTCGAATAAATAATATAAGGTTTTGACTTCTTCCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL11094 Chironomidae sp. water mite diet isolate 11094-BHL110116-GBD13996_10029-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGACCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATCGGAGGATTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.7% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11095 Chironomidae sp. water mite diet isolate 11095-BHL110116-GBD21901_25089-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGTATAGTAGTCACTTCTTTAAGAATTTTAATTCGACTAGATTTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCATATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGAGTTGTCCGCGAATAAATAAAATAAGATTTTGACTTCTTCCCCCCTCTTTAAC---TCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11096 Psectrocladius sp. water mite diet isolate 11096-BHL110116-GBD8783_26179-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGTAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAAAAATATAAGTTTTTGATTACTTCCCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1110 Dicrotendipes tritomus water mite diet isolate 1110-BHL110116-GBD28516_11451-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCGCGGATAAATAATATAAGTTTTTGATTACTACCCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11101 Oligochaeta sp. water mite diet isolate 11101-BHL110116-GBD18472_12544-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTGAAGATTCAGACCACGACCACCATCTCTAACATAACTAAAATCTTCTGGAGCAGTAGAAAATGGAGCTGGAA	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG422806, identified in GenBank as Slavina appendiculata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL1111 Chironomidae sp. water mite diet isolate 1111-BHL110116-GBD21107_13946-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1112 Chironomidae sp. water mite diet isolate 1112-BHL110116-GBD26368_12372-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCGTGATCGGGAATAGTAGGAACTTCTCTTAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAAATTTAATTGGAGATGATCAAATTTATAATGTTATTGTAACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTGCCATTAATATTAGGAGCACCTGATATGGCATTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCTTCCTTAACATTACTTCTTTCTAGTTCTACTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR754220, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1113 Chironomidae sp. water mite diet isolate 1113-BHL110116-GBD12240_4172-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATCTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATGAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAAATCAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11130 Oligochaeta sp. water mite diet isolate 11130-BHL110116-GBD27682_11241-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGTAGGAATAATTGGAGCAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCCCATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGAGTTGGAAACTGATTAGTACCACTAATAATTGGAGCTCCAGATCAGGCTTTCCCCCGACTAAATAATTTAAGATTCTGACTACTACCCCCATCTCTAATCTTACTAATTTCCTCTGCAGCAGTAGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.7% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL1114 Chironomidae sp. water mite diet isolate 1114-BHL110116-GBD20753_4670-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCTGGGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACCTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL11145 Chymomyza sp. water mite diet isolate 11145-BHL110116-GBD13230_13046-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.0% identical to accession ID EU493571, identified in GenBank as Chymomyza procnemis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11149 Paratanytarsus sp. water mite diet isolate 11149-BHL110116-GBD16854_8421-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTAATTATAGTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTATGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGAGTTTGACTTATTCCCCCCTCTGTAACTCAGTCACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1115 Chironominae sp. water mite diet isolate 1115-BHL110116-GBD6857_21036-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTACTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGATTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGACCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11153 Chironominae sp. water mite diet isolate 11153-BHL110116-GBD25586_16035-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTAATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11154 Paratanytarsus sp. water mite diet isolate 11154-BHL110116-GBD21836_20404-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCCTTTCCCCCAATAAAAAAAATAAGATTTTGAATTATTCCCCCCTCCTTAACCCTTTTACCTTCAAGTAGAATAGTGGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR276243, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11155 Chironomidae sp. water mite diet isolate 11155-BHL110116-GBD27485_18019-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCACATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATAAAGCTTTTCCGCGAAAAAAAAAAAAAGATTTTGATTATCACCCCCTTCATTAACCTCACTTTTATCAAGATAAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1116 Chironomidae sp. water mite diet isolate 1116-BHL110116-GBD18416_9864-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACAACCAAGCTCATTAATCGGAAACGAACAAATTTATAATGTAATTGTTACAGCACATGCCTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11163 Psectrocladius sp. water mite diet isolate 11163-BHL110116-GBD12963_19339-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTATATTTTATTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACTTTAATTGGAGATGATTAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11176 Paratanytarsus sp. water mite diet isolate 11176-BHL110116-GBD28477_19160-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATTAGGAATAGTAGGAACTTACCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGACCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTTGGAACTGATTATTGCCTTTAATAGTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTATAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11181 Paratanytarsus sp. water mite diet isolate 11181-BHL110116-GBD9405_17267-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACCTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL1119 Chironomidae sp. water mite diet isolate 1119-BHL110116-GBD4158_13975-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCCTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAACGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTGCATTAACCTTACTTTTATCAAGGTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11190 Oligochaeta sp. water mite diet isolate 11190-BHL110116-GBD16263_28288-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGAAGGAATAATTGGAACAGGGACTGGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATACGGCTTTCCCACGACTAAATAAAATAAGATTCTGACTACTACCACCAGCGCTAAACTTACTAATGTCTTCTGCAGCAGTATAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11191 Oligochaeta sp. water mite diet isolate 11191-BHL110116-GBD23624_6011-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATAATTCTTAGGAAGAGATCAACTATATAACGCACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCAGTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL1120 Chironomidae sp. water mite diet isolate 1120-BHL110116-GBD20047_25564-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGAAGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGTCTCCTGATATAGCTTTTCCGCGAATAAAAAATATAAGATTTTGATTATTACCCCCCTCATTAACCTTACTTTTATCAAGATAAATAGTAGAAAATGGAGCCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11211 Chironomidae sp. water mite diet isolate 11211-BHL110116-GBD11750_28285-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATTTTCGGAGCTTGATCCGGCATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACTTTAATTGGATATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTGATCGGAGGCTTTGGAAATTGACTATTACCACTTATACTTGGAGCCCCTGATATGGCCTTTCCTCGAATAAATAACATAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1122 Chironomidae sp. water mite diet isolate 1122-BHL110116-GBD28640_19761-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTGATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACACAGGCTCATTAATCGGAAGCGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11246 Oligochaeta sp. water mite diet isolate 11246-BHL110116-GBD26382_17225-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGAGATGGCATTCCCACGACTAAATAATTTAAGATAATGACTACGACCACCATCGCTAAAATGACTAATGTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11248 Paratanytarsus sp. water mite diet isolate 11248-BHL110116-GBD27850_17719-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACTAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACTTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACACTATTACTTTCAAGTAGGATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11251 Oligochaeta sp. water mite diet isolate 11251-BHL110116-GBD6244_23457-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGTGCAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATCCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTGGTAATACCAGTATTTAATGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATACGACTTTCCCACGACAAAATAATTTAAGATTCTGACTACTACCACCATCGCTAATCTAACTAATTGCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11256 Paratanytarsus sp. water mite diet isolate 11256-BHL110116-GBD17997_27771-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTAATTGTCCTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCGTTAACTCTGTTACTTGCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL11257 Paratanytarsus sp. water mite diet isolate 11257-BHL110116-GBD23905_20637-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGCACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTGTAACGCGTTAACCTGCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11273 Chironomidae sp. water mite diet isolate 11273-BHL110116-GBD24213_16938-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCATGGCCGCGAATAAATAAAATAAGAATATGATTATTACCCCCGTCATTAACCTGACATTTATCAAGAGCAATAGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11278 Chironomidae sp. water mite diet isolate 11278-BHL110116-GBD15035_2076-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATTCCAATCTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11286 Chironomidae sp. water mite diet isolate 11286-BHL110116-GBD23296_25646-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGTGAAGATCAAATTTATAATGTAATTGTTACAGCACATGATTCTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAAGGGCTCCTTATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTGCTTTTATCAAGATCAATAGTAGAAAATGGCGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11287 Oligochaeta sp. water mite diet isolate 11287-BHL110116-GBD24299_5363-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATCCTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTA-TATAACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGAGTTTCCCACGGCAAAATAAATAAAGATTCTGACTTCTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.4% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11298 Paratanytarsus sp. water mite diet isolate 11298-BHL110116-GBD21957_23530-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGATCTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGTGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACGTCCCCCCTCTTTAACACATTAACAATCAAGTAGAAGAGTGGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11306 Oligochaeta sp. water mite diet isolate 11306-BHL110116-GBD27989_12200-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCCGATATGGCTTTCCCACGACAAAATAATATAAAATACTGACTACGACCACCATCTCTAAACTTACTAATTTCTTCTGCAGCAGTATAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11308 Paratanytarsus sp. water mite diet isolate 11308-BHL110116-GBD13238_24762-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTAATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATACAGGAACTTTTATTGGAGATGACCACATTTATAATGTAATTGTTACAGCTCATGCATTTATTCTAATTTTTTTCATAGTTATACATATTTTAATTGGGTGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11313 Paratanytarsus sp. water mite diet isolate 11313-BHL110116-GBD21139_9178-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACATATTTTAATTGGGGGATTTGGTAACTGATTATAGCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCATCTTTAACACTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11319 Chironominae sp. water mite diet isolate 11319-BHL110116-GBD16478_20672-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTACGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAACTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATCATTACCACCATCTCTTACTTAATTACAATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL1132 Oligochaeta sp. water mite diet isolate 1132-BHL110116-GBD7942_10538-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAACTTTAGGAGTATGAGCAGGAATAATTGGAACATGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGAACATTCTTAGGAAAAGATCAACTTTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATAAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11332 Paratanytarsus sp. water mite diet isolate 11332-BHL110116-GBD24021_10328-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACCTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTAGACTACTGCCCCCCACTTTAACACTTTAACATGCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR278321, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1134 Chironomidae sp. water mite diet isolate 1134-BHL110116-GBD19602_17976-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAG-TGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11364 Oligochaeta sp. water mite diet isolate 11364-BHL110116-GBD26219_11205-Lq77 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTTAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTGTCCCACGACTAAATAATATAAGAGTCAGACTACTACCACCATCGCTAATCTAACTAATTGCGTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL1138 Oligochaeta sp. water mite diet isolate 1138-BHL110116-GBD16060_24919-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACCGGGACTAGAATACTAATTCGAATTGAATTATCATAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTCGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACGACCACCATCTCTAATCTTACTAAAATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11394 Oligochaeta sp. water mite diet isolate 11394-BHL101516-GBD26287_21424-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAAAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTCCTAGTAATACCGATATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGTGCTCCAGATATAGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACCACCACCAACTCTAATCTAACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11396 Oligochaeta sp. water mite diet isolate 11396-BHL101516-GBD13789_7485-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAAAATACTAATTCGAATTGAATTATCATAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTATTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCCTTCCCACGAATAAATAACATAAGATTCTGATTACTACCACCATCTCTAACCTTACTAATTTCTACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11403 Oligochaeta sp. water mite diet isolate 11403-BHL101516-GBD4136_8458-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAAAACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCCCGACTAAATAATTTAAGAATCTGAATAATACCCCCATCTATAAACCTACTAATTACTTCTGCAGCAGTAGAAAATGGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.8% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11404 Oligochaeta sp. water mite diet isolate 11404-BHL101516-GBD27045_8096-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGCCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGTAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACGAATACTTGGAGCTCCAGATATGGCTTGCCCACGACTAAATAATTTAAGATTCTGACTACGACCACAATCTCTAATATTACAAATTTCTTCTGCAGCAGTATAAAATAGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11419 Oligochaeta sp. water mite diet isolate 11419-BHL101516-GBD22387_20089-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATACTTTATTTTAGGAGTTTGAGCAGGAATAATTGGACCTGGGTCTAAAATACTAATTCGAATCGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTTTAACACCCTAGTTACTGCACATGCTTTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL11425 Chironomidae sp. water mite diet isolate 11425-BHL101516-GBD8471_11663-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGAATTTGGAAACTGATTAGTTCCTTTAAAATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAATTTTTTGATTGTTGCCCACATCATTAACTTTATTGTAATCTAGATCAATTGTGGAAAATGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11431 Psectrocladius sp. water mite diet isolate 11431-BHL101516-GBD12335_21280-Lq78 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCATAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTATGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTTCTTCCCCCGTCAGTAACTTTACTATTAGCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11443 Hyalospheniidae sp. water mite diet isolate 11443-BHL101516-GBD14725_3074-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACACTATATTTAATATTTGGTTTAATAGCCGGTATTATAGGGACAATATTTTCAATATTAATTAGAATTGAATTAGCATATCCAGGAGTACAGATTCTTAATGGAAATTATCAGTTTTATAATGTTATTGTTACAGCAAATGCTTTTGTTATGATTTTTTTCATGGTAATGCCTGCAATGATAGGCGGTTTTGGGAATTGATTTGTTCCTTTATTAATAGGAGCTCCTGATATGGCTTTTCCACGTCTAAATAATTTAAGCTTTTGACTTCTTCCCCCTTCTTTTATTTTATTATTGTTATCTAGTATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.8% identical to accession ID JN849043, identified in GenBank as Alocodera cockayni. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11456 Chironomidae sp. water mite diet isolate 11456-BHL101516-GBD14030_17731-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATTTTTCGGAGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTATTTCGTGCAGAATTAGGACATCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTATAGTAATACCTATTTTGATCGGAGGCTTTGGAAATTGACTATTACCACTTATACTTGGAGCCCCTGATATGGCCTTTCCTCGAATAAATAACATAAGATTCTGGTTACTACCTCCGTCTATTTCTTTGCTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11461 Oligochaeta sp. water mite diet isolate 11461-BHL101516-GBD8683_17221-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTGTACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTCGAATACTGATTCGAATTGAATTATCATAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATACGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACGAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11463 Oligochaeta sp. water mite diet isolate 11463-BHL101516-GBD28630_18206-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATCTGGAAACTGATTAGTACCACTAATACTTAAAGCTCCAGATATGGCTTTCCCCCGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTATAAAATGGCGCTTGAACA	Using NCBI BLASTN in June 2018, this sequence was 85.2% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11488 Oligochaeta sp. water mite diet isolate 11488-BHL101516-GBD17006_27754-Lq79 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCGACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGGTTTGGAAACTGACTAGTTCCATTAATACTCGGAGCCCCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCACCATCTCTAAACTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.8% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11492 Cricotopus sp. water mite diet isolate 11492-BHL101516-GBD6572_14026-Lq80 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAAGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11493 Chironomidae sp. water mite diet isolate 11493-BHL101516-GBD15477_20025-Lq80 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACCTTATATTTTATTTTCGGGGCTTGATCCGGAATAGTGGGGACTTCTTTAAGTATATTAATTCGTGCAGAATTAGGACATCCAGGAACTTTGATTGGAGATGATCAAATTTATAATGTTATTGTCACTGCTCATGCATTTATTATAATTTTTTTTTATAGTAATACCTATTTTGATCGGAGGCTTTGGAAGTTGACTATTACCACTTATACTTGGAGCCCCTGATATGGCCTTTCCTCGAATAAATAACATAAGATTCTGGTTACTACCTCCGTCTATTTCTTTGCTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR273785, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1150 Chironomidae sp. water mite diet isolate 1150-BHL110116-GBD11110_26723-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTGTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAACCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACGTTTTATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL11501 Oligochaeta sp. water mite diet isolate 11501-BHL101516-GBD14742_14283-Lq80 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGGTTTGGAAACTGACTAGTTCCATTAATACTCGGAGCCCCAGATATGGCATTCCCACGACTAAATAATATAAAATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11510 Oligochaeta sp. water mite diet isolate 11510-BHL101516-GBD26615_18382-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTAGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGGTTTGGAAACTGACTAGTTCCATTAATACTCGGAGCCCCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCACCATCGCTAATCTTACTAATGTCATCTGCAGCAGTAGAAAAGGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.9% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11511 Nais barbata water mite diet isolate 11511-BHL101516-GBD21832_27420-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAAGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTAACATGACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTCGGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATAGAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATGTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11512 Oligochaeta sp. water mite diet isolate 11512-BHL101516-GBD20716_19183-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGGTTTGGAAACTGACTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KY633404, identified in GenBank as Slavina sp. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11513 Oligochaeta sp. water mite diet isolate 11513-BHL101516-GBD5510_20574-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGTAACTAGAATATTAATTTGAATCGCATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGGTTTGGAAACTGACTAGTTCCAATAATACTAGGAGCCCCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACAACCATCTCTAATCTTACTAATGTAATCTGCAGCAGTAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11520 Oligochaeta sp. water mite diet isolate 11520-BHL101516-GBD11035_24903-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGAATCATTCTTAGGAAGATATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTACTTATTGGATGATATTAAAACTGATTAGTACCACTAATACTTGAAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCTTCTGCAGCAGTATAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11521 Oligochaeta sp. water mite diet isolate 11521-BHL101516-GBD28122_20183-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAGTCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCGACTGTATAACACCCTAGTTCATGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATATATTGGCGGGTTTGGAAAGTGACTAGTTCCATTAATACTCGGAGGCCCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCACCAACTCTAAGCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.7% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11525 Oligochaeta sp. water mite diet isolate 11525-BHL101516-GBD17059_5449-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCAATTTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTCGAATCGAATTAGCACAACCAGGGTCATTCATAGGAAAAGACCAACTGTATAACACCCTAGTTACTGCACATGCATTCGTAATAATTTTCTTTCTTGTAATACCAGTTTTTATTGGCGGGTTTGGAAACTGAGTAGTTCCTTTAATACTCGGAGCCCCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCATCTGCACCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.9% identical to accession ID HQ961513, identified in GenBank as Stylaria lacustris. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11527 Oligochaeta sp. water mite diet isolate 11527-BHL101516-GBD5674_7645-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTTTATAACAACCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGCGGGTTTGGAAATTGACTAGTTCCATTAATATTCGGAGCCCCAGATATGGCATTCCCTCGACTAAATAATTTAAAATTCTGACTACTACCCCCATCTCTAACCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.6% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11533 Oligochaeta sp. water mite diet isolate 11533-BHL101516-GBD21844_5634-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAACAGGAACTAGAATATTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGACTAGTACCACTAATACTTGGAGCACCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL11535 Oligochaeta sp. water mite diet isolate 11535-BHL101516-GBD27813_15892-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAAAACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTCGTAATACCAGTATTTACTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGACTTGCCCACGACTAAATAATTAAAGATTCTGACTACTACCGCCATCGCTAATCTTACAAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11536 Oligochaeta sp. water mite diet isolate 11536-BHL101516-GBD9434_4727-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGGTTTGGAAACTGACTAGTTCCATTAATATTCGGAGCACCCGATATAGCATTCCCACGACTAAATAATATAAAATTCTGACTACTACCACCATCTCTAACCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11542 Oligochaeta sp. water mite diet isolate 11542-BHL101516-GBD19827_14225-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATCCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAACAACTTAAGATTCTGACCACGACCACCATCTCTAATATAACTAAAATCTTCTGCAGCAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11544 Oligochaeta sp. water mite diet isolate 11544-BHL101516-GBD18018_24308-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCCTTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGGTTTGGAAACTGACTAGTTCCATTAATACTCGTAGCCCCAGATATGGCATTCCCACGACAAAAAAAATTAAAATTCTGACTACTACCACCATCTCTAAACTTACTAATGACATCTGCAGCAGTAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.0% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11546 Oligochaeta sp. water mite diet isolate 11546-BHL101516-GBD26333_21348-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGAAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATGTATTGGAGGATATGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACAAAATAATTTAAGATTCTGACTACTACCACCATCACTAATCTAACTAAAAACTTCTGCAGCAGTAGAAAAAGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11555 Oligochaeta sp. water mite diet isolate 11555-BHL101516-GBD22712_17700-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAATTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTACTAATTGGCGGGTTTGGAAACTGACTAGTTCCATTAATACTAGGAGCCCCAGATATGGCATCCCCACGACTAAATAACATAAAATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.8% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11564 Oligochaeta sp. water mite diet isolate 11564-BHL101516-GBD25085_9224-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGGATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGGTAATACCTGTATTTATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.0% identical to accession ID LT905357, identified in GenBank as Nais pseudobtusa. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11565 Oligochaeta sp. water mite diet isolate 11565-BHL101516-GBD1962_14743-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTTTATACTTCATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTGATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTTTAAAACACCCTAGTTACTGCACATGCATTCATAATAATTTTTTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATCGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11566 Oligochaeta sp. water mite diet isolate 11566-BHL101516-GBD27144_22372-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAAATGTATAACACCCTAGTTACTGGACATGCATTCTTAATCATTTTCTTTCTTGTAATACCAGTATTTATTGGCCGGTTTGGAAACTAACGAGTTCCATTAATACTAGGAGCCCCAGATATGGCATTCCCACGACTAAATAATTTAAAAATCTGACTACTACCACCATCTCTAATCTTGCTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.3% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11569 Oligochaeta sp. water mite diet isolate 11569-BHL101516-GBD19305_14728-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGAAGCAGGAACTAGGATATTAATTTGAATCGAATTATCACAACCAGAGTCATTCTTAGGAAAAGATTAACTGTATAACACCATAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATCTATTGGCGGGTTTGGAAACTGTCTAGTTCCATTTATACTCGGAGCCCCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACAACTACCACCATCTCTAATCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.7% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL11570 Oligochaeta sp. water mite diet isolate 11570-BHL101516-GBD28441_10251-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGACCAACTTTATAATACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGTGGGTTTGGAAACTGACTAGTTCCATTAATACTCGGAGCCCCAGATATGGCATTCCCACGACTAAATAATATAAAATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.3% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11571 Oligochaeta sp. water mite diet isolate 11571-BHL101516-GBD27124_11536-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTTATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACTCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAGTATTTATTGGAGGATTAGGAAACTGATTAGTACCCCTAATACTTGGAGCTCCAGATAAGGCTTTCCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11581 Oligochaeta sp. water mite diet isolate 11581-BHL101516-GBD17089_6858-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAGTCGAATTATCACAACCAGGTTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTACTACCAGTATTTATTGTCGGGGTTGGAAACTGACTAGTTCCATTAATATTTGGAGCCCCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 83.9% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11584 Oligochaeta sp. water mite diet isolate 11584-BHL101516-GBD17940_20103-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAACAGGAACTAGAATATTAACTTGAATCGAGTTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGGTTTGGAAACTGACTAGTTCCATTAATACTCGGAGCCCCAGATATGGCATTCCCACGACTAAATAATATAAAATTCTGACTACTACCACCATCTCTAACCTTACTAATGTCATCTGCAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11586 Oligochaeta sp. water mite diet isolate 11586-BHL101516-GBD25202_19113-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGTACATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGCGGTTTTGGAAACTGACTTGTTCCATTAGTACTCGGAGCCCCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11589 Oligochaeta sp. water mite diet isolate 11589-BHL101516-GBD28344_15943-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAGTCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGGATTGTGAACTGACTAGTTCCATTAATATTCTGTGCCCCAGATATGGCATTCCCACGACTAAATAAATTAAAATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.9% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11592 Oligochaeta sp. water mite diet isolate 11592-BHL101516-GBD20088_13824-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACCGGGTCTTGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTGCCCACGACTAAATAATTTAAGATTCAGACTACGACCACCATCTCTAATCTAACAAAAATCTTCTGCAGCAGTAGAAAATGGAGCTG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11595 Oligochaeta sp. water mite diet isolate 11595-BHL101516-GBD23244_5369-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTTTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGAACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAAATATATAACATCCTAGTTACTGCACATGCATTTATAATAATTTTTTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGGAAACTGATTAGTCCCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATATAAGATTCTGACTACTACCACCATCTCTAACCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11597 Oligochaeta sp. water mite diet isolate 11597-BHL101516-GBD20800_6737-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTTATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGTACTAGAATATTAATTTGAGTCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCGGTATTTATTGGAGGGTTTGGAAACTGACTAGTTCCATTAATACTAGGAGCCCCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCACCATCTCTAACCTTACTAATGTCATCTACAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.9% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11600 Oligochaeta sp. water mite diet isolate 11600-BHL101516-GBD3902_17029-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTAATTGGCGGGGTTGGAAACTGACTAGTACCACTAATATTCGGAGCCCCAGATATAGCTTTCCCACGACTAAATAATATAAAATTCTGACTACTACCACCATCTCTAACCTTACTAATGTCATGTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL11603 Oligochaeta sp. water mite diet isolate 11603-BHL101516-GBD10042_26251-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTTTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAATTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTGTAACACTCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGAGGATTTGGAAACTGACTAGTTCCATTAATATTCGGAGCCCCAGATATGGCATTCCCACGACTAAATAATATAAAATTCTGACTACTACCACCATCTCTAAACTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.8% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11611 Oligochaeta sp. water mite diet isolate 11611-BHL101516-GBD24216_24112-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGCACAGGGACTAGAATACTAATTCGAACTGAATTATAACAACCAGGATCACTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATAGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCCAATCTTACTAATATCTTCCGCAGCAGTAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11612 Oligochaeta sp. water mite diet isolate 11612-BHL101516-GBD10178_10066-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTTTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGGTTTGGTAACTGACTAGTTCCATTAATATTCGGAGCCCCAGATATGGCATTCCCACGACTAAATGATATAAAATTCTGACTACTACCACCATCTCTAATCTTACTAATATCATCAACAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID HQ961513, identified in GenBank as Stylaria lacustris. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11616 Oligochaeta sp. water mite diet isolate 11616-BHL101516-GBD21053_14926-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTTATTTTAGGAGTATAATCAGGAATAATTGGAGCTGGATCTAGAATATTAATTCGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTTGTTACTGCACATGCATTCTTAATAATTTTTTTCTTGTAATACCAGTATTAATTGGCGGGTTTGGAAACTGACTAGTACCATTAATACTCGGAGCCCCAGATATGGCATTCCCACGAATAAATAATATAAAATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11623 Oligochaeta sp. water mite diet isolate 11623-BHL101516-GBD12295_20708-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGCCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCCTTCTTAATAATTTTCTTTATAGTAATACCAGTATTAATTGGAGGGTTTGGAAACTGACTAGTTCCACTAATACTCGGAGCCCCAGACATGGCATTCCCACGACTAAATAATATAAAATTCTGACTACTACCACCATCTCTAACCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.2% identical to accession ID KY633404, identified in GenBank as Slavina sp. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11628 Megascolecidae sp. water mite diet isolate 11628-BHL101516-GBD8646_17487-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCAATTTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGATCTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCATAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTCGTAATACCAGTATTTATTGGAGGTTTTGGAAACTGACTAGTTCCATTAATATTTGGAGCCCCAGATATGGCATTCCCACGAATAAATAATATAAAATTCTGACTACTACCACCATCTCTTACCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.1% identical to accession ID KF205971, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11630 Oligochaeta sp. water mite diet isolate 11630-BHL101516-GBD18435_23137-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAGGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGGTGTGGAAACTGACTAGTTCCATTAATACTCTGAGTCCCAGATATGGCATCCCCACGACTAAATAATTTAAAATTCTGACTACTACCACCATCTCTAAGCTTACGAAGGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.0% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11637 Oligochaeta sp. water mite diet isolate 11637-BHL101516-GBD14311_28098-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCAATTTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAATGATCAACTGTATAACACCATAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTTATACCAGTTTTTATTGGCGGCTTTGGAAACTGACTAGTTCCATTAATACTAGGAGCCCCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCCCCATCTCTAACCCTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11638 Oligochaeta sp. water mite diet isolate 11638-BHL101516-GBD14245_16639-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAGTCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAATTGTATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGGTGTGGAAACTGACTAGTTCCATTAATAATCGGAGCCCCAGATACGGCATTCCCACGACTAAATAATATAAAATTCTGACTACTACCACCATCTCTAATCTTACTAATGCCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11641 Oligochaeta sp. water mite diet isolate 11641-BHL101516-GBD28238_17953-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTCTTGTAATACCAGTTCTTATTGGCGGGTTTGGAAACTGACTAGTTCCATTAATACTCGGAGCCCCAGATATGGCTTTCCCACGACTAAATAATATAAAATTCTGACTACTACCACCATCTCTAACCTTACAAATGTCAACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.0% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL11642 Oligochaeta sp. water mite diet isolate 11642-BHL101516-GBD9401_26041-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTTATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGACATTCTTAGGAAAAGATCAACTGTATAACACACTAGTTACTGCTCATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGCGGGTTTGGAAACTGACTAGTTCCATTAATACTAGGAGCCCCAGATATGGCCTTCCCACGACTAAATAATATAAAATTCTGACTACTACCACCATCTCTAACCTTACTAATGTCATCAGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11650 Oligochaeta sp. water mite diet isolate 11650-BHL101516-GBD22718_21013-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGATCTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTACAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTTGTAATACCAATATTAATTGGCGGGTTTGGAAACTGACTAGTTCCATTAATACTCGGAGCCCCTGATATAGCATTCCCACGACTAAATAATATAAAATTCTGACTACTACCACCATCACTAACCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.9% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11652 Oligochaeta sp. water mite diet isolate 11652-BHL101516-GBD21635_18972-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGATTTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATCTAAGATTCAGACTACTACCACCCCCTCCAAACTAACAAAAATCTTCTGCATCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.0% identical to accession ID MG422806, identified in GenBank as Slavina appendiculata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11656 Oligochaeta sp. water mite diet isolate 11656-BHL101516-GBD16445_16844-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGGGTTGGAAACTGACTAGTTCCATTAATACACGTAGCCCCAGAGATGGCATTCCCACAACTAAATAATTTAAAAAACTGACTACTACCACCATCTCTAAACTGACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.7% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11657 Oligochaeta sp. water mite diet isolate 11657-BHL101516-GBD26153_21056-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGCGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGAGTAGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTGTCCCACGACAAAATAATTTAAGAGTCAGACTACTACCACCATCGCTAATCTTACTAATTGCTTCTGCAGCAGTATAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11659 Oligochaeta sp. water mite diet isolate 11659-BHL101516-GBD4384_19631-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTTTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAGTCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGCGGGTTTGGAAACTGAATACTTCCATTAATACTCGGGGCACCAGATATAGCATTCCCACGACTAAATAATATAAAATTCTGACTACTACCACCATCACTAATCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11662 Oligochaeta sp. water mite diet isolate 11662-BHL101516-GBD23256_12335-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCAATTTATACTTCATTTTAGGAGCATAAGCAGGAATAATTGGAGCATGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTTTATAACACCCTTGTTACTGCACATGCATTTTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGGTTTGGAAATTGACTAGTTCCATTAATACTCGGAGCCCCAGATATGCCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.0% identical to accession ID LN999371, identified in GenBank as Nais elinguis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11664 Oligochaeta sp. water mite diet isolate 11664-BHL101516-GBD14634_19372-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCTGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGCGGGTTTGGAAGCTGACTAGTTCCATTAATACTCGGTGCCCCAGATATGGCATTCCCACGACTAAATAATATAAAATTCTGACTACTACCACCATCTCTAAACTTACTAATGTCACCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.2% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11668 Oligochaeta sp. water mite diet isolate 11668-BHL101516-GBD16244_21133-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATAATCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAGTCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACATCATAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGGTTTGGAAACTGACTAGTTCCATTAATACTCGGAGCCCCAGATATGGCATTCCCACGAATAAATAATATAAAATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCAAGTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.2% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11673 Megascolecidae sp. water mite diet isolate 11673-BHL101516-GBD19214_12345-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTTTATACTTTATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACATCCTTGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGGTTTGGAAACTGACTAGTTCCATTAATACTCGGAGCCCCAGATATAGCATTCCCACGACTAAATAATATAAAATTCTGACTACTACCACCATCACTAATCTTACTAATGTCATGTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.1% identical to accession ID F0017589, identified in GenBank as Amynthas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL11676 Oligochaeta sp. water mite diet isolate 11676-BHL101516-GBD19774_21800-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCAATTTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACGTGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGGTTTTGAAACTGATTAGGTCCATTAATATTCTGAGTCCCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCACCATCTCTAAACTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	#N/A
>RL11680 Oligochaeta sp. water mite diet isolate 11680-BHL101516-GBD7733_6383-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACCAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTCCTAGTAATACCAGTATTTATTGGAGGGTTTGGAAACTGACTATTTCCATTAATATTCGGAGCCCCAGATATGGCATTCCCACGGCTAAATAATATAAAATTCTGACTACTACCACCATCTCTAACCTTATTAATGTCATCTGCAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID KY633404, identified in GenBank as Slavina sp. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11681 Oligochaeta sp. water mite diet isolate 11681-BHL101516-GBD16697_26087-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGCACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTATAGTAATACCAGTATTAATTGGCGGATTTGGAAACTGACTAGTTCCATTAATATTCGGAGCCCCAGATATAGCATTCCCACGACTAAATAATATAAAATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCATCTACAACAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11683 Oligochaeta sp. water mite diet isolate 11683-BHL101516-GBD28260_20452-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTCGAATCGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGATTTGGAAACTGACTAGTACCAGTAATAATCGGAGCCCCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCATCTGCAGCAGTATAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11686 Oligochaeta sp. water mite diet isolate 11686-BHL101516-GBD29076_15980-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATATTTGGAGCAGGAACTAGAATATTAATTTGAATCGATTTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGCATTTATTGGCGGGTTTGGAAACTGACTAGTTCCAGTAATACTCGGAGCCCCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCACCAACTCTAGTCTTACTAAAGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 83.5% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11687 Oligochaeta sp. water mite diet isolate 11687-BHL101516-GBD16640_14613-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCACTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCGCTAATACTTGGAGCCCCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11688 Oligochaeta sp. water mite diet isolate 11688-BHL101516-GBD10014_14318-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCAGGTTTGGAAACTGACTAGTTCCATTAATACTCTGAGCCCCAGATATGGCATTCCCACGACTATATAATATAAAATACTGACTACGACCACCATCTCTAAACTGACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.0% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11692 Nais sp. water mite diet isolate 11692-BHL101516-GBD27637_12242-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTTTATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTATTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGATTTGGAAACAGATTACTTCCACTAATACTAGGTGCTGGTGATATAGCATTCCCCCGATAAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTGCTTCTACAGCCCTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID LN810267, identified in GenBank as Nais bretscheri. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11693 Oligochaeta sp. water mite diet isolate 11693-BHL101516-GBD22178_16085-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAACAGGGACTAGAATATTAATTTGAATTGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGGTTTGGAAACTGATTAGTTCCATTAATACTCGGAGACCCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCACCATCTCTAAGCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.4% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL1170 Chironomidae sp. water mite diet isolate 1170-BHL110116-GBD8775_19617-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGAGCTTGATCCGGAATAGTAGGCACTTCTTTAAGAATTCTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAAAAGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAAAATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTAATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL11701 Oligochaeta sp. water mite diet isolate 11701-BHL101516-GBD26888_12926-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTAGCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTTATAATTTTTTTTCTAGTAATACCAGTATTTATTGGCGGGTTTGGAAACTGACTAGTTCCCTTAATACTTGGAGCCCCAGACATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCCCCATCTCTAACCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11702 Oligochaeta sp. water mite diet isolate 11702-BHL101516-GBD21411_27582-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGTAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCTCATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGGTTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAAAAATATAAGATTCTGACTACTACCGCCATCTCTAAACTAACAAATGTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11704 Oligochaeta sp. water mite diet isolate 11704-BHL101516-GBD27482_14916-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATACTTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGCTCATTCTTAGGAAGAGATCAACTGTATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGATTTGGAAACTGACTAGTTCCATTAATACTTGGAGCCCCAGGTATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.4% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11705 Oligochaeta sp. water mite diet isolate 11705-BHL101516-GBD14330_27419-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAATCTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATACTAATTCGAGTCGAATTATCACAACCAGGCTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGACTAGTTCCATTAATACTCGGAGCCCCAGATATGGCATTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11707 Oligochaeta sp. water mite diet isolate 11707-BHL101516-GBD2193_15028-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTTATTTTAGGAGTATAAGCAGGAATAATTGGAACAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAAATGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTATAGTAATACCAGTACTAATTGGCGGGTTTGGAAATTGATTAGTTCCATTAATATTCGGAGCCCCAGATATGGCATTCCCACGACTAAATAATATAAAATTCTGACTACTACCACCATCTCTAACCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11708 Oligochaeta sp. water mite diet isolate 11708-BHL101516-GBD13646_2909-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTCGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTTTTTATTGGCGGGTTTGGAAACTGACTAGTTCCATTAATAATCGGAGCCCCAGATATGGCATTCCCTCGACTAAATAATTTAAAATTCTGACTACTACCCCCATCTCTAATCTTTCTAATTTCATCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11710 Oligochaeta sp. water mite diet isolate 11710-BHL101516-GBD21714_19326-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATAAGCGGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTTTATAACACACTAGTTACTGCACATGCATTCTTGATAATTTTCTTTCTTGTAATACCAGTATTAATTGGCGGGTTTGGAAACTGACTAGTTCCATTAATACTCGGAGCCCCAGATATGGCATTCCCACGAATAAATAATATAAAATTCTGACTACTACCACCATCTCTAACCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11713 Oligochaeta sp. water mite diet isolate 11713-BHL101516-GBD17185_26873-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATAATCAGGAATAATTGGAGCAGGAACTAGAATATTAATTCGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAATATTAATTGGAGGGTTTGGAAACTGATTAGTTCCATTAATAATCGGAGCCCCAGATATAGCATTCCCACGACTAAATAATATAAAATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.1% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11715 Oligochaeta sp. water mite diet isolate 11715-BHL101516-GBD19656_14141-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCCTTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGGTTTGGAAATTGACGAGTTCCATTAATACTAGGAGCCCCAGATATGGCATTCCCACGACTAAATAATATAAAATTCTGACTACTACCACCATCTCTAATCGTACTAAGGTCAACTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11716 Oligochaeta sp. water mite diet isolate 11716-BHL101516-GBD21546_27553-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGGGCAGGAATTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCTAGTAATACCAGTATTTATTGGAGGGTTTGGAAACTGATTAGTTCCATTAATACTCGGAGCCCCAGATATGGCATTCCCACGACTAAATAATATAAAATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCATCTACAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL11719 Nais barbata water mite diet isolate 11719-BHL101516-GBD5564_6810-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGTAGTATGATCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTTAACTCTCACAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGGAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGCTTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGATTAAATAATCTAAGATGTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11721 Oligochaeta sp. water mite diet isolate 11721-BHL101516-GBD22264_9791-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCAATTTATACTTTATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGATCTAGAATATTAATTTGAATCGAATTATCCCAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGGTTTGGAAACTGATTAGTTCCATTAATATTTGGTGCCCCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCACCATCTCTAACCTTACTAATATCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	#N/A
>RL11722 Oligochaeta sp. water mite diet isolate 11722-BHL101516-GBD18271_27642-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGGTTTGGAAACTGACTAGTTCCATTAATACTCGGAGCCCCAGATATGACATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCACCAGCTCTAAACCTACAAATGGCATCTGCAGCAGTAGAAAATGGAGCTGAAACAG	Using NCBI BLASTN in June 2018, this sequence was 83.9% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11723 Oligochaeta sp. water mite diet isolate 11723-BHL101516-GBD22105_5289-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAGTTGGATTATCACAACCAGGGTCATTCTTTGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATGTTCTTTCATGTAATACCAGTATTTATTGGCGGGTTTGGAAACTGACTAGTGCCATTAATACCCGGAGCCCCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.6% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11725 Oligochaeta sp. water mite diet isolate 11725-BHL101516-GBD13285_2056-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTCGAATCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGGTTTTGAAACTGACTAGTTCCATTAATACTCGGAGCCCCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACGACCACCATCACTAAACTGACGAATGGCATCTGCAGCAGGAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.9% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11728 Oligochaeta sp. water mite diet isolate 11728-BHL101516-GBD11050_25973-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATAATCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGATCATTCTTAGGAAAAGATCAACTGTATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTTTTTATTGTAATACCAGTATTAATTGGTGGGTTTGGAAACTGACTAGTTCCATTAATACTCGGAGCACCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCCCCATCTCTAATCTTACTAATGTCATATGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11735 Oligochaeta sp. water mite diet isolate 11735-BHL101516-GBD7169_21097-Lq81 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTTATTTTAGGAGTATAAGCAGGAATAATTGGAACCGGAATTAGAATATTAATTTGAATCGAATTATCACGACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTAATTGGCGGGTTTGGAAACTGACTAGTACCATTAATACTCGGAGCCCCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11736 Oligochaeta sp. water mite diet isolate 11736-BHL101516-GBD14720_26962-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCCTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11737 Cricotopus sp. water mite diet isolate 11737-BHL101516-GBD18037_22251-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTCCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAAAGTTAGGGGCCCCTGATATAGCTTTCCCCCGAATAAATAAAATAAGTTTTTTGATTATTACCCCCTTCCCTCACCTTACTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11738 Cricotopus sp. water mite diet isolate 11738-BHL101516-GBD12851_27015-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGGGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGTTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL11740 Lebertia sp. water mite diet isolate 11740-BHL101516-GBD12845_28915-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATACTTCGCTTTTGGGGCTTGATCAGGAATGGTGGGAGCAAGACTAAGAACTTTAATTCGTTTAGAATTAGGACGACCAGGAACTCTCCTAGGAAGAGACTAAATTTATAATACTATCGTAACAGCTCACGCCTTCGTTATAAATTTCTTTATAGTTATGCCAATAATAATTGGAGGATTCGGAAATTGAATAGTTCCATTGATGATTAGAGCTCCAGATATAGCATCTCCCCCAATAAACAATATAAGATTTTGACTTTTTACCCCCCTCTTTAACTCTTCTACTATCTAGTTCATTCACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG811666, identified in GenBank as Lebertia quinquemaculosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11744 Cricotopus sp. water mite diet isolate 11744-BHL101516-GBD22214_22572-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTTAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGACCAAAATTATAACGTTATTGTTGCAGCTCATGATTTTATAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAAGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGATTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCCTTCCCTCACCTTACTTCGTTCAAGTTTAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11746 Cricotopus sp. water mite diet isolate 11746-BHL101516-GBD24173_10563-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCATTGAGAATCTTAATTCGAGCTGAATTAGGACATGCCGGATCATTAATTGGAGATGATTAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTATTACCCCCTTCTCTCACCCTACTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1175 Chironomidae sp. water mite diet isolate 1175-BHL110116-GBD15466_16137-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTGCTTTAAGCATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAAGAGAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTAATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11761 Cricotopus sp. water mite diet isolate 11761-BHL101516-GBD21335_27430-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCCTTTAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGTCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTAACCTAACTACTATCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11763 Oligochaeta sp. water mite diet isolate 11763-BHL101516-GBD5265_12592-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11766 Pleuroxus sp. water mite diet isolate 11766-BHL101516-GBD28322_16599-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTGTATTTTTTATTTGGAATTTGAGCGGGGATAGTAGGAACTGCTTTAAGTTTATTGATTCGAGCTGAGTTAGCTGAAAGCGGATCTGTTATTGGGGATGATCAAATTTATAACGGAATTGTTACAGCCCATGCGTTTGTTATGATTTTTTTTTATAGTTATGCCTATTATAATTGGAGGGTTTGGTAATTGATTGGTACCTTTAATATTAGGAGCTCCCGATATGGCTTTCCCTCGACTTAATAATTTGAGTTTTTGATTATTACCTCCGGCTCTTACTCTTCTTTTAGCAGGAGGAGCCGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID MG449534, identified in GenBank as Pleuroxus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11767 Cricotopus sp. water mite diet isolate 11767-BHL101516-GBD12897_27355-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATATTAGGTACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCTAATCATTAATTGGAGATGATCAAATTTATCACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGTGGATCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1177 Chironomidae sp. water mite diet isolate 1177-BHL110116-GBD12254_16151-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTCGGAGCTTGATCGGGAATAGTCGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCACATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTTATAGTGATACCTATTTTAATTGGTGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11776 Oligochaeta sp. water mite diet isolate 11776-BHL101516-GBD27092_13721-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTAACACTAATACTTGGAGCTCCAGATATGACTTGCCCACGACTAAATAATTTAAGAGTCTGACTACTACCACCATCTCGAATCTAACTAATTTCTGCAGCAGCAGTATAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL11778 Cricotopus sp. water mite diet isolate 11778-BHL101516-GBD4890_12637-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTCGGGGCTTGCTCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAAATTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTGCCCTCGAATAAATAATATAAGTTTTTGATTATAACCCCCTTCGCTCACCTTACTTCTTTCAAGTACAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11801 Cricotopus sp. water mite diet isolate 11801-BHL101516-GBD21075_3169-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTTATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGTTCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATAATTACCCCCTTCTCACACCTTACTACATACAAGTGCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11804 Cricotopus sp. water mite diet isolate 11804-BHL101516-GBD28967_14580-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATCGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTTTGCCTCGAATAAATAATATAAGTTTTTGATTATAACCCCCTTCTCTCACCTTACTGCTTTCAAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11811 Cricotopus sp. water mite diet isolate 11811-BHL101516-GBD29560_14358-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTCCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTCATAGTTATACCTCTTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTATGGTCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTCCCCCCTTCTCTAACCTAACTTCTTTCAAGTTCAATTGTTGAAAATGGCGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11817 Cricotopus sp. water mite diet isolate 11817-BHL101516-GBD11694_5774-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTCCCTTGAGACTCTTAATTCGAGCTGAATTAGGTCATGCCGGATAATTAATTGGAGATGACCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTCATATTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGTCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGGGTTTGATTATTACCCCCTTCTCTCACCTTACCTCTTTCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11818 Cricotopus sp. water mite diet isolate 11818-BHL101516-GBD17244_18270-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGTGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATTATTAATTGGTGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGTGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTCTCACCTAACTTCGTGCAAGATCAATTGTTGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1182 Chironomidae sp. water mite diet isolate 1182-BHL110116-GBD17771_2746-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGTCTCATTAATCGGAGACGATCTAATATAGAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTAACTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCCATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11820 Cricotopus sp. water mite diet isolate 11820-BHL101516-GBD6348_8615-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTCTTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTGAGAATCTAAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTCATAGTTATACCTATTTTAATTGGAGGAGTTGGAAACTGATTAGTTCCTTTAATGTTCTGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTGACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11846 Chironomidae sp. water mite diet isolate 11846-BHL101516-GBD27320_14516-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTTTTTCATAGTTATACCTATTTTAATAGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTGTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11850 Oligochaeta sp. water mite diet isolate 11850-BHL101516-GBD25619_22845-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACTCTAGTTACTGCATATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTGGTACCACTAATACTTGGAGCTCCAGATAAGGCTTTCCCACGACAAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATAACTTCTGCATCAGTATAAGATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL11855 Chironomidae sp. water mite diet isolate 11855-BHL101516-GBD3930_18141-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGAAGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGACTGTTGCCCCCATCATTAACTTTATTGTTATCTAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11861 Cricotopus sp. water mite diet isolate 11861-BHL101516-GBD25283_9697-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGATTTCCTTGAGAATCTTAATTCGAGCGGAATTAGGTCATGCCGTATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGCAGACTAATTAGTTCCTTTAATGTTAGGGACTCCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11862 Cricotopus sp. water mite diet isolate 11862-BHL101516-GBD5304_19424-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTGAGAAGCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTACTCTCACCTAACTTCAATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11883 Cricotopus sp. water mite diet isolate 11883-BHL101516-GBD13168_17730-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGATATGATCAAATTTATAACGTTATTGTTACAGCTCATACTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGTGATCCTGATATAGCATTCACTCGAATAAATAATATAAGTTTATGATTATTAACCCCCTGCTCTCACCTTACTTCATTCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11886 Oligochaeta sp. water mite diet isolate 11886-BHL101516-GBD26805_23000-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTACTGGAGGATTTGGAAACTGATTAGTACCCCTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCCCCCACTCCAACCTAACTAAAATCTTCTGCAGCAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11887 Oligochaeta sp. water mite diet isolate 11887-BHL101516-GBD21290_27533-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGGAACTAGAATATTAATTTGAGTCGAATTATCACAACCAGGGTCATTCTTAGGAAAAGATCAACTGTATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTCGTAATACCAGTATTTATTGGCGGGTTTGGAAACTGACTAGTTCCATTAATACTCGGAGCCCCAGATATGGCATTCCCACGACTAAATAATATAAAATTCTGACTACTACCACCATCTCTAATCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.8% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL1189 Chironomidae sp. water mite diet isolate 1189-BHL110116-GBD28572_14568-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTCGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGTTCAAATTTATAACGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTATTACCTTTGAAATTAGGGGCTCCTGATATAGCTTTTCCGCGAAAAAATAAAATAAGATTTTGAATATTACCCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11900 Oligochaeta sp. water mite diet isolate 11900-BHL101516-GBD16437_7703-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTAATTTTAGGAGTATAAGCAGGAATAATTGGAGCAGCAACTAGAATATTAATTTGAATCGAATTATCACAACCAGGCTCATTCTTAGGAAAAGATCAACTGAATAACACACTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGCGGGTTTGGAAACTGACTAGTTCCATTAATATTAGGAGTCCCAGATATGGCATTCCCACGACTAAATAATTTAAAATTCTGACTACTACCACCATCACTAATCTTACTAATGTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID LN810254, identified in GenBank as Piguetiella blanci. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL11905 Cricotopus sp. water mite diet isolate 11905-BHL101516-GBD2081_17778-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTAAAACGTTATTGTTACAGATCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGACTCCTGATATAGCTTGCCCTCGAATAAATAATATAAGTTATTGATCATTACCACCTTCTCTCACCTTACATCATTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11911 Oligochaeta sp. water mite diet isolate 11911-BHL101516-GBD4505_16650-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTACTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACCAAATAATCTAAGATTCAGACCACGACCACCATCTCCAATATAACAAAAATCTTCTGCAGCAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 84.6% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL11975 Cricotopus sp. water mite diet isolate 11975-BHL101516-GBD21400_23245-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCATGAATAGTAGGTACTTCCTTGTGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTACTCTAACCTAACCACTTGCAAGTACAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1198 Chironomidae sp. water mite diet isolate 1198-BHL110116-GBD26848_16612-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGTACTTCTTTATGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGAGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAACAATAGTATAAAATGGAGCTGAAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL11999 Cricotopus sp. water mite diet isolate 11999-BHL101516-GBD8143_15054-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGTTCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTAATTAGTTCCTTTAATGTTAGGGGCTCCTGATAGAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTGCTCTCACCTTACTTCTTTCAAGTGCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12018 Cricotopus sp. water mite diet isolate 12018-BHL101516-GBD28966_12319-Lq82 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTACTTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTGTGATCATTACCCCCTTCGCTCACCTAACATCAAGCAAGTTCAATAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12039 Chironomus sp. water mite diet isolate 12039-BHL040517-GBD4215_15758-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACACTATACTTTATTTTTGGTCCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATCACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCTTTTAATATTTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12040 Phaenopsectra sp. water mite diet isolate 12040-BHL040517-GBD17100_7762-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCCTCTCTTACTCGTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12041 Chironomus riparius water mite diet isolate 12041-BHL040517-GBD21793_20932-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGAAATAGTGGGAACTTCATTAAAAATGCTTATTCGAGCAGAATTAGGACGATCCGGAACTTTCATTGGAGGTGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTAGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGTTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12042 Chironomus sp. water mite diet isolate 12042-BHL040517-GBD17238_23764-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATAATTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12044 Chironomus sp. water mite diet isolate 12044-BHL040517-GBD10051_12899-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGGGGCTTCATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGAAGACCCGGGACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCCTAATTCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12046 Chironominae sp. water mite diet isolate 12046-BHL040517-GBD10479_15350-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTAGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAGATAATATAAGATTTTGATTATTACCACCATCTCTTACATTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12047 Chironomus sp. water mite diet isolate 12047-BHL040517-GBD12604_8302-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGGTTTTATTATAATTTTTCTCATAGTTATACCAATTTTAATTGGAGGGTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGCTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12048 Chironominae sp. water mite diet isolate 12048-BHL040517-GBD16198_12104-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGTCGGACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCACGCATTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12051 Phaenopsectra sp. water mite diet isolate 12051-BHL040517-GBD23752_14539-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATAAAGCATTTCCTCGGATAAAAAATATAAGTATTTGACTTTTACCCCCCTTCTTTAACTTTACTTCTTTCTACTACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12053 Chironomus sp. water mite diet isolate 12053-BHL040517-GBD15239_5482-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGAGCCGAAATAGTGGGAACTTCATTAAGAATGCTTATGCGAGCAGAATTAGGACGATCCGGAACTTTCATTGGAGATGACCAATTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTGGGAAACTGACATGTCCCCCTAATACTTGGAACACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12055 Phaenopsectra sp. water mite diet isolate 12055-BHL040517-GBD5856_19047-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGGTTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.7% identical to accession ID KR274695, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12057 Oligochaeta sp. water mite diet isolate 12057-BHL040517-GBD25313_7665-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACCCTATACTTAATTTTAGGAGTTTGAGCCGGAATAATTGGAACCGGAACTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTCCTAGGGGAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGC-TTTCCTACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL12058 Chironomus sp. water mite diet isolate 12058-BHL040517-GBD27961_10108-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAACTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACACCCCTCTCATGCTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12061 Oligochaeta sp. water mite diet isolate 12061-BHL040517-GBD19681_26852-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAACTGGAACAGGAACTAGAATATTAATTCGGATTAAATTATCTCAACCAGGATCATTACTATGGAAGAGATCAACTAGATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCGTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL12063 Chironomus sp. water mite diet isolate 12063-BHL040517-GBD20151_8827-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAACTTATAATGTTGTAGTTACTGCACATGCTTTTATTATATTTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACATTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KC750313, identified in GenBank as Chironomus nepeanensis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12065 Chironomus sp. water mite diet isolate 12065-BHL040517-GBD27330_16804-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTATTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTCTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAACACCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12066 Cricotopus sp. water mite diet isolate 12066-BHL040517-GBD21524_16189-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGTACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTCTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12067 Chironomus sp. water mite diet isolate 12067-BHL040517-GBD13973_12701-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACGTTATACTTTATTCTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTGTTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTCGTCCCCCTAATACTTGGAGCACCTGACGTAGCTTTTCCTCGAATAAATAATAAAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTGCTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12068 Phaenopsectra sp. water mite diet isolate 12068-BHL040517-GBD14320_11225-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCGTGATCGGGAATAGTAGGAACTTCTCTTAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAAATTTAATTGGAGATGATCAAATTTATAATGTTATTGTAACAGCCCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTCTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAGATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR723136, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1207 Chironomidae sp. water mite diet isolate 1207-BHL110116-GBD28187_11241-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATCATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGGGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTTATGTTAGGGGCTCCTGATTTAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGAACGATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12072 Oligochaeta sp. water mite diet isolate 12072-BHL040517-GBD14009_10259-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACCTAATCTTAGGAGTTTGAGCTGGAAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGGTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTGTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTAGTAGTTGCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL12073 Chydorus sp. water mite diet isolate 12073-BHL040517-GBD13737_24214-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTAATTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAACGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGGTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCGTTCCCTCGTCTTAATAAATTAAGTTTCTGGCGTCTTCCCCCAGCTTTAACCCTTCTTTTAGAAGGGAGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12074 Phaenopsectra sp. water mite diet isolate 12074-BHL040517-GBD4063_18566-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTTGGTACTTCTTTAAGTATGCTAATTCGAGCAGATCTTGGACGACCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTGTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR274695, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12075 Oligochaeta sp. water mite diet isolate 12075-BHL040517-GBD16760_5797-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAGTCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATAAAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTTGTTATACCATTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCCCCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL12076 Chironomus sp. water mite diet isolate 12076-BHL040517-GBD27616_16925-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTAACTAGT-CCCTTTATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCCTTACTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12078 Phaenopsectra sp. water mite diet isolate 12078-BHL040517-GBD5283_21744-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTTTGGAGCTTGATAAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGGGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR769945, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12079 Chironomus sp. water mite diet isolate 12079-BHL040517-GBD7315_16703-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAGCTTCCCTTAGATTATTTATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTTGGTGATGACCAAATTTATAATGTATTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGATCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTCTTGACTTCTCCCCCCATCCTTAACTCTACTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1208 Paratanytarsus sp. water mite diet isolate 1208-BHL110116-GBD16708_7240-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTGTAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.1% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12080 Chironomus sp. water mite diet isolate 12080-BHL040517-GBD24983_17920-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGAAAACTAACTTGT-CCCATAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTATCTAACTCTACTAATTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12081 Chironominae sp. water mite diet isolate 12081-BHL040517-GBD25256_5984-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGTGGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAATAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12083 Chironomus sp. water mite diet isolate 12083-BHL040517-GBD29111_15313-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTCGGACGACCTGGATCTTTTATTGGTTATGACCAAATTTATAATGTAGTTGTTACAGCTCACGCATTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTAACTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12085 Chironomidae sp. water mite diet isolate 12085-BHL040517-GBD21425_25842-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTTATTCGACTCGAATTAGGACACCCAGGCTCATTAATCGGAGAAGAACAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCGTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12086 Chironominae sp. water mite diet isolate 12086-BHL040517-GBD20246_15945-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGCAGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12087 Chironominae sp. water mite diet isolate 12087-BHL040517-GBD21521_19523-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACCTCCTCCATCTCTAACACTACTTCTTTCAAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12088 Chironomus sp. water mite diet isolate 12088-BHL040517-GBD22518_14953-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGAGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGGTTTTATTATAATTTTTCTCATAGTTATACCAATTTTAATTGGAGGGTTCGGAAACTGACTTGCCCCCCTAATACTTGGAGCACCTGACATAGCTTCTCCTCGAATAAATAATATAAGCTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12092 Chironomus sp. water mite diet isolate 12092-BHL040517-GBD20373_8490-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTTGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACTGG	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12093 Chironomus sp. water mite diet isolate 12093-BHL040517-GBD8111_23015-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12094 Oligochaeta sp. water mite diet isolate 12094-BHL040517-GBD3151_16979-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATCGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCCTTCCCACGATTTAACCATTTAAGATTCTGACTACTACCACCTTCCCTAATCCTATTAGTTTCTTCTGCCGCCGTAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL12099 Phaenopsectra sp. water mite diet isolate 12099-BHL040517-GBD3552_13420-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTGTAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGATCTTGGACGACTTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR274695, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12100 Chironomus sp. water mite diet isolate 12100-BHL040517-GBD19449_17936-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGCTATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTACTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAATTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTTTCCTCGAATAAATAATATAAGCTGCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12112 Chironomus sp. water mite diet isolate 12112-BHL040517-GBD11982_17182-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTAGAGCTTGATCAGGAATAGTAGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTTAATGCTTGGAGCATATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCATCTTCTTTCTAGTTATTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12116 Oligochaeta sp. water mite diet isolate 12116-BHL040517-GBD16896_20122-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGATTAAACCAGTATTTATTGGGGGAGTTGAAAATTGACTTCTACCTCTAATACTTGGAGCATCAGATATAGCTTTCCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL12117 Chironomus riparius water mite diet isolate 12117-BHL040517-GBD19352_27814-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGAGGCTTCATCCGGAATATTGGGAACTTCATTAAGAATGCTTATTCGAGCATAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATTCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCATCTTCTGTCTAGTTCTTGCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12122 Chironominae sp. water mite diet isolate 12122-BHL040517-GBD16417_5250-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTAATCAGGAATGGTAGGAACTTCTTCAAGGATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12128 Chironomus sp. water mite diet isolate 12128-BHL040517-GBD19172_11638-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTAAAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATACAAGTTTCTGACTTTGACCCCCCTCTCTTACGCGTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12129 Chironomidae sp. water mite diet isolate 12129-BHL040517-GBD11780_19114-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGTACAAGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGTTATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KR723136, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL1213 Chironomidae sp. water mite diet isolate 1213-BHL110116-GBD27173_11266-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTGCTTTAAGAATTTTAATTCGACTAGATTTAGGATACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACGCCCTTCATTAACCTTTCATTAATCAAGATCAATAGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12131 Chironomus sp. water mite diet isolate 12131-BHL040517-GBD9942_20697-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCATTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTGTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12134 Oligochaeta sp. water mite diet isolate 12134-BHL040517-GBD22933_23760-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAATTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAAATTATATCAACCAGGATCATTCCTAGGAAGAGATCAACTTTTTAATACTCTAGTAACTGCACATGCTTTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGACTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL12135 Phaenopsectra sp. water mite diet isolate 12135-BHL040517-GBD11739_25220-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACTCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATATGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12137 Chironominae sp. water mite diet isolate 12137-BHL040517-GBD27540_12920-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGAAGCTTGACCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12139 Chironominae sp. water mite diet isolate 12139-BHL040517-GBD23615_26607-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTTGGAACTTGGTCAGGAATGGTGGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTATTTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCCTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1214 Oligochaeta sp. water mite diet isolate 1214-BHL110116-GBD15765_6012-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACGAGAATACTAATTCGAATTGAATTATAACAACCAGTATCATTCTAAGTAAGAGATCATCTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTACAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL12143 Chironomus sp. water mite diet isolate 12143-BHL040517-GBD17356_28909-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTCTGGGGCTTCATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTTCATAGTTAGACCAATTTTATTTGGAGGATTCGGAAACTGACTTTTCCCCCTAATGTTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12148 Chironomus sp. water mite diet isolate 12148-BHL040517-GBD24295_20371-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGG-AACTGACTTGTCCCCCTAATGCTTGGAACACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12149 Oligochaeta sp. water mite diet isolate 12149-BHL040517-GBD12435_15255-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATCATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTATGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAACCCTATAAGAATCTTCTGCTGCCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 85.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL1215 Chironomidae sp. water mite diet isolate 1215-BHL110116-GBD26957_16894-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCGCATTAATCGGAGGTGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTGATATTAGGGCATCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12160 Chironomidae sp. water mite diet isolate 12160-BHL040517-GBD16869_11523-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAAC---CCTTCTTT-TAGTGGGGGGGGGCA---GTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.8% identical to accession ID KR769945, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12162 Phaenopsectra sp. water mite diet isolate 12162-BHL040517-GBD27139_17794-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATTTTAATTCGAGCAGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGTAATTGATTAGTACCTCTAATATTGGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTTCCCCCGTCTTTAACTTTACTACTATCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12163 Chironomus sp. water mite diet isolate 12163-BHL040517-GBD9428_20258-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACCCTATACTTTATTTTTGGAGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTCTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTAACATGT-CCCATAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12168 Chironominae sp. water mite diet isolate 12168-BHL040517-GBD26348_23409-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAAGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATACTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1217 Chironomidae sp. water mite diet isolate 1217-BHL110116-GBD21743_21613-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGTTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACAAACAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCCATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATAAGGGGCTCCTGATATAGCTTTCCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12171 Chironomus sp. water mite diet isolate 12171-BHL040517-GBD26701_23039-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGGGGCTTCATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGTACTTTCATTGGAGATGACAAAATTTATAATGTTGAAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGCATTCGGAAACTTTCTTGTCCCCCTAATGCTTGGATCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTATCCCCCTCTCTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12181 Chironomidae sp. water mite diet isolate 12181-BHL040517-GBD24338_11106-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12183 Chironomidae sp. water mite diet isolate 12183-BHL040517-GBD6376_13530-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCC------ATCACTAATTCTAT-TAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.3% identical to accession ID KR769945, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12184 Chironominae sp. water mite diet isolate 12184-BHL040517-GBD23546_15511-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCGTGATCGGGAATAGTAGGAACTTCTCTTAGAATATTAATTCGAGCTGAATTAGGATATCCTGGAAATTTAATTGGAGATGATCAAATTTATAATGTTATTGTAACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12185 Chironomidae sp. water mite diet isolate 12185-BHL040517-GBD23627_4541-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGACCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGTCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAACAATAAAAGTTTTTGATTTCTTCCTCCATCTCTAACTCTTCTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ166684, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12186 Chydorus sp. water mite diet isolate 12186-BHL040517-GBD22933_6642-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATAAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12188 Chironomidae sp. water mite diet isolate 12188-BHL040517-GBD4998_20214-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAGTCGGGACTTCTCTAAGAATGCTTACTCAAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGC-TTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12194 Phaenopsectra sp. water mite diet isolate 12194-BHL040517-GBD27698_12003-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTAGTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTACACTAATCCAATTAGTTTCTTCTGCTGC---CGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12200 Oligochaeta sp. water mite diet isolate 12200-BHL040517-GBD23332_24006-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAAATTATCTCAACCAGGATCATTCCTAGGAAGAGTTCAACTTTATAATACTCTAGTAACTGCACAGGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCCTCACTAAACCTATTAGTTTCTTCTGGGGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL12201 Phaenopsectra sp. water mite diet isolate 12201-BHL040517-GBD16110_13472-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGTAATTGATTAGTACCACTAATATTAGGAGCCCCTGATATAGCATTTCCACGAATAAATAATATAAGTTTTTGACTATTACCACCATCTCTAACTTTACTTCTTTCAAGAACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR723136, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12202 Polypedilum sp. water mite diet isolate 12202-BHL040517-GBD14321_13584-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCGTGATCGGGAATAGTAGGAACTTCTCTTAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAAATTTAATTGGAGATGATCAAATTTATAATGTTATTGTAACAGCCCATGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGCTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID MG449714, identified in GenBank as Polypedilum sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12209 Phaenopsectra sp. water mite diet isolate 12209-BHL040517-GBD23497_23812-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCACCTGATATAGCATTTCCCCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTAACCGTACTTCTTTCAAGTACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR723136, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12210 Chironomus sp. water mite diet isolate 12210-BHL040517-GBD22090_27588-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGGGGCTTCATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCTGAATTAGGACGACCCGGGACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAAATGGAGGATTCGGAAACTGATTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCACGAATAAATAATATAAGTTTCTGACTGTTACCCCCCTTCTCTAACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12212 Chironomus sp. water mite diet isolate 12212-BHL040517-GBD13253_24058-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAGGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAAAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12213 Chironomus riparius water mite diet isolate 12213-BHL040517-GBD24199_22520-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGTTCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGTACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAACACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTACTGACTTTTACCCCCCTCTCTTACTCATCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12217 Chironomidae sp. water mite diet isolate 12217-BHL040517-GBD19868_7999-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCGTGATCGGGAATAGTAGGAACTTCTTTTAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAAATTTAATTGGAGATGATCAAATTTATAATGTTATTGTAACAGCCCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTAACTTGTCCCA-TAATACTTGGAGGACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR754220, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12219 Oligochaeta sp. water mite diet isolate 12219-BHL040517-GBD21512_11110-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTAGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTATCTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTTGGAAATTGACTTTTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACATTATAAGATTCTGACTACTACCCCCTTCATTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL12221 Chironomus sp. water mite diet isolate 12221-BHL040517-GBD26744_15814-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGGTTTTATTATAATTTTTCTCATAGTTATACCAATTTTAATTGGAGGGTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCCCGAAAAAAAAAAAATAAGCTTCTGAATTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12228 Phaenopsectra sp. water mite diet isolate 12228-BHL040517-GBD28206_9485-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTAGGGAGCATGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTATTACCCCC------ATCACTAATTCTAT-TAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12230 Phaenopsectra sp. water mite diet isolate 12230-BHL040517-GBD14923_17700-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAACTCGGCCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCATTAACTTTACTACTATCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12239 Chironomidae sp. water mite diet isolate 12239-BHL040517-GBD28939_15856-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACGTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCCTGTTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTAACTGCTCATGCATTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTATTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGATTTTGATTACTTCCTCCATCTCTATCCCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.7% identical to accession ID GU944724, identified in GenBank as Chironomus circumdatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12241 Lebertia sp. water mite diet isolate 12241-BHL040517-GBD11542_26900-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGATTTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTCTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTACACTAATAATCAGAGCCCAAGATATAGCTTTTCCACGAAAAAATAATATAAGATTATGACTTCTTCCTCCATCCTTAACACTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12248 Chironomus sp. water mite diet isolate 12248-BHL040517-GBD5097_12440-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTAGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGGTTTTATTATAATTTTTCTCATAGTTATACCAATTTTAAAATGGAGGCTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGCTTCTGACGTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12250 Lebertia sp. water mite diet isolate 12250-BHL040517-GBD17180_4142-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCATTTCCACGAATAATTAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTATTTCTATCAAGTTCCTTTACCGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12254 Chironomidae sp. water mite diet isolate 12254-BHL040517-GBD18118_8460-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTTGGAGCGTGATCGGGAATAGTAGGAACTTCTCTTAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAAATTTAATTGGAGATGATCAAATTTATAATGTTATTGTAACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGATATTGACTAGTGCCATTAATGTTAGGAGCACCTGATATGGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCATTCGTAGAAGATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR754220, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12255 Chironominae sp. water mite diet isolate 12255-BHL040517-GBD12513_6409-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGTCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTGTTTTATAGTTATACCTATTTTAATTGGAGG-TTTGGATATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12256 Culex pipiens water mite diet isolate 12256-BHL040517-GBD3323_14037-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCTTATATGGCCTTTCCTCGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACACTTCTACTTTCAAGTAGTTTAGTATAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.4% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12259 Chydorus sp. water mite diet isolate 12259-BHL040517-GBD21640_5621-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCATAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAACGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGACACCTGATATAGCCTTCCCTCGTCCTAATAATTTAAGTTTCTGGCTTCTTTCCCCCAGCTTTAACCCTACTTATAGTAGGGGGGGCAGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12261 Chydorus brevilabris water mite diet isolate 12261-BHL040517-GBD6011_23008-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTGGGGCTTGATCCGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCAAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTATGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.8% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12269 Phaenopsectra sp. water mite diet isolate 12269-BHL040517-GBD20854_16478-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTTGAGGATTCGGAAACTAACTTGT-CCCATAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1227 Chironomidae sp. water mite diet isolate 1227-BHL110116-GBD23025_26709-Lq44 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATCGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCGTTAACCTTACTTTTACCAAGATCACTAGTATAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12278 Oligochaeta sp. water mite diet isolate 12278-BHL040517-GBD26015_15507-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTATGAGTTTGAGCTGGAATAATTGGAACAGGAACCAGAATATTAATTCGGATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGAGATCAACTATATAGTACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 81.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL1228 Oligochaeta sp. water mite diet isolate 1228-BHL110116-GBD23784_9198-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTCTCCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL12283 Culex sp. water mite diet isolate 12283-BHL040517-GBD11749_10795-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAGGTCAACCAGGTGTATTTATTGGAAATGGTCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCAATTATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGACCTTTCCTCGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL1229 Chironomidae sp. water mite diet isolate 1229-BHL110116-GBD14681_27180-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCTTATACGTTAAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTTGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12295 Oligochaeta sp. water mite diet isolate 12295-BHL040517-GBD21688_24794-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATATTTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATATTATGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.2% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL1230 Dicrotendipes tritomus water mite diet isolate 1230-BHL110116-GBD13202_16094-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGG-ACAGGA	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12302 Psectrocladius sp. water mite diet isolate 12302-BHL040517-GBD8577_15214-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGAACAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.1% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12306 Chydorus sp. water mite diet isolate 12306-BHL040517-GBD24116_23339-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAATGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTTGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCCTTTGTTATAATCTTTTTTATAGTTATACCCATTTTAATTGGGGGGTATGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGACATAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12309 Phaenopsectra sp. water mite diet isolate 12309-BHL040517-GBD24411_24034-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGTTGAATTATGTCAACCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTATTACCCCCATCTCTAACTTTACTACTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1231 Chironominae sp. water mite diet isolate 1231-BHL110116-GBD23375_5449-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCCTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12310 Phaenopsectra sp. water mite diet isolate 12310-BHL040517-GBD21915_19318-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATACTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTTAGTAATACCTATTTTTAATTGTGGGATTTGGAAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCATTAACTTTACTACTATCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12315 Phaenopsectra sp. water mite diet isolate 12315-BHL040517-GBD22875_13078-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTTATTTTTGGGGCTTGATCCGAAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAGACTTAGGACGATCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATCATAATTTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KR274695, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12317 Chydoridae sp. water mite diet isolate 12317-BHL040517-GBD10067_16901-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTCGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCTTAATATTAGGGGCACATGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTAACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATC-GTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL1232 Chironomidae sp. water mite diet isolate 1232-BHL110116-GBD17484_27969-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCTACTAGAATTAGGACACCCAGCCTCATTAATCGGAGACGATCAAATTTATCATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGCGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12320 Phaenopsectra sp. water mite diet isolate 12320-BHL040517-GBD14579_12902-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTTTACTTTATTTTTTTGGAGCTTGATCAGGACTAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTCTTTGACTTTGACCCCCTTCTTTAACATTACATCAATCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12323 Chironominae sp. water mite diet isolate 12323-BHL040517-GBD21672_26345-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTCTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTTGGCCATCCGGGTACCTTTATTGGAGAAGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTAACTCTTCTTCTTTCAAGTTCAATTGTAGAAAGTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12325 Phaenopsectra sp. water mite diet isolate 12325-BHL040517-GBD20790_9019-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATACTTTATTTTTGGAGCTTGATCAGGAATAGTGGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGACACCCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCCTCTTTAACTTTACTTCTTTCTAGTTCGATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12327 Chydorus brevilabris water mite diet isolate 12327-BHL040517-GBD5919_6196-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTTTTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCGTTATTGGAGATGATCAAATTTACAATGTTATTGTCATTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGTGGGGTTTGGAAACTGACTCTTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1233 Lebertia quinquemaculosa water mite diet isolate 1233-BHL110116-GBD18986_4492-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATACTTCGCTTTTGGGGCTTGATCAGGAATGGTGGGAGCAAGACTAAGAACTTTAATCCGTTTAGAATTAGGACAACCAGGAACTCTCCTAGGAAGAGACCAAATTTATAATACTATCGTAACAGCGCACGCCTTCGTTATAATTTTCTTTATAGTTATGCCAATAATAATTGGAGGATTAAGAAATTGACTAGTCCCATTGATAATTAGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGACTTTTACCCCCCCTCTTTAACTCTCCTACTATCTAGTTCTTTCCCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID MG773261, identified in GenBank as Lebertia quinquemaculosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12336 Phaenopsectra sp. water mite diet isolate 12336-BHL040517-GBD9441_25190-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGTTCAGGAATAGTAGGAACTTCTTTAACTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTTATAGTTACTGCACATGGTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATCTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGTATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1234 Paratanytarsus sp. water mite diet isolate 1234-BHL110116-GBD13610_14718-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTTATTATACTTCATTTTTGGCGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAGCTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTCTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR289581, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12345 Chironomus sp. water mite diet isolate 12345-BHL040517-GBD11455_7316-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGGCTGATCCGGAATAGTGGGCACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTCATTGGAGATGACCAAATTTACAATGTTGTAGTTACTGCACATGGTTTTATTATAATTTTTCTCATAGTTATACCAATTTTAATTGGAGGGTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGCTTCTGACTTTTACCCCCGTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1235 Chironomidae sp. water mite diet isolate 1235-BHL110116-GBD19445_28139-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTTGGAGCTTGCTCGGGAATAGTAGTCACTTCTTTAAGAATTTTAATTCGACTAGACTTAGGACACCCAGGCTAATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGACTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12353 Chironomus sp. water mite diet isolate 12353-BHL040517-GBD6870_8778-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTTTATATTTTATTTTTGGTACTTGATCAGGAATAGTTGGAACTTCCCTTAGAATATTAATTCGAGCAGAACTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAAATTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTTCCTTTAATATTAGGAGCTCCAGATTTGGCCTTCCCATCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12357 Chydorus brevilabris water mite diet isolate 12357-BHL040517-GBD16810_24834-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAATAGGGACCCTTATTGGAGATGATCAAATTTAGAACGTTACTGTCACTGCACATGCTTTTGTTATAATCTTTTCTATAGTTATACCCATCATAATTGGTGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGAGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1236 Chironomidae sp. water mite diet isolate 1236-BHL110116-GBD27397_12767-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACAACCAGGCTCATTAATCGGAAACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAACAAATAATATAAGAATTTGATTATTACCCCCCTTCATTAACCTTACTTTTATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12365 Chironomus sp. water mite diet isolate 12365-BHL040517-GBD12614_21012-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTT-GGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.1% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12369 Lebertia sp. water mite diet isolate 12369-BHL040517-GBD9610_4168-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAAATCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCGTGCTTTCGTTATAATTTTCCTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTATTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCCTTCTTTATCTTTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1237 Chironomidae sp. water mite diet isolate 1237-BHL110116-GBD5224_14931-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCTGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTAGAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTGTGATATTATGGTGTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12370 Oligochaeta sp. water mite diet isolate 12370-BHL040517-GBD24315_17984-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGCGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGCATCATTCCTAGGAAGAGATCAACTATTTAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTTCTGGTTATACCAGTATTTATTGATGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATTCTGACTACTACCCCCTTTACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL12373 Diptera sp. water mite diet isolate 12373-BHL040517-GBD15269_21757-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTACATTATATTTTATTTTTGGAGCTTGATTAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATGGCATTCCCACGACTTAACAATATAAGATTTTGACTTCTACCACCTTCACTAACCCTACTGGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACTGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID JF966742, identified in GenBank as Anopheles claviger. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12376 Chironomidae sp. water mite diet isolate 12376-BHL040517-GBD7191_17693-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTAGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCACCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCATCATTAACCTTATTATCAACTAGAACACTAGCTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12379 Chironominae sp. water mite diet isolate 12379-BHL040517-GBD21457_10516-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTTTTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTTTACCTATTTTAATTGGAGGATTTGGAAATTGATTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAACAATATAAGATTTTGATTACTTCCACCATCTCTAACTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL1238 Chironomidae sp. water mite diet isolate 1238-BHL110116-GBD18421_15340-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGTCTCATTAATCGGAGACAATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATAGAAGATTTTGATTATTACCCCCGTCATTAACCTTGCTTTGATCAAGATCAAGAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12381 Chironominae sp. water mite diet isolate 12381-BHL040517-GBD11601_27027-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTTAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAACAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTTTTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTATTACTTTCAAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12384 Phaenopsectra sp. water mite diet isolate 12384-BHL040517-GBD9409_17973-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTATGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTATTTCGAGCTGAATTGGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCTTTTATTATATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCCTCTTTAACTTTACTACTATCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12385 Lebertia sp. water mite diet isolate 12385-BHL040517-GBD8584_8438-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTCTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTACTTCGACTTGGATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTTTAACTGCTCATGCTTTCGTTATAATTTTCTTCATAGTAATACCAATGATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12387 Oligochaeta sp. water mite diet isolate 12387-BHL040517-GBD22030_24545-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTTAACCAGGATCATTCCTGGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTATCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTATAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCATTAATCTTATTAGTTTCTTCTGCTGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL12390 Oligochaeta sp. water mite diet isolate 12390-BHL040517-GBD24122_16692-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATAGTTTATCTTAGGAGTTTGAGCTGGAATAATTGGTACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATTAACTATACAATACTCTAGTAACTGCACATGCATTCGTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGATGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL12395 Chironominae sp. water mite diet isolate 12395-BHL040517-GBD18532_2668-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACTGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTTTTTTACTTTCAAGTGCTACTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12398 Phaenopsectra sp. water mite diet isolate 12398-BHL040517-GBD26833_14431-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACATTATCCTTTATTTTTGGAGCTTAATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGTAATTGAATAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCGTCTTTAACTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR293527, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12400 Phaenopsectra sp. water mite diet isolate 12400-BHL040517-GBD25821_20988-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTACGTATATTAATTCGAGCTGAATTAGGTCACCAAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12406 Chironomidae sp. water mite diet isolate 12406-BHL040517-GBD5891_20847-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGAGCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATGGCCTTCCCACGACTTAACAATTTAAGATTTTGACTTCTACCACCTTCACTAATCCTACTGGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID KT104776, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12407 Chironomus riparius water mite diet isolate 12407-BHL040517-GBD12587_7296-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTGTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATTGTTATACCAA-TTTAATTGGAGGATTCGGAAACTAACTTGT-CCCCTGATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGAC-TTTATCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1241 Chironominae sp. water mite diet isolate 1241-BHL110116-GBD8669_23853-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTATGTATGCTGATTCGAGCAGAACGTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGCATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12412 Chironomus sp. water mite diet isolate 12412-BHL040517-GBD20849_8979-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGCATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTAACTTGT-CCCATAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCGCGCTTACACTACTGCTGTCTAGTGCTTGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12417 Chironomus riparius water mite diet isolate 12417-BHL040517-GBD11686_4770-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGCGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGAGTTGGAAACTGACTTGTCCCCCTAATACTTGGAACACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTCTTACCCCCCCTCTCTTACTCGTCTTCTGTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12420 Chydorus brevilabris water mite diet isolate 12420-BHL040517-GBD11774_5177-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAAAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATGTAGCCTCCCCTCGTCTTAATAATTGAAGTTTCTGGGTCCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGTGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12427 Oligochaeta sp. water mite diet isolate 12427-BHL040517-GBD3360_15151-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTTCTTAGTAATACCAATTTTCATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTA--TCT-TTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL12433 Oligochaeta sp. water mite diet isolate 12433-BHL040517-GBD26839_22673-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCATCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTAATAACAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGTACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTATAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 86.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL12436 Chironominae sp. water mite diet isolate 12436-BHL040517-GBD27041_9089-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTCTAAGTATGCTAATTCGAGTAGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGCAATTGTCACAACACATGCTTTTATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGATTTATTCCTTTAATGTTAGGACCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12438 Chironomus sp. water mite diet isolate 12438-BHL040517-GBD28116_15117-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGATGTCCTGGAACTTTTATTAGTGATGACCAAATTTATAATGTAGTAGTTATAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTAAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCTTTCCCTTGAATAAATAAAATAAGTTATTGACTTCTCCCCCCAATCTTTAACTCTT-ATCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 95.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12447 Phaenopsectra sp. water mite diet isolate 12447-BHL040517-GBD9633_27875-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGATCTTTAATTGGAGATGATTAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCATTAACTTTGCTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12448 Chironomus sp. water mite diet isolate 12448-BHL040517-GBD27760_19474-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAAAGTTATACATTATTTTTGGGGGCTTGATCCGGAATAGTGGGAACTTCATTAGGAATGCTTGTTCGAGTAGAGTTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGATACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAAGATTCGGAAACTGACTCGTCCCCCTAATACTTGGAGCACCTGACGTAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12451 Chironomus sp. water mite diet isolate 12451-BHL040517-GBD6485_25389-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGATCTTGGACGACCTGGTACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACATGT-CCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12453 Chironomus sp. water mite diet isolate 12453-BHL040517-GBD9945_26388-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTCTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTAACTTGT-CCCATAATACTTGGAGCACCTGACATAGCTTTTCTTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTGTCTTTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12460 Chironomus sp. water mite diet isolate 12460-BHL040517-GBD6605_16857-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTT-GGTGCTTGGTCAGGAATAGTAGGAACTTCCCTTGGAATATTAATTCGAACAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTAACTTGT-CCCATAATACTTGGAGCACCTGACATAGCTTTTCCTAGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12466 Phaenopsectra sp. water mite diet isolate 12466-BHL040517-GBD23838_18586-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTATACTATACTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCTGGTTCTTTAATTTGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGAAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCGTCTTTAACTTTACTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1247 Chironomidae sp. water mite diet isolate 1247-BHL110116-GBD22753_21124-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGAACTTCTTTATGAATTTTAATTCGACTAGAATTAGGACACCCAAGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGACTCCTGATATAGCATTTCCGCGAATAAAAAATATAAAATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12474 Oligochaeta sp. water mite diet isolate 12474-BHL040517-GBD7714_25383-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACCCTATACTTAATTTTAGGAGTTTGAGCCGGAATAATTGGAACCGGAACTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTCCTAGGGAGAGATCAGCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTTTAGTTATACCAGTATTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.1% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL12476 Chironomus sp. water mite diet isolate 12476-BHL040517-GBD7356_11797-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGAGGCTTGATCCGGAATAGTGGTAACTTCAATAAGATTACTTATTCGAGCATAATTAGGACAACCCGGAACTTTCATTGGAGGTGACCAAATTTATAATGTTGTAGTTACTGCACATGGTTTTAATACAATTTTTCTCATAGTTATACCAATTTTAATTGGAGGGTTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGCTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTATCTAGCTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12481 Lebertia sp. water mite diet isolate 12481-BHL040517-GBD17317_22005-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGCTCCGGTATAATTGGAGCTAGATTAAGAACCCTAATTCGACATGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATAAAGCCTTTCCACGAATAAATAAAATAAGATTTTGACTTCTTCCCCCATCCTTAACTCTGCTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12489 Phaenopsectra sp. water mite diet isolate 12489-BHL040517-GBD24680_8231-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATATTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTAAATTAGGTCACCCAGGAACTTTAATTGGGGATGATCAAATTTTTAATGTAATTGTAACTGCCCATGCATTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTATCCCCCTTTTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR723136, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12491 Chironomidae sp. water mite diet isolate 12491-BHL040517-GBD7730_23439-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTGTATATTTTATTTTTGGAGCTTGATCGGGAATAGTATGCACTTCTTTAAGAATTTTAATTCGACTATAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACATATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGCATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12492 Psectrocladius sp. water mite diet isolate 12492-BHL040517-GBD16311_4213-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCATGAGCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCTATTTTAGAATGTAATTGTTACAGCACACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTACTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12493 Chironomidae sp. water mite diet isolate 12493-BHL040517-GBD11826_28218-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGTTCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAACCGGAGACGATTAAATTTATAATGTAATTGTTACAGTACATGCTTTTGTAATAATTTTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAGTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12494 Chironominae sp. water mite diet isolate 12494-BHL040517-GBD22246_15415-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCTAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12495 Psectrocladius sp. water mite diet isolate 12495-BHL040517-GBD25857_10862-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAAAACTCGGTCACGCAGGTTCCTTACTTGGAGATGATCAACTTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGTAGGAATTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATATTATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12497 Chironomidae sp. water mite diet isolate 12497-BHL040517-GBD6718_21996-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTAGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATGATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12498 Chironomidae sp. water mite diet isolate 12498-BHL040517-GBD25735_21249-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTAGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGATACCCCGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATTCTTTTGTAATAATTTTTTTTAATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGACTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12499 Chironominae sp. water mite diet isolate 12499-BHL040517-GBD24993_21245-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACTACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGATGGTTTGGAAATTGATTAGTTCCTTTAATATCGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12500 Chironomidae sp. water mite diet isolate 12500-BHL040517-GBD25762_23327-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGGTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTCATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12502 Chironominae sp. water mite diet isolate 12502-BHL040517-GBD3014_20602-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTATTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACATCACACGCTTTTATTATATTTTTTTTTTTATAGTTATGCCAATTTTAATTGGATGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTTTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12503 Psectrocladius sp. water mite diet isolate 12503-BHL040517-GBD19023_27910-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAATAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACCATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATAACTATTTTAATTGGAGGGTTAGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCCCGAAAAAAAAATATAAGTTTTTGAATACTTCCCCCGTCATTAACTTTACTATTAATCTAACTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12504 Chironomidae sp. water mite diet isolate 12504-BHL040517-GBD19772_7387-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTGGGAAATTGATTAGTACCTTTGAGATTATGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGAATAAGATTATTACCCCCTGCATTAACCTTGCTTTAATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12505 Psectrocladius sp. water mite diet isolate 12505-BHL040517-GBD24854_17893-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTGGGTACATCTTTAAGAATTTTTATTTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCCTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAATTTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACTTTACTATTATCTAACACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12506 Psectrocladius sp. water mite diet isolate 12506-BHL040517-GBD15176_7979-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAAAATTTTAATTCGAGCAGAACTCTGTCACGCTGGTTCTTTCATCGGAAACGATCAACTTTATAATGTCATTGTTACCGCTCACGCTTTTTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTGATTACTTCCCCCCGTCACTAACTTTACTATTATCTAGCTCTGTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12508 Psectrocladius sp. water mite diet isolate 12508-BHL040517-GBD21111_25553-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTCATTGTTACCGCTCACGCCTTTGTAATAATTTTTTTATAGTGATACCTATTTTAAATGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCCCGAATAAAAAATATAAGTTTTTGATTACTTACCCCGTCATTAAATTTACTATTTATGTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12510 Psectrocladius sp. water mite diet isolate 12510-BHL040517-GBD13713_11593-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATGTAGCATTCCCTCGAATAAATAATATAAGTTTGTGATCACGTCCCCCGTCATTAACATTACTAAAATCTAGCGCTCTAGTTGAAGATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12512 Psectrocladius sp. water mite diet isolate 12512-BHL040517-GBD15808_18850-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGAAAAAGCATTTCCCCGAAAAAAAAAAAAAATTTTTGAATACTTCCCCCTGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12513 Psectrocladius sp. water mite diet isolate 12513-BHL040517-GBD17547_10953-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACATCTTTAAGAATTTTTATTTCGAGCAGAACTCGGTCACGCTGGATCTTTATTCGGAGTCGATCAAATTTTTAATGTAATTGTTACCGCTCACGCTTTTGTATTATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12514 Psectrocladius sp. water mite diet isolate 12514-BHL040517-GBD28706_12174-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCCCGCTGGTTCTTTAATCGGAAACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATAACTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGTGAGCCCCTGATATAGCATTCCCTCGAATAAATAAGATAAGGATTTGATTACTTCCCCCGTCATTAACTTTACTATTATCCAGCTCTATAGTTGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12515 Psectrocladius sp. water mite diet isolate 12515-BHL040517-GBD25869_16369-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATAAGGTATAGTAGGTACATATTTAAGAATTTTAATTCGAGCAGAACTCGGCCAATCTGGTTCCTTAATCGGAGACGATCGAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTATTATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTATTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTTAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12516 Chironominae sp. water mite diet isolate 12516-BHL040517-GBD6455_18836-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCGGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12518 Parachironomus sp. water mite diet isolate 12518-BHL040517-GBD16768_17927-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAACGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATTGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCACTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12519 Psectrocladius sp. water mite diet isolate 12519-BHL040517-GBD10572_19273-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACCCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTTTAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTACTTTAATATTGAGAGCCTCTGATATAGCATTCCCTCGAAAAAATAATATAAGGGTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACGCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12520 Chironominae sp. water mite diet isolate 12520-BHL040517-GBD19316_17829-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGATATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12521 Psectrocladius sp. water mite diet isolate 12521-BHL040517-GBD7951_13317-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATAAATTTTATAATGTAATGGTTACCGCTCACGCTTTTGTAATATTTTTTTTTATAGTGATACCTATATTAATTGGAGGGTTGGGAAATTGATAAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAAAAATATAAGTTTTTGATTACTTCCCCCGTCATAAACTTTACTATTATCTAACTCTCTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12522 Psectrocladius sp. water mite diet isolate 12522-BHL040517-GBD28986_17063-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTATTATAGTGATACCTATTTTATTGGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAGATAAAATAAGAGTTTGATTACTCCCCCCGTCATTAACTGTACTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12524 Chironomidae sp. water mite diet isolate 12524-BHL040517-GBD2643_17750-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAACTCGAGCAGAACTCGGTCACACTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12526 Cricotopus sp. water mite diet isolate 12526-BHL040517-GBD27910_11592-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGACTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12527 Chironomidae sp. water mite diet isolate 12527-BHL040517-GBD9291_16918-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCATGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAATTAGGGCACCCAGGAACATTGATTGGGGATGATCAAATTTACAATGTAATTGTAACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGTGGATTTGGAAATTGGCTTTTACCTTTAATACTTGGAGCCCCTGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCATCTATTTCATTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID KP043758, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1253 Oligochaeta sp. water mite diet isolate 1253-BHL110116-GBD5573_19694-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAGCAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.5% identical to accession ID LN810268, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL12530 Psectrocladius sp. water mite diet isolate 12530-BHL040517-GBD8290_17910-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGGGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAAATTTTTTTAATGATGATACCTATATTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGACATAGCATTCCCTCGAATAAACAATATAAGTTTTTGATTACTTCTCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12532 Chironomidae sp. water mite diet isolate 12532-BHL040517-GBD14307_18130-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATTCCTATTTTAATTGGTGGTTTTGGAAATTGGTAAGTACCTTTGTTATTAGTGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTAATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12533 Psectrocladius sp. water mite diet isolate 12533-BHL040517-GBD14975_2617-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCGAATTTATAATGTAATAGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTGCTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR288763, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12534 Chironomidae sp. water mite diet isolate 12534-BHL040517-GBD11618_8779-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAAGTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATGATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12538 Phaenopsectra sp. water mite diet isolate 12538-BHL040517-GBD6274_16499-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTAAATTAGGTCACCCAGGATCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCTCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTAACTTTACTTCTATCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12539 Psectrocladius sp. water mite diet isolate 12539-BHL040517-GBD16727_2213-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATAAGGAATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGATCACGCTGGTTCTTTAATCGGAGGCGCTCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTATAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACGTCCCCCGTCATTAACTTTTCTATTATCTAGCTCTCTAGTTGAAAGTGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12540 Chironomus riparius water mite diet isolate 12540-BHL040517-GBD24731_17542-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGTACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATATTTTTTTTCGTAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12541 Psectrocladius sp. water mite diet isolate 12541-BHL040517-GBD19301_19825-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCTCGTTAATATTAGGAGCCCCCAACATAGCATTCCCTCGAATAAAAAATATAAGGATTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12542 Paratanytarsus sp. water mite diet isolate 12542-BHL040517-GBD21713_22826-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTGCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCGCACTCTTTAACTCTTTTACTATCTAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12543 Psectrocladius sp. water mite diet isolate 12543-BHL040517-GBD10536_12792-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCATGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGGTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGAAAAAACCATCCCCTC-AAAAAAAAATAAAAGTTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12545 Psectrocladius sp. water mite diet isolate 12545-BHL040517-GBD10538_13876-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGATTCTTTAATCTGAGACGATCAAATTTATAATGCAATTGTTACCGCTCACGACTTTTGTAATACTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGGTTTTGATTACTTCCCCCGTCATTAACTTAACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12546 Psectrocladius sp. water mite diet isolate 12546-BHL040517-GBD11078_17174-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCCTGATCAGGAATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTATGTCACGCTGGTTCTTTAATAGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCCCCAATAAATAATATAAGTATTTGATCACTTCCCCCGTCATTAACTTTACTTTTATCTAGCTCTCTAGTTGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12547 Psectrocladius sp. water mite diet isolate 12547-BHL040517-GBD20095_22494-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCAAGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTAATATAGGGAGCCCCTGATATAGCATTCCCTCAAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12548 Psectrocladius sp. water mite diet isolate 12548-BHL040517-GBD18664_27106-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGTCTGATCAGGTATAGTAGGTACATCTTTTAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATCATTTTTTTTTATAGTGATACCTATTTTAATTGGAAGGTTTGGAAATTGATTAGTTCCTTTAATATTGTGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTATTGATTACTTCCCCCATCATTAACTTGACTATTATCTAGCTCTCTAGTTGCAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12549 Psectrocladius sp. water mite diet isolate 12549-BHL040517-GBD18726_12684-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCCTGATCAGCTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACAATCAAATTTATAATGTAATTGTTTCCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGAAGCCCCTGATATAACATGCCCCTCGAATAAATAATATAAGGTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1255 Chironomidae sp. water mite diet isolate 1255-BHL110116-GBD12349_15731-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCACATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTTATTGGAAGCTTTTGGAAATTGATTATTACCTTTAATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTACTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12552 Psectrocladius sp. water mite diet isolate 12552-BHL040517-GBD24290_25467-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTTGGAGTTTGATAAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGTTTCTTTAATCGTACACGATCAAATTTATAATGTAATTGTTACCGCTCCCGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTCATTAGTTCCTTTATTATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12554 Psectrocladius sp. water mite diet isolate 12554-BHL040517-GBD19542_2941-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAACTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12556 Chironomidae sp. water mite diet isolate 12556-BHL040517-GBD21383_19133-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTCGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCATTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCATCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12557 Psectrocladius sp. water mite diet isolate 12557-BHL040517-GBD27941_19805-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGCAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCTCGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGTAGCCCCTGATATAGCATTCCCTCGAATAAATAAGATAAGTTTTTGATGACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTTAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL1256 Oligochaeta sp. water mite diet isolate 1256-BHL110116-GBD6602_11552-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGAAAAGCCTTTCCCACGACTAAATAAATAAAGATTCTGACTACTACCACCACCTCTACTCTTCCTAATTTCTTCTGAAGCAGTAAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL12560 Psectrocladius sp. water mite diet isolate 12560-BHL040517-GBD27963_11723-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGTTCACGCCGGTTCTTTAATAGGAGACGATAAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATCATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTGGGAAATTGATTAGTACCTTTAATATTGGGAGCCCCATGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGGCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12562 Psectrocladius sp. water mite diet isolate 12562-BHL040517-GBD14477_11794-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGCACTCGGTCACGCTGGTTCTTTAATCGGAGCCGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAAAAAAAGTTATTGATTACGTCCCCCGTCAGTAACTTTACAATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12564 Psectrocladius sp. water mite diet isolate 12564-BHL040517-GBD14406_3699-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGTTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTCATTGGAGGGTTTGGAAATTGATTTGTTCCTTTCATATTGGGAGCCCCATGATATAGCATTCCCTCGACTAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTCACTCTCTAGTTGAAAATGGCGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12565 Chironomidae sp. water mite diet isolate 12565-BHL040517-GBD21349_9566-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGTCTGATCAGGTATAGTAGATACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATAAAGCATCCCCAAAAAAAAAAAAATAATTTTTTAATTCCCCCCCCCGCCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12566 Psectrocladius sp. water mite diet isolate 12566-BHL040517-GBD19286_5557-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGTACATCTTTAAGAATTTTAATTTGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTACTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCAAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCTTTAACTTTACTATCATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12567 Chironomidae sp. water mite diet isolate 12567-BHL040517-GBD13190_17948-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GACACTTTACTTTATTTTTGGAGCTTGATCCGGAATAGTAGGAACATCTTTAAGAATATTAATTCGAGCAGAATTAGGGCACCCAGGAACGTTGATTGGGGATGATCAAATTTACAATGTAATTGTAACAGCCCATGCCTTTATTACAAATTTTTTTATAGTTATACCATTTTTAATTGGTGGATTTGGAAATTGGCTTTTACCTTTAATACTTGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTATACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.3% identical to accession ID KP043758, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12572 Psectrocladius sp. water mite diet isolate 12572-BHL040517-GBD28494_19402-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGGTCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATTAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTAGAAATTGATTAGTTCCCTTAATATTGGGAGCCCCTGATATATCATTCCCTTGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCTTTAACTTTACTATTATATAGCTATCTAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12573 Psectrocladius sp. water mite diet isolate 12573-BHL040517-GBD18948_14831-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACCCGGTCACGCTGGTTCTTTAATCGGAGACGGTCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTACTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAAAAATAAAAGTTATTGAATACTTCCCCCGTCATTAACATTACTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12574 Psectrocladius sp. water mite diet isolate 12574-BHL040517-GBD25844_15413-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGTAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGATCAAGCTGGTTATTTAATCGGAGACGGTCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTTCTTTAATATTGGGAGCACCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12575 Psectrocladius sp. water mite diet isolate 12575-BHL040517-GBD10116_26783-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGGATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGATTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTAACGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATTCCTATTTTAATTGAATGGTTTGGAAATTAATTAGTTCCTTTAAAATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12576 Psectrocladius sp. water mite diet isolate 12576-BHL040517-GBD18888_25643-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAGTTTTAATTCGAGCAGAATTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGACCCCCTGATATAGCATTCCCGCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGATCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12577 Psectrocladius sp. water mite diet isolate 12577-BHL040517-GBD24860_13397-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCATGATCAGGAATAGTAGGAACATCTTTAAGAATTTTAATTCGAGTAGAACTCGGTCACGCTGGTTCTTTAATAGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTTTAATAATTTTTTTTCTAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCATGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCGTCATTAACTTTACTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12578 Psectrocladius sp. water mite diet isolate 12578-BHL040517-GBD22313_19076-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAACTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTCCCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGTCCCTGATATAGCATTCCCTCTAATAAATAATATAAGCTGTTGATTACTTCCTCCGTCATTAACTTTACGATTATCTAGCACGCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12579 Chironomidae sp. water mite diet isolate 12579-BHL040517-GBD29356_17869-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTGATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCAGGAACGGGACGAGGAGCGAGCGCGCGAGGGGAAAAGGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12580 Psectrocladius sp. water mite diet isolate 12580-BHL040517-GBD10518_9923-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCTGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAGCTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTTGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACCTTACTATCATCTAGAACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12583 Psectrocladius sp. water mite diet isolate 12583-BHL040517-GBD11104_27076-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGTTACTTATTTTAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCCTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAAATGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAATTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12587 Psectrocladius sp. water mite diet isolate 12587-BHL040517-GBD15890_25310-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGTAGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTACATTGATACCTATTTTAATTGTAGGGTTTGGAAATTGATTAGTTCCTTTAATATTTGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACGTCCCCCGTCATTAACATTACTATTATCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12588 Psectrocladius sp. water mite diet isolate 12588-BHL040517-GBD25996_17377-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGACACGCTGGTTCTTTAATCGGTGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12590 Psectrocladius sp. water mite diet isolate 12590-BHL040517-GBD23440_23045-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTATGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGAGACATATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGAGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGGGTTTGATTACTTCCCCCGTCATTAACTTAACTATTATCTAGCACTCGAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12592 Psectrocladius sp. water mite diet isolate 12592-BHL040517-GBD7450_14668-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTATGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGACCAAATTTATAATGTAATTGTTACCTCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCTGTTAATATTGGGAGCTCCTGATATAGCAGTCCCTCGAATAAACAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAACTCTCTAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12593 Chironomidae sp. water mite diet isolate 12593-BHL040517-GBD13217_18079-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTAGATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTTGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12594 Psectrocladius sp. water mite diet isolate 12594-BHL040517-GBD21657_14941-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCATTAGTCGGAAACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTTTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGATATTGATTAGTTCCTTTAATATTGGGAGCTCCATGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCATTAACTTTACTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12598 Chironomidae sp. water mite diet isolate 12598-BHL040517-GBD17034_14134-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGTGGATTTGGAAATTGGCTTTTACCTTTAATACTTGGAGCCCCTGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCATCTATTTCATTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.3% identical to accession ID KP043758, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1260 Chironomidae sp. water mite diet isolate 1260-BHL110116-GBD19459_15568-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATGGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAGTCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATCATTACCCCCTTCATTAACCTTACATTAATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12601 Psectrocladius sp. water mite diet isolate 12601-BHL040517-GBD22455_15479-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCGTTTATTGGTGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCATCATTAACTTTACTATTATCTAGCACACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12603 Psectrocladius sp. water mite diet isolate 12603-BHL040517-GBD9744_22932-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTTAATATTGGGAGCCCCTGAAATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCGTCATTAACGTTACTATAAGCTAGCTCACTAGCGGAAAATGGAGCTGGAAAAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12604 Psectrocladius sp. water mite diet isolate 12604-BHL040517-GBD7556_8810-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGTAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATGCCTAATTTAATTGGAAGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAACCCCTGAAATATCAATCCCTCGAAAAAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTAATATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12605 Psectrocladius sp. water mite diet isolate 12605-BHL040517-GBD4178_16561-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCATGCTGATTCTTTAATCGGATACGATCAATTTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTACTTTAATATTGGGAGCCCCTGATACAGCATTCCCTCGAATAAATAATATAAGGGTTTGATTACTTCCCCCGTCATTAACTTTACCATTATCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12609 Psectrocladius sp. water mite diet isolate 12609-BHL040517-GBD6422_9820-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTGTTGGAGCCTGATCAGGTATAGTAGGAACATCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTACAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTAATAGTGATCCCTATTTTAATTGGAGGTTTTGGAAATTGATAAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGCTCTCTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12610 Psectrocladius sp. water mite diet isolate 12610-BHL040517-GBD25829_20697-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTGTATTTTATTTTTGGAGCCTGATCAGGTGTAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAAGTTATAATGTAATTGTTACCGCTCACGCTTTTGTTATAATTTTTTTTATAGTGATACCTATTTTAATTTGAGGGTTTGAAAATGGATTAGTTCCTTTAATATTGGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTATTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12611 Psectrocladius sp. water mite diet isolate 12611-BHL040517-GBD23524_10582-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGGGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATAAAGCATTCCCTCGAACAAAAAAAATAAATATTTGATTTCTTCCCCCGTCATTAACTTTACTAATATCTAGCTCTCTAGTTGGAAAATCGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12612 Psectrocladius sp. water mite diet isolate 12612-BHL040517-GBD16888_20797-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTATTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTATAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCCCGAATAAATAACATAAGTCTTTGATTACTTCCCCCGTCATTAACCTTACTACTATCTAGCACACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12614 Psectrocladius sp. water mite diet isolate 12614-BHL040517-GBD4956_12905-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATGCCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATGGCATTCCCTCGAATAAATAATATAAGGTTTTGAATACTACCCCCGTCATTAACTTTACTATTAGCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12615 Chironominae sp. water mite diet isolate 12615-BHL040517-GBD16295_22135-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGTCGACCTGGTACTTTTATTGGAGATGATCAAATTTACATTGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCATTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12618 Psectrocladius sp. water mite diet isolate 12618-BHL040517-GBD6098_12603-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTGTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGTTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAGTGTAATTGTTACCGCTCAAGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGAATAGTTCCTTTAATATTGGGAGCCCCTTAATATAGCATTCCCTCGCATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACATTACTATTATCTAGCTCTCTAGTTTAAAATCGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12622 Psectrocladius sp. water mite diet isolate 12622-BHL040517-GBD2173_16294-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGATCACGCTGGTTCTTTAATCGGAGACGATCAAGTTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGAGTAGTTCCTTTAATATTGAGAAGCCCTGATATAGCATTTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12623 Chironominae sp. water mite diet isolate 12623-BHL040517-GBD29230_18980-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGACATTGACTTTTTCCTTTAATGTTAGGAGCCCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12631 Chironomidae sp. water mite diet isolate 12631-BHL040517-GBD4371_10864-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTCTATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCTGGCTCATTACTCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTGATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGTCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTGATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12632 Lebertia sp. water mite diet isolate 12632-BHL040517-GBD12247_15532-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAGTTGGAGCTAGATTAAGAACCTTAATTCGACTTGAAATAGGACAACCAGGCTCACTCCTAGGAAGTAACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACACTGCTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12633 Psectrocladius sp. water mite diet isolate 12633-BHL040517-GBD29430_16413-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATAAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCAGTGACGGGACGAGTAGCTAACTCTCTAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12636 Oligochaeta sp. water mite diet isolate 12636-BHL040517-GBD10049_21593-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAACTGGAACAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTTCTAATAATTTTCTTTCTAGTTATACCAGTATTTATGTGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCCCCTTCTCTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL12643 Chironomidae sp. water mite diet isolate 12643-BHL040517-GBD8706_15988-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGATCATTAATCGGAGACGATCAGATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAATACCTTTGATATTATGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12647 Psectrocladius sp. water mite diet isolate 12647-BHL040517-GBD18824_16532-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTTATTCGAGCTGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATATTTTTTTTTATAGTGATTCCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCCTTAATATTGGGAGCCCCATGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGAATACTACCCCCGTCATTAACTTTACCATTATCTAGCACGCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12648 Psectrocladius sp. water mite diet isolate 12648-BHL040517-GBD27245_20541-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTTACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACGGCTCACGCTTTTGTAATAATTTTTTTTATAGCGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATCCCCTCGAATAAATAAGATAAGTTTTTGAGTACTCCCCCCGTCATTAAACTTTACTATAATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12649 Psectrocladius sp. water mite diet isolate 12649-BHL040517-GBD21992_5297-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGTGCCTGATAAGGTATAGTAGGTACATCTTTAAGATTTTTACTTCGAGCGGAACTCGGTGACGCTGTTTCTTTATTCGGAGACGATCAAATTTATAATGTAATTGTTATCGCTTACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1265 Chironomidae sp. water mite diet isolate 1265-BHL110116-GBD22834_10427-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTTATTGTTACAGCACATGCTTTTGTAATAAATTTTTTTATAGTGATACCCATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTTATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCCTTCACTAACCTTACTTTTATCAAGATCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12650 Psectrocladius sp. water mite diet isolate 12650-BHL040517-GBD10332_23012-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGTATAACTCGGTCACGCTGATTCTTTAATCGGAGACGATCAAATTTATTATTTAATTGTTACCGCTCACTCTTTTGTAATAATTTTTTTTATAGTGATATCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTTCATTAACTTTACTATTATCTAGCGCCCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12653 Psectrocladius sp. water mite diet isolate 12653-BHL040517-GBD22238_21137-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTAAATTCGAGCAGAACTCGGTCATGCTGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACTTTACTATTATCAAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12655 Psectrocladius sp. water mite diet isolate 12655-BHL040517-GBD13400_1990-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCATGCTGGTTCTTTAATCGGGGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTCATGATTTTTTTTATAGTGATACCTTTTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12659 Psectrocladius sp. water mite diet isolate 12659-BHL040517-GBD13280_13075-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGTACATCTTTAAGTATTTTTATTTCGAACAGAATTCGGCCACGCTGGTTCTTTAATCGGAGACGATCAATTTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGTGGGTTTGGGAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12661 Psectrocladius sp. water mite diet isolate 12661-BHL040517-GBD20118_9790-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAGTTTTTATTTTCTTTTTGGAGCCTGATCCGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATACAAGTTTTTGATCACGGCCCCCGTCATTAACATTACAAAAAGCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12668 Chironomidae sp. water mite diet isolate 12668-BHL040517-GBD14922_15541-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAACTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTATTTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGTGAGCCCCTGATATACCATCCCCTAAAAAAAAAAATAAAAGTTTTTGATCCCCCCCCCCGCCATTAACTTTACTATAATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12672 Psectrocladius sp. water mite diet isolate 12672-BHL040517-GBD11446_13057-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTCGGAGCCTGATCAGGTATAGTAGGAACTTCTTTAAGAATTCTAATTCGAGCAGAACTAGGACATGCTGGCTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCTCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR761745, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12673 Psectrocladius sp. water mite diet isolate 12673-BHL040517-GBD21626_10821-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTATGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATAAGTGCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12676 Psectrocladius sp. water mite diet isolate 12676-BHL040517-GBD25267_22679-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTGTATATTTTATTGTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTAGAGCAGAACTCGGTCACGCTTGTTCTTTAATAGGAGACGATCAAACTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGAGAGCCACTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1268 Chironomidae sp. water mite diet isolate 1268-BHL110116-GBD24402_17576-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATCTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTTATTCGACTAGAATTAGGACACCCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAACTTTTCCGCGAATAAAAAGTATAAGATTTTGATTATTACCCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12686 Psectrocladius sp. water mite diet isolate 12686-BHL040517-GBD11398_4933-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACCCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTGATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCAAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12691 Psectrocladius sp. water mite diet isolate 12691-BHL040517-GBD9767_14315-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCTTGTTCAGGAATAGTAGGTACTTCTTTAAGATTTTTAATTCGAGCAGAACTCGGTCACGTTGTTTCTTTAATTGGAGCCGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTAAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12700 Psectrocladius sp. water mite diet isolate 12700-BHL040517-GBD15904_28845-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAACTCGGTCACTCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTGATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACTCTAGGTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12702 Chironominae sp. water mite diet isolate 12702-BHL040517-GBD17881_12242-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAATTTGGACGACCTGGTACTTTTATTGGAGATGACCAACTTTACAATGTACTTGTTACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTGTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12704 Psectrocladius sp. water mite diet isolate 12704-BHL040517-GBD16543_2689-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGTTACTGTCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAAGAATTTTTTTTATAGAGATACCTATTTTAATTGTAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCCTTCCCCCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12711 Orthocladius sp. water mite diet isolate 12711-BHL040517-GBD13275_17490-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCTGAATTCGGACATGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTTATAGCTCATGCTTTTGTTATAATTTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATAGTAGAAAATGGAGCTGGAACGGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1272 Chironominae sp. water mite diet isolate 1272-BHL110116-GBD25926_5951-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATGGTAGGGACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCATGGATCTTTTATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTACTTTCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR754526, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12721 Chironominae sp. water mite diet isolate 12721-BHL040517-GBD15102_16341-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTTGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGTACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTGTTTGACTTCTTCCCCCTTCATTAACTCTTGGACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12725 Psectrocladius sp. water mite diet isolate 12725-BHL040517-GBD9838_25302-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGATCTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCTCTCACGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTAATGGATTACGTCCCCCGTCATTAACATTACTATTAGCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12728 Psectrocladius sp. water mite diet isolate 12728-BHL040517-GBD22127_26043-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGTTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTATTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGTAGCCCCTGTTATAGCATTCCCTCGCATAAATACTATAAGTATTTGATTGCTTCCCCAGTCATTAACTTTACTATTATCTAGCTCTCTAGCTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12733 Psectrocladius sp. water mite diet isolate 12733-BHL040517-GBD24099_17529-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTAATCAGATATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGCTCACACTGGTTCTTTAATCTGAGACGATCAAATTTATATTGTTATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTCATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12737 Psectrocladius sp. water mite diet isolate 12737-BHL040517-GBD15847_26512-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACCTCTTTTAGAATTTTAATTCGAGCAGAATTCGGTCATGCTGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTCTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACAATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12741 Psectrocladius sp. water mite diet isolate 12741-BHL040517-GBD12119_12795-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCCGGTATAGTAGGTACTTCTTTAAGAATTTTTATTTCGAGCAGATCTCGGTCACGCTGCTTCTTTAATCGGAGACGATCAAATTTATAATGTATTTGTTACCGCTCACGCTTTTGTAATAATTTTTCTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAACATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATCATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12744 Psectrocladius sp. water mite diet isolate 12744-BHL040517-GBD21859_22957-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGGATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTACTCGGAGAAGATCAAATTTATAATGTAATTGTTACCCCTCACGCGTTTGTAATAATTTTTTTTATAATGATACCTATTTTAATTGGAGGGTTTGGAATTTGATTAGTTCCTTTAATATTGCGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTAATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAATAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12745 Psectrocladius sp. water mite diet isolate 12745-BHL040517-GBD26757_18605-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCATGATCAGGTATAGTAGGGACATATTTAAGAATTTTAATTCGAGCAGAACTCGGTAACGCTGGTTCTTTAATCGGAGACGATCAAATTTATACTGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAAGTGATAAGTTCAGTTAATATTGGGAGCCCCATGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATAATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12748 Psectrocladius sp. water mite diet isolate 12748-BHL040517-GBD16942_28273-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTGTATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAATTAGGTCACGCTGGTTCTTTAATCGGAGAAGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTTATAAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACATTACTATTATCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12754 Psectrocladius sp. water mite diet isolate 12754-BHL040517-GBD5290_15008-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACCTCTTTAAGAATTTTAATTCGAGCAGATCTCGGGCACGCTGGTTCTTTAATCGGAGAAGAACAAATTTATTGTGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTTCTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12755 Chironomidae sp. water mite diet isolate 12755-BHL040517-GBD3267_20632-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATCTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAAGTCGACTAGAATTAGGACAACCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCATATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGACTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTTCTTTTATCAAGATCAATAGTATAAAATGGCGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12756 Psectrocladius sp. water mite diet isolate 12756-BHL040517-GBD19172_10698-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACACTGGTTCTTTCATCGGAGACGATCAAATTTATAATGTAAATGTTACCGCTCACGCCTTTGTAATAATTTTTTTTATAGTGATACCAGTTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAACATTGGGAGCCCCAGATATAGCATCCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12761 Psectrocladius sp. water mite diet isolate 12761-BHL040517-GBD8705_25329-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGTAGAACTTTGTCACGCTGGATCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTATTGTAATAATTTTTTTTAAAGTGATACCTATTTTAATTGGAGGGTTTGGAAAATGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCCAGAATAAATAATATAAGTTTTTGATTACTTGCCCCGTCATTAACTCTACTATTATCTAGCTCTCTAGTTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12764 Chironomidae sp. water mite diet isolate 12764-BHL040517-GBD11543_5525-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATCTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGTAGATGATCAAATTTATAATGTAATTGTTACATCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGTCTCCTGATATAGCTTTGCCGCGAATAAATAATATAAGGTTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12766 Psectrocladius sp. water mite diet isolate 12766-BHL040517-GBD18817_27753-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGGCGACCAATTTTATAATTAAATTGTTACCGCTCACGCTTTTTTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGTTTGGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAACTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12769 Chironominae sp. water mite diet isolate 12769-BHL040517-GBD11852_13122-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGTTACTTTTATTGGAGATGACCAAATTTACAATGTGATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCATTTTTAATTGGAGGTTTTGGAAATCGGCTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCACTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGATGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12771 Psectrocladius sp. water mite diet isolate 12771-BHL040517-GBD23395_8086-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAACCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCATGCTGGTTCTTTAATCGGAGAAGATTAAATTTATAATGTAATTGCTACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12778 Psectrocladius sp. water mite diet isolate 12778-BHL040517-GBD11118_8665-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGCACATCTTTAAGAATTTTAATTCGAGCATAACTCGGTCATGCTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTACTACCCCCGTCATTAACATTACTATTATCTAGCTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1278 Chironominae sp. water mite diet isolate 1278-BHL110116-GBD8053_8560-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGTTGGATTTGGCAATTGATTAGTTTCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGCATAAATAATATGAGATTTTCATTACTTCCCCCTTCTTTAACTCTTCTTCTCTCTAGCTCACTTGTAGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR754526, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12780 Psectrocladius sp. water mite diet isolate 12780-BHL040517-GBD18262_5014-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTATATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATGCGAGCAGAACTCGGTCACGCTTGTTCTTTAATCGGAGACGATCAAATTTCGAATGTAATTGTTACCGCGCACGCTTTTGTAAGAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTCATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12782 Psectrocladius sp. water mite diet isolate 12782-BHL040517-GBD25271_9252-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCCAATTTATAATGTAATTGTTATCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATTCCTGTTTTAATTGGAGGGGGTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACGTCCCCCGTCATAAACTTTACTATGATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12788 Chironomidae sp. water mite diet isolate 12788-BHL040517-GBD20455_14401-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGTTCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTAAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAACCTTTCCGCGAATAAATAATATAAGATTTTGATTATTATCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12790 Orthocladiinae sp. water mite diet isolate 12790-BHL040517-GBD20386_21821-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCTATTTCATTACTTCTT---TCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KR725429, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12791 Psectrocladius sp. water mite diet isolate 12791-BHL040517-GBD29163_15437-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGTCTGATCAGGTATAGCAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGAACAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTAACTATAAGCTAACGCTCTAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12792 Psectrocladius sp. water mite diet isolate 12792-BHL040517-GBD15493_5740-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGAACAGGCAGAGTAGGGACATCTTTAAGAATTTTAATGCGAGCAGAACTCGGTCACTCTGTTTCTTTAATCGGAGACGATCAAATTTAGAATGTAATTGTTACCTCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTATCTTTACTATTATCTAGCTCTCTAGTTGAAAATGGCGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12800 Chironominae sp. water mite diet isolate 12800-BHL040517-GBD21817_3632-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAAAACTTTGACGACCTGGTTCTTTTATTGGAGATGACCAAATTTACAATGTCATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTATAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12812 Parachironomus sp. water mite diet isolate 12812-BHL040517-GBD11490_11692-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATTAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGTGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCTTTAACTCTTTTACTATCTAATTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12818 Psectrocladius sp. water mite diet isolate 12818-BHL040517-GBD14686_15084-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATCTTTTATTTCTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGAAGATCAAATTTATAATGTAATTGTTACCGATCACTCTTTTGTAATGATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGTGAGCCCCTGATATAGCATTCCCTCTAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCGCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12821 Psectrocladius sp. water mite diet isolate 12821-BHL040517-GBD27328_10962-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTAATCAGGAATAGTAGGAATATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGAGGATCAAATTTATAATGTTATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12823 Psectrocladius sp. water mite diet isolate 12823-BHL040517-GBD27282_16658-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGCTAAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCGTTAATCGGAGCCGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAAAAATATAAGTTATTGATTACGTCCGCCGTCATTAACGTTACTATTATCTAGCGCTCGAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12825 Psectrocladius sp. water mite diet isolate 12825-BHL040517-GBD7889_24862-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCCTTAAGTATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGGTCATGCTTTTGTTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCATCATTAACTTTACTATTATCGAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12826 Psectrocladius sp. water mite diet isolate 12826-BHL040517-GBD27194_16428-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCATGAGCAGGTATAGTAGGTACATATTTAAGAATTTTAATTCGAACAGAACTCGGTCACGCTGGTTCTTTAATCGGAAACGATCAAATTTATAATGTAATTGTTACCGCTCACGCATTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAATCTGATTAGTTCCTTTAATATTTGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR751697, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12832 Psectrocladius sp. water mite diet isolate 12832-BHL040517-GBD8770_7917-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCCGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGTGCAGAACTCGGGCACCCTGGTTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAACATAAGTTTTTGATTACTTCCCCCGTCAATAACTTTACTAGTATCTAGATCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12833 Psectrocladius sp. water mite diet isolate 12833-BHL040517-GBD4164_15038-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGTGCCTGATCTGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGACACGCTGGTTCTTTAATTGGAGATGATCAAATTTATAATGTTATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTTTTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAACTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12835 Psectrocladius sp. water mite diet isolate 12835-BHL040517-GBD25384_18067-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCAAGCTGGTTCTTTAATCGGAAACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCATTAACCTTACTAATATCAAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12836 Chironominae sp. water mite diet isolate 12836-BHL040517-GBD23717_18239-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTCGGTACTTCTTTAAGTATGCTAATTCGAGTAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGACTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTACTATCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12838 Psectrocladius sp. water mite diet isolate 12838-BHL040517-GBD13633_14536-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTTATATTGGGAGCCCCTGGTATAGCAATTCCCCGGAAT-AATAATAATAATTTTTGAATACCTCCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12841 Psectrocladius sp. water mite diet isolate 12841-BHL040517-GBD11310_25462-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCATTAATCGGAGACGATCAAATTTAAAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCATTAACTTTACTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12849 Paratanytarsus sp. water mite diet isolate 12849-BHL040517-GBD28130_19300-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAACTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATATCTATTTTAATTGGAGGATTTGGGAACTGATTATTGACTTTAATATTAGGAGTCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTAACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12852 Psectrocladius sp. water mite diet isolate 12852-BHL040517-GBD8682_14840-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCATAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGAGACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGTGAGCCCCTGATACAGCATTCCCTCGAATAAATAATATAAGTGTTTGATTACTCCCCCCGTCAGTAACTTTGCTATTATCTAGCACGCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12853 Psectrocladius sp. water mite diet isolate 12853-BHL040517-GBD6515_6195-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTAGTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCAGTCCCTCGAATAAATAATATAAGGGTTTGATTACTTCCCCCGTCAGTAACTTTACTATTAGCGAGCTCGCGAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12854 Psectrocladius sp. water mite diet isolate 12854-BHL040517-GBD22150_25361-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGATTACTTAAATGGAGATGATCCAATTTATAATGTAATTGTTACCGCTCACGCTTTTTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAAAAATATAAGTTATAGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12861 Psectrocladius sp. water mite diet isolate 12861-BHL040517-GBD18669_10508-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACCTCTTTAAGAATTTTAATTCGAGCAGAACTCGGGCACGCTGGTTCTTTAATCGGAAACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCAGTTATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTGCCCCGTCATTAACATTACTATTATCAAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12866 Chironomidae sp. water mite diet isolate 12866-BHL040517-GBD25330_23400-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCATTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAATTTTATAATGTAATTGTTACAGCACATGCTTTTATAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTATTACCCCCTTAATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12871 Psectrocladius sp. water mite diet isolate 12871-BHL040517-GBD26814_8810-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTGTATATTTTATTTTTGGAGCCTGATAAGCTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTATTCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTTGAGGGTTTGGAAACTGATTAGTTCCTTTAAGATTGTGCGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATGATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR751697, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12874 Psectrocladius sp. water mite diet isolate 12874-BHL040517-GBD17385_19491-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATGAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGTTTCTTTAATCGGAGACGATCAAATTTATAATGTCATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGATGTTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTGCCCCCGTCATTAACTTTACTATTATCTAGCTCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12875 Chironomidae sp. water mite diet isolate 12875-BHL040517-GBD15118_29045-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCATTAACTTTACTATAATCGAGCTCTCTAGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12879 Psectrocladius sp. water mite diet isolate 12879-BHL040517-GBD24644_8622-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATAATTTATTTTTGGAGCCTGAACAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTAAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTTAAATAACATTCCCCCCAATAAATAAAAAAAGGTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12883 Psectrocladius sp. water mite diet isolate 12883-BHL040517-GBD3370_9884-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGAATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCACGCTGGATCCTTACTCGGAGACTATCAAATTTATAATTTAATTGTTACCGTTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTAATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12888 Chironominae sp. water mite diet isolate 12888-BHL040517-GBD26121_6896-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGTTAATTCGAGCAGAACTCGGACGACCTGGTTCTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCATTAACTCTATTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12891 Psectrocladius sp. water mite diet isolate 12891-BHL040517-GBD11337_24752-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACATCTTTAGGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATCATCTAGCACACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1290 Chironominae sp. water mite diet isolate 1290-BHL110116-GBD15379_19908-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTTGGGACATCACTTAGTATATTAATTCGAGCGGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTTCTGTCTAGCACAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988908, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12902 Chironomidae sp. water mite diet isolate 12902-BHL040517-GBD24596_25064-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACACGCAGGCTCATTAATTGGAGAAGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATATTAATAGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACCTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12903 Nais christinae water mite diet isolate 12903-BHL040517-GBD7551_11822-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTTTATCTAATTTTAGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGATTACTTATTCGAATTGAGTTATCACAACCAGGATCATTTCTTGGAAGAGATCAATTATATAATACTCTTGTAACAGCACATGCATTCTTAATAATTTTCTTCTTAGTAATACCTGTATTTATTGGAGGGTTCGGAAACTGACTTCTTCCACTAATATTAGGTGCTGCTGATATAGCATTTCCTCGATTAAATAATCTTAGATTTTGACTACTACCACCTTCATTAATTCTATTAATTTCTTCTGCAGCAGTAGAAAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID LT903844, identified in GenBank as Nais christinae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL12904 Chironomidae sp. water mite diet isolate 12904-BHL040517-GBD11175_3459-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCTTTAATTGGAGACGATCAAATTTATAAAGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12905 Chironomidae sp. water mite diet isolate 12905-BHL040517-GBD21103_4924-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATGCTAATTCGAGCAGAATTAGGACATGCAGGTTCATTAATTGGAGAAGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCCTTAATATTAGGAGCACCTGACATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATCGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12906 Chironomidae sp. water mite diet isolate 12906-BHL040517-GBD12420_19749-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGTAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATGGTTATACCAATCTTAATTGGAGGAATTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATACGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTCTATTATTATCTAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12908 Chironomidae sp. water mite diet isolate 12908-BHL040517-GBD27139_16617-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTCTTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTATGAATTCTAAATCGAACAGAATTAGGACATGCAGGCTCATTAATTGGAGACTATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTAGAAGCTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12909 Chironomidae sp. water mite diet isolate 12909-BHL040517-GBD7493_26123-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGTAACTTCTTTAAGAATTCTAATTCGAGTATAATTTGGACATGCAGGATCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTGCAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAAATGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12910 Orthocladiinae sp. water mite diet isolate 12910-BHL040517-GBD15827_28362-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTCTAATATTAGGAGCACCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGACTGTTGCCCCCATCATTAACTTTATTATTATCTAGAACAATTGTGGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12911 Chironomidae sp. water mite diet isolate 12911-BHL040517-GBD23660_15613-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTCGATCAGGTATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGATTTCGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATATTGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTCTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12913 Chironomidae sp. water mite diet isolate 12913-BHL040517-GBD13068_16121-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGTATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGCATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAATTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCAACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCGTCATTAGCTTTATTATTATCTAGAGCAATTGTGGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12914 Chironomidae sp. water mite diet isolate 12914-BHL040517-GBD20561_27794-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTTGGACATGCAGGCTCATTAATTGGAGAAGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACAAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGAACCTGAGATGGCTTTCCCACGAATAAATAATATAAGTTCTTGATTGTTGCCCACATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12915 Chironomidae sp. water mite diet isolate 12915-BHL040517-GBD28571_10493-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGTAACTTCTTTAAGAATTCCAATTCGAGCAGACTTAGGACCTGCATGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATCATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCATCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12917 Chironomidae sp. water mite diet isolate 12917-BHL040517-GBD26734_8134-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTTATTAATTGGAGACGTTCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAAATGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAAAAAAAAAAGTTTTTGATTGTTGCCCCCATCATTAACTTGATTATAATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12918 Chironomidae sp. water mite diet isolate 12918-BHL040517-GBD14509_5905-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGAGATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACATCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAACTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCACCATCATTAACGTTATTATTATCTAAATCAATTGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12919 Chironomidae sp. water mite diet isolate 12919-BHL040517-GBD8921_25200-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTATTTTCGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGTTCATTAATTGGAGACGATCAAATTTATAATATAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAAGATTTGGCAACTGGCTAGTTCCTTTAATATTATGAGCACCTGATATGGCTTTCCCACGAATAAATAAAATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12920 Chironomidae sp. water mite diet isolate 12920-BHL040517-GBD13454_19389-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGGATTCTAATTCGACTAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTATTTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12921 Orthocladiinae sp. water mite diet isolate 12921-BHL040517-GBD9619_11806-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTATTTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATGTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAAGATAAGTTTTTGATTGTAGCCCCCATCATTAACTTTATTATTATCTAGAACAATTGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR513498, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12922 Chironomidae sp. water mite diet isolate 12922-BHL040517-GBD7803_18142-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTGGGAACTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACATGCAGGATCATTAATTGGAGAAGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTGCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12925 Orthocladiinae sp. water mite diet isolate 12925-BHL040517-GBD22414_3614-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGAACAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAATTTGACTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTCCCACGAATAAATAATATAAGATTTTGATTATTACCCCCATCATTAACTTTATTATTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12926 Chironomidae sp. water mite diet isolate 12926-BHL040517-GBD23351_11971-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGCGCGGAATTAGGACTTGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTTTTATAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGCAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGGTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12927 Orthocladiinae sp. water mite diet isolate 12927-BHL040517-GBD27702_17009-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTAATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTTGAGCTGAATTAGGACATGCAGGCTCATTAATTGGAGACTATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGAACAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12928 Chironomidae sp. water mite diet isolate 12928-BHL040517-GBD6603_19638-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTATTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGTTTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAGTATAAGTTTTTGATTGTAGCCCCCATCATTAAAATTATTATGATCTAGAACAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12929 Chironomidae sp. water mite diet isolate 12929-BHL040517-GBD2214_16463-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GACACTTTACTTTATTTTTGGAGCTTGATCCGGAATAGTAGGAACATCTTTAAGAATATTAAATCGAGCAGAATTAGGACATCCAGGAACATTGATTGGGGATGATCAAATTTACAATGTAATTGTAACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAAATGGTGGGTTTGGAAATTGGCTTTTACCTTTAATACTCGGGGCCCCTGATATAGCCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KP043758, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12930 Chironomidae sp. water mite diet isolate 12930-BHL040517-GBD19967_26694-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATAAGGAATAGTTGGAACTTCTTTAAGAATTCAAATTCGAGCAGAATTAGGACATGAAGGCTAATTAATTGGAGACGATCAAATTTATAATGTAATTGTAAAAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12932 Chironomidae sp. water mite diet isolate 12932-BHL040517-GBD7156_16757-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGTTCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGCATTATGACATGCAGGCTCATTAATTGGAGACGATCATATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACGGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATCGTTGCCCCCATCAGTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12933 Chironomidae sp. water mite diet isolate 12933-BHL040517-GBD13654_5504-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAAAATTAGGACATGCAGGCTCATTAATTGGAGACGATCTAATTTATAATGTAATTGTTACAGCTCATGCGTTTTTCATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGAATTGGAAACTGACTAGTTCCTTTAATATTAGGAGCAACTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12934 Chironomus riparius water mite diet isolate 12934-BHL040517-GBD16152_19231-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12935 Chironomidae sp. water mite diet isolate 12935-BHL040517-GBD24297_6794-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTCGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATTCTAATTCGAGCAGAATTTGGACATGCAGGTTCATTAACTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCCTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12938 Chironomidae sp. water mite diet isolate 12938-BHL040517-GBD11044_12275-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTTATTCGAGCAGAGTTAGGACATGCAGGCTCATTAATTGGAGACGATCAGATTTATAATGTAATTGTTACAGCTCATGCTTTTGCTATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATAGGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12939 Orthocladiinae sp. water mite diet isolate 12939-BHL040517-GBD6032_20485-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGATCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATATCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12942 Chironomidae sp. water mite diet isolate 12942-BHL040517-GBD17565_4525-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAAATCGAGCAGAAGTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAGTATTAGGAGCTCCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTACCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12944 Chironomidae sp. water mite diet isolate 12944-BHL040517-GBD29029_18982-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACCTGCAGGATCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGAGATGGCATTCCCACGAATAAATAATATAAGTTTTTAATTGTTGCCCCCATCAGTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12946 Chironomidae sp. water mite diet isolate 12946-BHL040517-GBD4666_22662-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGAGCAAATTTATAATGTAATTGTTACAGTTCATTCTTTTGTCATAATTTTTTTTATAGTTATACCAATCTTATTTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAAGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12948 Chironominae sp. water mite diet isolate 12948-BHL040517-GBD5021_6579-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTATGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCGCTGCGTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12949 Chironomidae sp. water mite diet isolate 12949-BHL040517-GBD26027_12958-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGTACTTCTTTAGGAATTCTAATTCGAGCAGAATTAGGACACGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTACACCAATCTTAATTGGAGGATTTAGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATGAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12950 Chironomidae sp. water mite diet isolate 12950-BHL040517-GBD27551_14903-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTCGGAGCTTGATCGGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGAACAAATTTATAATGTAATTGTTACAGCTCATGCCTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCTCCTGATATGGCTTTCCGACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12951 Chironomidae sp. water mite diet isolate 12951-BHL040517-GBD11269_26460-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATGTTCGGAGCTTGATCGGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGGCATGAAGGCTCATTAATTGGAAACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTATAGTTATACCAGTCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTCTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCAGCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12952 Chironomidae sp. water mite diet isolate 12952-BHL040517-GBD19802_21246-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCCGCAATCGTTGGAACTTCTTTAAGAATTCTTATTCGAGCAGAATTCGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACAAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12953 Chironomidae sp. water mite diet isolate 12953-BHL040517-GBD15485_10384-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTATTTTATTTTCGGAGCCTGATCAGGAATAGTTGGTACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCATGCAGGTTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATAGTGGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 95.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12954 Chironomidae sp. water mite diet isolate 12954-BHL040517-GBD5882_24710-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATGCTGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCGCGCTTTTGTAATAATTTTTTTTATAGTTATGCCAATCTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAAATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12955 Chironomidae sp. water mite diet isolate 12955-BHL040517-GBD14622_18532-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAGTAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAAAATTAGGACATGCAGGATCATTAATTGGAGACGAACAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTTCAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12957 Chironomidae sp. water mite diet isolate 12957-BHL040517-GBD19063_3116-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTGTTTAAGAATTCTAATTCGAGTAGAATTAGGACATGCAGGCTCATTACTTGGAGACGATCAAATTTATAATGAAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCATTTAATATTAAGAGCACCTGATATGGCTTTCCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTACCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12958 Chironomidae sp. water mite diet isolate 12958-BHL040517-GBD4715_11547-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTCATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTACACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCAACTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGACCCCATCATTAAAATTATGATTATCTAGATCAATTGTGGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12959 Chironomidae sp. water mite diet isolate 12959-BHL040517-GBD25145_17575-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGAAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTTTAATAATTTTTTTTATAGTTATACCAATCTTAATTTGAGGATTTGGAAACTTACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAAAAAAAAATATAAGTTTTTGAATGTTGCCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12960 Orthocladiinae sp. water mite diet isolate 12960-BHL040517-GBD15682_6387-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTATTTTCGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAATAATTCTAATTCGAGCAGAATTAGGACATGCAGGCACATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTATTAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTCCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12961 Chironomidae sp. water mite diet isolate 12961-BHL040517-GBD27618_20398-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTCTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACATGCAGGCTCATTAATTAGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCCTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAGTAAATAATATAAGTTTTCGATTGTTGCCCCCATCATTAACTTAATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12964 Psectrocladius sp. water mite diet isolate 12964-BHL040517-GBD27173_23164-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGTCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAACTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.1% identical to accession ID KR761745, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12965 Chironomidae sp. water mite diet isolate 12965-BHL040517-GBD19710_5936-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACGTCTTTAAGAATTCTAATTCGAACAGAATTAGGACATGCAGGCCCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATGTGGCTTTCCCACGAATAAATAATGTAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTATGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12966 Chironomidae sp. water mite diet isolate 12966-BHL040517-GBD21018_12864-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTATAATTCGAGCAGTATTAGGACATGCAGGCTCATTAATTGGAGACAATAAAATTTATAATGTAATTGTTAAAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATATTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAGTATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12968 Chironomidae sp. water mite diet isolate 12968-BHL040517-GBD19044_3126-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTTGGCACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGGTTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGAAAAGGCTTTCCCCGCGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12971 Chironomidae sp. water mite diet isolate 12971-BHL040517-GBD13708_19755-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTATTTTCGGAGCTTGCTCCGGAATAGTTGTAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTATTTGATTGTTGCGCCCATCATTAACTTTATAATTATCTAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12972 Orthocladiinae sp. water mite diet isolate 12972-BHL040517-GBD25641_11149-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTATTTTCGGAGCTTGATTAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGATGATCAAATTTTTAATGTAATTGTTACAGCTCATGCTTTTGTAATATTTTTTTTATAGTTATATCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTTAATATTAGGAGCACCGGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGCTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12974 Chironomidae sp. water mite diet isolate 12974-BHL040517-GBD7812_18509-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTTATTCGAGCTGAATTAGGACAAGGAGGCTCATTAATTGGAGAAGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATCATCTGGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12977 Chironomidae sp. water mite diet isolate 12977-BHL040517-GBD2621_16437-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTATTCTCGGAGCTTGATCAGGAATAGTTTGAACTTCTTTAAGAATTCTAATTCGAGAAGAATTAGGACATGCAAGCTCATTAATTGGATACGATCAAATTTATAATGTAATTGTTACATCTCATGCTTTTGGAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL12978 Chironomidae sp. water mite diet isolate 12978-BHL040517-GBD22379_8341-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTATTTTCGGAGTTTGATCAGGAATAGTTGGAACTTCTTCTAGAATTCTAATTCGAGTTGAATTAGGACATACAGGCTCATTAATTGGAGACGATCAAATTTATAATGTACTTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAAATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12979 Chironomidae sp. water mite diet isolate 12979-BHL040517-GBD9677_12704-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGACTTAGGACATGCAGGTTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTATGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGACACTGACTAGTTCCTTCAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12981 Chironomidae sp. water mite diet isolate 12981-BHL040517-GBD2740_18638-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGAAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAAGTAGGACATGCAGGCTCATTATTTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCCTAATTGGATGATATGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGGTATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12983 Chironomidae sp. water mite diet isolate 12983-BHL040517-GBD23673_24793-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTACTTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTCCCGTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCTCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12987 Chironomidae sp. water mite diet isolate 12987-BHL040517-GBD16679_12831-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAATTGGAACTTCTTTTAGAATTCTAATTCGAGTAGAATTATGACATGCAGGCTCATTCTTAGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTTTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCACCATCATTAACCTTATTATTATCTAGAGCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12988 Chironomidae sp. water mite diet isolate 12988-BHL040517-GBD12135_2148-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAAAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAATTTTATAATGTCATTATTACAGCTCATGCTTTTGTAATATTTTTTTTTTATAGTTATACCAAACTTAATTGGAGGATTTGGAAGCTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTGTGATTGTTGCCCCCAGCATTAACTTTAGTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12989 Chironomidae sp. water mite diet isolate 12989-BHL040517-GBD15440_18966-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTTCGGATCTTGATCAGGAGTAGTTGGAACTTCTTTGAGAATTCTAATTCGAGCTGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTATTGATTGTTGCCCCCATCATTAACATTATTATTATCCAGAGCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12991 Chironomidae sp. water mite diet isolate 12991-BHL040517-GBD18134_3545-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTGTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCTAAGTTATAATGTAATGGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATAACAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCCCCTGACATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL12993 Chironomidae sp. water mite diet isolate 12993-BHL040517-GBD9904_10966-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACGTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATTAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAAATTTTTTTTATAGTTATACCAATCTTAATAAGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGAATGTTGCCCCCATCATTAACTTTATTATTATCTAGATTAAGTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1300 Chironominae sp. water mite diet isolate 1300-BHL110116-GBD25003_9742-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTGCTGCCCCCTTCTTTAACTCTATTACTATCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM988908, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13000 Chironomidae sp. water mite diet isolate 13000-BHL040517-GBD19691_5931-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGGAGGCTCATTAATTGGAGACAATCAAATTTATAATGTAATTGTTACAGCCCATGTTTTTGTAATAATTTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTCACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTAGCCCCCATCATTAACTTTATTATTATCTAGATTAATTATGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13001 Dicrotendipes sp. water mite diet isolate 13001-BHL040517-GBD23126_20535-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGACATTGATTAGTCCCTTTAATATTAGGAGTCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTCTCTGACTATTACCTCCTTCTCTAACCCGTCTTCTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13002 Chironomidae sp. water mite diet isolate 13002-BHL040517-GBD27638_19234-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGAAATGCAGGCTCATTAATTAGAGAAGAACAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGAGCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13003 Orthocladiinae sp. water mite diet isolate 13003-BHL040517-GBD25925_6218-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGAAATAATTTTTTTTTATAGTTATACCTTTTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGAACAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13004 Chironomidae sp. water mite diet isolate 13004-BHL040517-GBD23607_20649-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCATGAATAGTTGGAACTTCTTTAAGACTTCTAATTCGAGCAGACTTAGGACATGAAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTATAGTTATACCAATCTTAATTGGAGGAGTTGGACACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGAGCAATTGTGGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13009 Chironomidae sp. water mite diet isolate 13009-BHL040517-GBD11695_11091-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATGATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTATAAGAACCTGGTATGGCTTTCCCACGAATAAATAATATAAATTTTTGATTGTTGCCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13011 Chironomidae sp. water mite diet isolate 13011-BHL040517-GBD5487_11909-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTCGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATCCTGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGACTGTTGCCCCCATCATTAACATTATTATTAGCTAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13013 Chironomidae sp. water mite diet isolate 13013-BHL040517-GBD28034_19723-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTTAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAACTTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATAATAGGAGCACCTGATATGGCTTTCCCACGAATAAAAAAAATAAGTATTTGATTTTTGCCCCCCATCATTAACTTTATTATTATCTGGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13016 Chironomidae sp. water mite diet isolate 13016-BHL040517-GBD6928_9867-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTCTTTTATTTTCGGCGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAACTCGGGCAGAATTAGGACATGCATGCTCATTCATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13019 Chironomidae sp. water mite diet isolate 13019-BHL040517-GBD19928_22212-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATAAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAGTTGGAGACGATCAAATTTATACTGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTATGATTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGTTTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13020 Chironomidae sp. water mite diet isolate 13020-BHL040517-GBD24670_24867-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACAGTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTATTTAAGAATTCTAATTCGAGTAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGATTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGTAGGATTTGAAAACTGACTAGTTCCTCTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13021 Chironomidae sp. water mite diet isolate 13021-BHL040517-GBD28061_12771-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTAGGAGCTTGACCAGGAATAGTTGGAACTTCTTTAAGAATTCTAAATCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACAATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTTTAATAATTTTTTTTATAGGTATACCAATCTTAATTAAAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13024 Orthocladiinae sp. water mite diet isolate 13024-BHL040517-GBD7543_17009-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATATTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGGTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTTTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACTTGATATAGCTTTCCCACGAATAAATAACATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGAACAATTGTGGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13029 Chironomidae sp. water mite diet isolate 13029-BHL040517-GBD23257_25531-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGTAACTTCTTTAAGAATGCTAATTCGAGCGGAATTAGGACATGCAGGCTCATTAATTGGAGAAGATCAAATATATAATGTAATTTTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13030 Chironomidae sp. water mite diet isolate 13030-BHL040517-GBD4697_19900-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCATGATCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGACTTTTCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTATCCTTATTATCATCTAGATCAATTGCGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13032 Chironomidae sp. water mite diet isolate 13032-BHL040517-GBD27571_16371-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTTTTTTATTTTCGGAGCTTGATTAGGAATAGTTGGTACTTCTTTAAGAATTCTAGTTCGCGCAGAATTAGGACATGCAGACTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCGATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13034 Chironomidae sp. water mite diet isolate 13034-BHL040517-GBD4306_15515-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTTTTACAGGTCAAGCTTTTGTAATAATTTTTTTTATAATTATACCATTCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGACTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTTTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13035 Chironomidae sp. water mite diet isolate 13035-BHL040517-GBD23568_26519-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATTCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATATTAATTGGAGGATTTGGAAACTGACTAGTACCTTTAATATTAGGAGCTCCTGATATGGCTTTCCCACGACTAAACAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTCGATCAATTGTGTAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13045 Chironomidae sp. water mite diet isolate 13045-BHL040517-GBD27423_13265-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGTAGCTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGAACAAATTTATAATGTAATTGTTCCAGCTCATGCTTTTATAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTCTCCCACGAATAAATAATATAAGTTGTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13046 Chironomidae sp. water mite diet isolate 13046-BHL040517-GBD6377_14081-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCCGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACATGCAGGCTCATTACTTGGAAACGATCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTCTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCACCATCATTAACTTTATTATAATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13047 Chironomidae sp. water mite diet isolate 13047-BHL040517-GBD5563_20680-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCAGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAAATCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGATCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTGTGATTGTGGCCCCCATCATTAACTTAATTATTATCTAGAGCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13051 Chironomidae sp. water mite diet isolate 13051-BHL040517-GBD17013_21689-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATGAAGGTTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATCTTAATTGGAGGATTCGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAACTCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13055 Chironomidae sp. water mite diet isolate 13055-BHL040517-GBD10587_11204-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTATCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTAGCCCAAATCATGAACATTATTATGAACTAGATCAATTGTGGAAAATGGAGCAGGAAAAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13061 Chironomidae sp. water mite diet isolate 13061-BHL040517-GBD11397_15291-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGTTCAGGAATAGTTGGAACTTCTTTATGAATTCTAATTCGCGCTGAATTAGGTCATGCAGGCTCATTAATTTGAGACGATCAATTTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATATTTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13062 Orthocladiinae sp. water mite diet isolate 13062-BHL040517-GBD13690_13205-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTACTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAAAATTAGGACATGCAGGCTCATTCATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAAAAATAAAAATTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGGGGAAAATGGAGCCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13065 Chironomidae sp. water mite diet isolate 13065-BHL040517-GBD19255_21567-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATAAGGTATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGTAGAATTAGGACATCCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCCCGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13069 Chironomidae sp. water mite diet isolate 13069-BHL040517-GBD20489_3317-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCCGGAATAGTTGGAACTTCTTTAAGAATGCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTCATTGGAGACGATCAAATTTATAATGTAATTGTTACAACTAATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATGGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTCTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1307 Chironomidae sp. water mite diet isolate 1307-BHL110116-GBD18029_2086-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGAGAATAGTAAGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGGGAAGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGGGCCCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13070 Chironomidae sp. water mite diet isolate 13070-BHL040517-GBD20803_27040-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAGGAATTCTAATTCGAGCAGAATTAGGACATGCAGGATCATTAATTGGAGACAATCAAATTTATAATGTAATTGTTACAGCTCATGCCTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAATCTGACTAGTTCCTTTAATATTAGGAGCAACTGATATGGCTCTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCTCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13071 Chironomidae sp. water mite diet isolate 13071-BHL040517-GBD14830_2986-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTGTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATGAGTACATGCAGGCTCATTAATTGGAGACGATCTAATTTATAATGTAATTGTTACAGCACATGCTTGTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTCGATCAATTGTGTAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13072 Chironomidae sp. water mite diet isolate 13072-BHL040517-GBD12489_27307-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGAATAGTTCCTTTAATATTAGGTGCACCTGATATGGCCTTCCCACGAAAAAATAAAATAAGGTTTTGATTGTTGCCCCCCTCATTAAATTTATTATTATCTAGATCAATTGGGAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13073 Chironomidae sp. water mite diet isolate 13073-BHL040517-GBD14912_6165-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCATGCTCATTTATTTGAGACGATCTAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGTAGGATTTGGAAACTGACTAGTTCCTTTATTATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCTCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13075 Chironomidae sp. water mite diet isolate 13075-BHL040517-GBD10195_12510-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTCGGAGTTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAATAGAATTATGACATGCAGGCTCATTAATTGGAGGCGAACAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTATAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13076 Chironomidae sp. water mite diet isolate 13076-BHL040517-GBD6130_12236-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGCATTGGGACATGCAGGCTCATTAATTGGAGACGATCATATTTATAATGTAATTGTTCCAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTAGACCAATCGTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTAGCCCCCATCATTAACTTTATTATTATCTAGAGCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13077 Chironomidae sp. water mite diet isolate 13077-BHL040517-GBD27653_15547-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGACCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGCCGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAAGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGGTTTTGATTGTTGCCCCCAGCATTAACTTTATTATTATCTAGAGCAATTGT-GAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13079 Chironomidae sp. water mite diet isolate 13079-BHL040517-GBD20007_2179-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTACGAATTCTAATTCGAGCAGAATTAGGCCATGCAGGATCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCAGTAACATTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13084 Chironomidae sp. water mite diet isolate 13084-BHL040517-GBD25174_5752-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATTAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATATTAATTGGATGTTTTGGAAACTGATTAGTTCCTTTAATTTTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTACTATTATCTAGATCATTTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13087 Chironomidae sp. water mite diet isolate 13087-BHL040517-GBD25391_10577-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGTACTTCTTTAAGTATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAATTGACTAGTACCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTGTTTGATTGTTGCCCCCATCATTAACTTAATTATTATCTCGAACAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13089 Orthocladiinae sp. water mite diet isolate 13089-BHL040517-GBD18579_27293-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTGGAGCAGAATTAGGACATGCAGTCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTGCCCACGAATAAATAATATAAGTTTTGGATTGTAGCCCCCAGCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13096 Chironomidae sp. water mite diet isolate 13096-BHL040517-GBD10964_28307-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAACAATATAAGTTTTTGATCGTGGCCCCCATCATTAACTTTATTATAATCTAAAGCAATTGTGGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13099 Chironomidae sp. water mite diet isolate 13099-BHL040517-GBD9247_15442-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTATTTTCGGAGCTTGATCAGGAATAATTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACCTGCAGGCTCATTAATTGGAGACGATCAAATTTATAAAGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCCTTAATATTAGGAGCACCTGGTATGGCTTTCCAACGAATAAATAATATAAGTCTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1310 Chironominae sp. water mite diet isolate 1310-BHL110116-GBD11775_28135-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTAGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCCTTCTTTAACTCTTCTTCTATCTAGCGCAATTGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR754526, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13101 Chironomidae sp. water mite diet isolate 13101-BHL040517-GBD28209_11359-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTATTTTCGGAGCTTGATCATGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTGGGAGCACCTGATATGACTTTCCCACGAATAAATAATATAAGTTTTTGACTATTTCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13108 Chironomidae sp. water mite diet isolate 13108-BHL040517-GBD7288_14360-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTTATCAGGAATAGTTGGAACTTCTTTAAGACTTCTAATTCGAGTAGAATTATGACATGCAGGCTCATTAATTGGAGACGATCAATTTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGAGTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACGTTATTATAATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13111 Chironomidae sp. water mite diet isolate 13111-BHL040517-GBD9168_26534-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATGCAGGTTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCCCCTGATATTGCTTTCCCACGAATAAATAATATAAGTTTTTTATTGTTGCCCCCATCATTAACTTTATTATTATCTTGATCAATTGTGTAAAATGGAGCTGGGACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13114 Chironomidae sp. water mite diet isolate 13114-BHL040517-GBD4206_7727-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGACTTCTAATTCGCGCATAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACATCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGAATTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTGTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGAACAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13118 Chironomidae sp. water mite diet isolate 13118-BHL040517-GBD7145_23098-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACTTCCCTAAGAATACTAATTCATGCTGAATTAGGTCACCCAGGAACATTCATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTATCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTATTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13119 Chironomidae sp. water mite diet isolate 13119-BHL040517-GBD15264_21224-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGA-TTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTCTCCCACGAATAAATAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCGGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1312 Chironomidae sp. water mite diet isolate 1312-BHL110116-GBD9361_4130-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGAGGCTCCTGAGATAGCTTTTCCGCGACTAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTGGCTTTAAACAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13122 Orthocladiinae sp. water mite diet isolate 13122-BHL040517-GBD23755_21940-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGATGGAACTTCTTTAAGAATTCTCATTCGAGCAGAATTAGGCTATGCAGGCTCATTAATTGGAGATGATCAGATTTATAATGTAATTGTTACAGCTCATGCTTTTCTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTAGTATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATTAATTGT-GAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13123 Chironomidae sp. water mite diet isolate 13123-BHL040517-GBD14275_11210-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTATTTTCGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGTAAACTGACTAGTTCCTTTAATAATAGTAGCACCTGATATTGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTGATTATCATCTAGAGCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13133 Chironomidae sp. water mite diet isolate 13133-BHL040517-GBD24119_11749-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGGATTAATATTTCGAGCAGAATTAGGACCTACAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTTTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGAACAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13135 Chironomidae sp. water mite diet isolate 13135-BHL040517-GBD4178_8782-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTACTTCGAGCAGAATTAGGACATGCAGGTTCATTAATTGGAGACGATCAAATTTATCATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGATACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATAGAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATAAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13139 Chironomidae sp. water mite diet isolate 13139-BHL040517-GBD18836_25546-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGAAGATGTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGAGTGTTGCCCCCAGCATTAACTTTATTATAATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13145 Chironomidae sp. water mite diet isolate 13145-BHL040517-GBD17608_1913-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTATTTTTCGGAGCTTGTCCAGGAATAGTTGGAACTTCTTTATGAATTCTATTTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGACCCCATCATTAACTTTATTATTATCTAGAACAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13149 Chironomidae sp. water mite diet isolate 13149-BHL040517-GBD25722_10895-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTAGAGCAGAATTAGGACATGCAGGCTCATTCATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTAATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTATTTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACATGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCACCAGCATTAACTTTATTATAATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13150 Chironomidae sp. water mite diet isolate 13150-BHL040517-GBD26293_9089-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACATCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGAAGCACCTGATATGGCTTTCCCACGAAAAAAAAATAAAAGTTTTGGATGGTTG-CCCCATCATTAACTGTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13151 Chironomidae sp. water mite diet isolate 13151-BHL040517-GBD17446_17006-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTATTTTCGGAGCTTGATCTGGAATAGTTGGAACTTCTTTTAGAATTCTAATTCGAGCAGAATTAGGACATGAAGGCTCATTAATTGGAGACGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGGCTAATTCCTTTAATATTAGGAGCACCTGATATGACTTTCCCACGAATAAATAATATAAATTTTTGATTGTTGCCCCCCATCATTAACTTTATTATTAGCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13155 Chironomidae sp. water mite diet isolate 13155-BHL040517-GBD22243_20780-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAACAATATAAGGTTTTGAATATTGCCCCCATCATTAACTTTATTATTATCTAGAACAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13156 Chironomidae sp. water mite diet isolate 13156-BHL040517-GBD15861_24962-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAAAATTAGGACATGCAGGCCCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGAAGGATTTGGAAAATGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTGGCACCAATAAGTAACTTGATTATTATCTAGAACAATTATGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL1316 Chironomidae sp. water mite diet isolate 1316-BHL110116-GBD16680_9094-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGCACTTCTTTAAGTATTTTAATTCGACTAGAACTTGGACACCCAGGTTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAATACCTTTGATATTAGGAGCTCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13165 Paratanytarsus sp. water mite diet isolate 13165-BHL040517-GBD11200_6426-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACTTCCTTAAGTATACTAATTCGAGCAGAATTATGTCACCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGTTTTGGAAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAAAAGATTAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13166 Cricotopus sp. water mite diet isolate 13166-BHL040517-GBD13709_27166-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGGTTATTACCCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13167 Chironomidae sp. water mite diet isolate 13167-BHL040517-GBD29064_17182-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGGAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13168 Paratanytarsus sp. water mite diet isolate 13168-BHL040517-GBD20982_17594-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTTGTCAGTAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCATCCTGTAACATTTATTGGAGATTACCAAAACTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGAAGCTCCCGAGATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCAACTTTAACCCTACTTCTATCAAGAAGATTAGTGGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR672858, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13169 Chironomidae sp. water mite diet isolate 13169-BHL040517-GBD15513_25242-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTATGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13170 Psectrocladius sp. water mite diet isolate 13170-BHL040517-GBD13531_15790-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATATTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13171 Chironomidae sp. water mite diet isolate 13171-BHL040517-GBD21461_21508-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTCATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGTTGAATTAGGACATCCGGGTACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTTTAATTTTTTTTTTATAGTTATACCAATTTTAATTGTAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13172 Paratanytarsus sp. water mite diet isolate 13172-BHL040517-GBD21196_5498-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR740890, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13173 Paratanytarsus sp. water mite diet isolate 13173-BHL040517-GBD6903_8776-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAAAAATAATCGGAACATCCCTAAGTATACTAATTCGAGAAAAATTAGGGCGCCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATATTTTTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCCTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR639844, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13174 Paratanytarsus sp. water mite diet isolate 13174-BHL040517-GBD18590_24438-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAATATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCCTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAATTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13175 Chironomidae sp. water mite diet isolate 13175-BHL040517-GBD23419_9819-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGATTATTATTTCGAGCTGAATTAGTACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATAACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13176 Chironomidae sp. water mite diet isolate 13176-BHL040517-GBD9835_10993-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13177 Chironomidae sp. water mite diet isolate 13177-BHL040517-GBD16603_6504-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCCCGATCAGGAATAGTTGGTACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCATATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGATGCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13178 Chironomidae sp. water mite diet isolate 13178-BHL040517-GBD25802_19846-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCCCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13179 Chironomidae sp. water mite diet isolate 13179-BHL040517-GBD6608_19722-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCCTGGTCAGGAATAATCGGAACATCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTGTAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13180 Chironomidae sp. water mite diet isolate 13180-BHL040517-GBD19950_28330-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGGGCTGAATTACGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAACCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTATCAAAAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13181 Diptera sp. water mite diet isolate 13181-BHL040517-GBD3205_13714-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAGTTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTCTAATTGGAGGGTTTGGAAATTGTTTAGTTCCTCTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAGTATAAGTTTTTGATTATTTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.4% identical to accession ID KM455055, identified in GenBank as Philophylla caesio. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13182 Chironomidae sp. water mite diet isolate 13182-BHL040517-GBD20197_11261-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTTGGACATCCTGGTACTTTTATTGGAGATGACCATATTTATAATGTAATTGTTACCGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTTCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13183 Chironomus riparius water mite diet isolate 13183-BHL040517-GBD5566_24857-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATCTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCATTTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13184 Paratanytarsus sp. water mite diet isolate 13184-BHL040517-GBD14387_7700-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTCTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCAATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KM994688, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13185 Chironomidae sp. water mite diet isolate 13185-BHL040517-GBD24277_12824-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTTGAGATGATCAAATTTATAATGTAATTGTCACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTTTTTTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13186 Paratanytarsus sp. water mite diet isolate 13186-BHL040517-GBD12901_21213-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTTTATTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATCAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13187 Paratanytarsus sp. water mite diet isolate 13187-BHL040517-GBD14514_16401-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGGACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGCTTTTGGGAATTGACTTCTTCCTTTAATATTAGAAGCTCCCGATATAGCTTTTCCCCGTATAAATAGCATAAGGTTTTGATTACTTCCCCCATCTTTAACCCTGCCTCTATCAAAAAGATTAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13188 Chironomidae sp. water mite diet isolate 13188-BHL040517-GBD20632_19757-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTTATAGTGATACCTATTTTAATTGGAGTGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13189 Orthocladius sp. water mite diet isolate 13189-BHL040517-GBD8092_13392-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATCAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID JF870185, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13190 Chironomidae sp. water mite diet isolate 13190-BHL040517-GBD20435_9189-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTTGGAGATGATCAAATTTATATTGTAATTGTTACTGTACATGCTTTCTTTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTTTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13192 Chironomidae sp. water mite diet isolate 13192-BHL040517-GBD22557_24888-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTTTGAGCCTGATCAGTAATAGTTGGACCTTCCTTAAAAATATTAATTCGAGCTGAATTAGGACATCCTGTTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCTTTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGATTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATGATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13193 Chironomidae sp. water mite diet isolate 13193-BHL040517-GBD10070_24916-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTGCATTATATGTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTTGGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGTAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTATTGAATATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATAGTAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13194 Paratanytarsus sp. water mite diet isolate 13194-BHL040517-GBD25950_19062-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCGCCCTGAAACATTTATTGGAAATGACAAATTCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATGGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTGCTATCAAAAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR742514, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13195 Paratanytarsus sp. water mite diet isolate 13195-BHL040517-GBD26514_17486-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATGCTTAGGTATACTAATTCGAGCAGAATTATGGCACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTATTTGGGGGTTTTGGAAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTAAAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR753366, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13197 Chironomidae sp. water mite diet isolate 13197-BHL040517-GBD13602_4404-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGGAGCCTGAGCAGGAAGAGTTGGAACTTCCTTAAGAATATTAATGCGAGCTGAATTAGGACATCCTGTTACTTTTATTGGAGATGATCAATTTTAGAATGTAATTGTAACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCAAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACAATATTACTTTCAAGAAGTATTGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13198 Paratanytarsus sp. water mite diet isolate 13198-BHL040517-GBD14050_21967-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATATTCGTAACATCCTTAGGTATATTAATTCAAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGGTGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATATTTTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAAAAGATTAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13199 Chironomidae sp. water mite diet isolate 13199-BHL040517-GBD24832_14970-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTGTATTTTATTTTTGGGGCCTGATCAGGAATAGTTGGAACTTCCTTTAGAATATTAATTCAAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATAATTACTTGCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13201 Chironomidae sp. water mite diet isolate 13201-BHL040517-GBD11618_2514-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAACAAATCATAAAGATATTGGCTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACAGCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGAAACATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTTATAGTGATACCGATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTATTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTCGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.7% identical to accession ID JF764756, identified in GenBank as Orthocladius telochaetus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13202 Chironomidae sp. water mite diet isolate 13202-BHL040517-GBD10791_20383-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAACGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATAAAGCTTTTCCCCGAATAAATAAAAAAAAGTTTTGATTATTACCCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13204 Chironomidae sp. water mite diet isolate 13204-BHL040517-GBD10229_22753-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCGGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTATTTAATCGGAGACGATCAGATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13205 Chironomidae sp. water mite diet isolate 13205-BHL040517-GBD25159_22485-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGTATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGATCATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAACATTTCCTCGAATAAAAAATATAAGTTTTTGATTATTACCCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTATAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13206 Chironomidae sp. water mite diet isolate 13206-BHL040517-GBD7216_25358-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAAATCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAGTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGTCTCCTGATATAGCTTATCCGCGAATAAATAATATAAGTTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13207 Chironomidae sp. water mite diet isolate 13207-BHL040517-GBD8111_12228-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATCTTAATTCGAGCAAAACTCGGTCAAGCTGGTTCTTTATTCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTCGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATCGGGAGCCCCTGATATAGCATTCCCTCGAATAAAAAATATAAGTATTTGATTACTTCCCCCCGTCATTAACTTTATTATTATCTAGCGCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13208 Chironomidae sp. water mite diet isolate 13208-BHL040517-GBD7413_6120-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGTATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13209 Psectrocladius sp. water mite diet isolate 13209-BHL040517-GBD4895_6643-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAAAAGATTAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13210 Paratanytarsus sp. water mite diet isolate 13210-BHL040517-GBD5243_18145-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KP043139, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13212 Chironomidae sp. water mite diet isolate 13212-BHL040517-GBD8768_14939-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCGTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTTATAGTTATACCAATTTTTATTGGAGGCTTTGGTAATTGACTTTTGCCATTAATACTAGGAGCCCCAGATATGGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACACTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13215 Chironomidae sp. water mite diet isolate 13215-BHL040517-GBD28324_18372-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGTACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGATCATTAATCGGAAACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTATTACCTTTGATATTAGATGCTCCTGATATAGCTTTTCCGCGAATGAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13216 Chironomidae sp. water mite diet isolate 13216-BHL040517-GBD27413_22174-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTAGAACTTCCTTAAGAATATTAATTCGAGCTGAATTCGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGTGCCCCAGATATAGCTTTTCCTCGAATAAATAAAATAAGTTTTTGATTATTACCCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13217 Chironomidae sp. water mite diet isolate 13217-BHL040517-GBD8622_9895-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATCATGACCCCCATCTCTAACATTACTACAATCAAGAAGTAGTGTAGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM995398, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13218 Chironomidae sp. water mite diet isolate 13218-BHL040517-GBD8630_5715-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTGATTATATTTTATTTTTGAAGCATGATCAGGAATCGTTGGAACTTCCTTAAGAATATTAATTAGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAATAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13219 Chironomidae sp. water mite diet isolate 13219-BHL040517-GBD5849_21185-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCTGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGATGATATGGAAATTGACTAGTTCCTTTAATATTAGGAGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCATTTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13220 Chironomidae sp. water mite diet isolate 13220-BHL040517-GBD21739_3863-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAATTTATATTTTATTTTTGGAGCGTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAGTCGTAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACTTTTGATATTAGGGGCTCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGGAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13221 Chironomidae sp. water mite diet isolate 13221-BHL040517-GBD22318_19880-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13222 Chironomidae sp. water mite diet isolate 13222-BHL040517-GBD18000_28947-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGCATATTAATTCGAGCTGAATTAGGACATCCTGTTACCTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTATTACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTGTTACCCCCATCGCTAACATTATTACTTTCAAGAAGTATTGTAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13223 Chironomidae sp. water mite diet isolate 13223-BHL040517-GBD19546_21884-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGTTGAATTAGGACATCCTGGTACATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGGGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCATCACTAACATTATTTCTATCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13225 Chironomidae sp. water mite diet isolate 13225-BHL040517-GBD17191_5697-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCGGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGATACTTTTATTGGAGATGATCAAATTTATAATGTAATTGGTACTTCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCGAGAAGTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13227 Chironomidae sp. water mite diet isolate 13227-BHL040517-GBD28831_16501-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATTGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTATAGTTATACTAATTTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTATTTGATAATTACCCCCATGGCGAACATGAATACGTTCAAAAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13229 Psectrocladius sp. water mite diet isolate 13229-BHL040517-GBD10879_26214-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAGCATCCTTAAGTATACTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAGATTTATAATGTAATTGTTACCGCTCACGCTTTTATAATAATTTTTTTTATAGTGATACCTATTATAATTGGAGGGTTTGGAAATTGATTAGTTCCTTCAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCTCCCGTCATTAACTTTATTATGATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KR761745, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13230 Diaphanosoma sp. water mite diet isolate 13230-BHL040517-GBD11548_24940-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCCTAAGTTTACTTTTTCGAGCTGAATTGGGGCACTGTGGCAGTTTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13231 Chironomidae sp. water mite diet isolate 13231-BHL040517-GBD21829_6473-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTTTATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGTACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCCTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCGCTAACATTATTAAAATCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13232 Chironomidae sp. water mite diet isolate 13232-BHL040517-GBD22997_26503-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTTGGAGCCTGATCAGGATTAGTTGGAACTTCTTTAAGAATATTAATTCGAGATGAATTAGGAAATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13234 Chironomidae sp. water mite diet isolate 13234-BHL040517-GBD7904_15842-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCATGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCGATTTTAATTGGAGGATTTGGTAATTGACTCTTGTCATTAATACTAGGAGCCTCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCAAACATTATTACGTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13236 Paratanytarsus sp. water mite diet isolate 13236-BHL040517-GBD7086_23062-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTCTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTCAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTATAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATATTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13237 Chironomidae sp. water mite diet isolate 13237-BHL040517-GBD25680_10538-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTAATTAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTATTGCCATTAAGACTAGGAGCCCCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13238 Chironomidae sp. water mite diet isolate 13238-BHL040517-GBD19771_28401-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGTAACTTACTTATGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAAATGATCAAATTTATAATGTAATTGATACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAAGTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13239 Chironomidae sp. water mite diet isolate 13239-BHL040517-GBD8057_25610-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAACTTATAGTGTAATTGTTACTGCACATGCGTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTCTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13241 Dicrotendipes sp. water mite diet isolate 13241-BHL040517-GBD21213_11118-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTAGAGCTTGATCTGGATTAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAAATTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTGTTACCTCCTTCTCTGACCCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13242 Chironomidae sp. water mite diet isolate 13242-BHL040517-GBD22993_16393-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTCGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCACATACTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAAATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13243 Chironomidae sp. water mite diet isolate 13243-BHL040517-GBD22585_4748-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGGGATGATCAAATTTATAATGTAATTGTTACTGCACATGTTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGAATCTTGACATTAATACTAGGAGCCCCAGATATAGCTTTTCCCCGAAAAAATAATATAAGTATTTGATTATTAACCCCATCTATAACACTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13244 Chironomidae sp. water mite diet isolate 13244-BHL040517-GBD13902_24539-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13245 Paratanytarsus sp. water mite diet isolate 13245-BHL040517-GBD23222_4788-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTGTATATTTTACTTTCGGAGCTTGCTCAGGAATAATCGTTACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGCAAAAATAACATAAGTTTTTGATTACTTCCCCCATCTTCAACCCTTCTGCTATCAAGAAGATTAGTGGAAAATCGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13248 Chironomidae sp. water mite diet isolate 13248-BHL040517-GBD18395_27588-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAAGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCGCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.7% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13249 Chironomidae sp. water mite diet isolate 13249-BHL040517-GBD13431_23225-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAAAATTAATTCGAGCTGAATTAGGACATGCTGGTTCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTAATATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCACTAACATTATTACCATCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13253 Chironomidae sp. water mite diet isolate 13253-BHL040517-GBD29636_13842-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTTAGACTATTAATTCGAGCTGAATTAGGACATCCTGGTACTCTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTCTAGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13254 Chironomidae sp. water mite diet isolate 13254-BHL040517-GBD11332_3265-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGGATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCACATGCATTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTTCTGTCAAGAAGTGCTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13257 Paratanytarsus sp. water mite diet isolate 13257-BHL040517-GBD12739_28437-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACTTCTTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAACATTAGGAGCTCCTGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTACTACTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13259 Chironomidae sp. water mite diet isolate 13259-BHL040517-GBD20019_20694-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGCATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTCGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCATGTCCGCGAATAAATAAAATAAGATTTTGATTATTACCCCCGTCAGTAACCTTACTTTTATCAAGAGCAATAGTAGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13261 Chironomidae sp. water mite diet isolate 13261-BHL040517-GBD28921_13310-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGCATCGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGATACTTTTCTTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTCTTATAGTTATACCATTTTTAATTGGAGGATTTGGTAATTGACTTTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTGTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13262 Paratanytarsus sp. water mite diet isolate 13262-BHL040517-GBD27788_11725-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATACTTAAGTATACTAATTCGAGTAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTATTACTTTAATATTAAGAGCTCCCGATATAGCTTTTCACCGTATAAATAAAATAAGTTTTTGATTACTTCCTGCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGTAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13263 Paratanytarsus sp. water mite diet isolate 13263-BHL040517-GBD21654_16945-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCCCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAATTATACCTATTTTAATTGGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR740890, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13264 Paratanytarsus sp. water mite diet isolate 13264-BHL040517-GBD13845_2718-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTAATTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTTGAACATTTATTGGATATGACCAAATCTATAATGTAATTGTTACAGTTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCATTATAGCTTTTCCCCTTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR742514, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13265 Chironomidae sp. water mite diet isolate 13265-BHL040517-GBD13106_18941-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTTCTTTTATTGGAGATGATCAAATTTATAACGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTAAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGTAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13266 Chironomidae sp. water mite diet isolate 13266-BHL040517-GBD25868_24550-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATATTAATTCGAGCTGAATTAGGACACCCTGGTTCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCGTGCCATTAATACTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTATCAAGAAGTATTGTAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13269 Chironomidae sp. water mite diet isolate 13269-BHL040517-GBD25207_20929-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTTTATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGACTATTAATTCGAGCTGAATTAGAACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAGTATAAGTTTTTGATTATTACCCCCAGCTCTAACATTATTACTAGCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13271 Paratanytarsus sp. water mite diet isolate 13271-BHL040517-GBD28313_20921-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTTGGAGCTTGGTCAGGAATAATCGGAACTTCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAAATGACCAAATCTATAATGTAATTGTTACTGCTCATGCTTTTATTATAAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTAGAAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGAATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13273 Chironomidae sp. water mite diet isolate 13273-BHL040517-GBD22955_26011-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTTGGAACTTCCTTAAGAATTTTAATTCGAGCTGAATTCGGTCAACCTGGTACTTTTATTGGAGATGATCAAATTTATAACGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGTGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTATCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13274 Chironomidae sp. water mite diet isolate 13274-BHL040517-GBD9821_22952-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTAAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTAGAGGATTTGGTAATTGATTCTTGCCATTAATACTAGAAGACCCAGATATAGATTTTCCTCGAATAAATAAAATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACGTTCAAGAAGCATTGTAGAAAATGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13277 Chironomidae sp. water mite diet isolate 13277-BHL040517-GBD15329_9492-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTACTGGAGATGATCAAGTTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGAAATAGCTTTTCCCCGAATAAATAATATAAGTTTTTGATTATTACCCCCAGCTCTAACATGATTACTTATCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13279 Chironomidae sp. water mite diet isolate 13279-BHL040517-GBD26479_11618-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTACTTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTCTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCCTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTATTATGATCTAGCTCTTTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13281 Chironomidae sp. water mite diet isolate 13281-BHL040517-GBD6830_15144-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGCGCTTGATCGGGAATAGTATGCACTTCTTTAAGAATTTTAATTCGACTAAAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGAGACCTATTTTAATTGTAGGCTTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACCTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13285 Chironomidae sp. water mite diet isolate 13285-BHL040517-GBD21005_27143-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTTGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCACATTCTTTCATTATATTTTTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTTTTGCCATTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTCTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13286 Chironomidae sp. water mite diet isolate 13286-BHL040517-GBD22796_6612-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTATTGATTATTACCGCCAGCTCGAACATTATTACATGCAAGAAGCATTGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KM995398, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13287 Chironomidae sp. water mite diet isolate 13287-BHL040517-GBD9666_21017-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTCAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATAATAAGCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13288 Chironomidae sp. water mite diet isolate 13288-BHL040517-GBD22919_3911-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTCAAGAATTTTAATTCGAGCAGAACTCTGTCACGCTGTTTCTTTAATCGGAGACTATCAAATTTATAATGTCATTGTTACCGCTCACGCTTTTGTAATACTTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATACAGCATTCCCTCGAAAAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13289 Cryptochironomus sp. water mite diet isolate 13289-BHL040517-GBD8456_21788-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGAACAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATGGTTATATCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGTCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTATTACCCCCATCCTTGACTCTACTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13290 Diptera sp. water mite diet isolate 13290-BHL040517-GBD11922_17439-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAACTTTAACTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGAACAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATACCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAAAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.3% identical to accession ID KM455055, identified in GenBank as Philophylla caesio. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13291 Chironomidae sp. water mite diet isolate 13291-BHL040517-GBD28152_20014-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTTAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAAGTATACCAATTTTAATTGGAGGATTTGGTAATTGTCTCTTGCCATTAATACTAGGGTCCCCAGATATAGCTTTTCCTCGAATAAATAATAAAAGTTTTTGGTTATTACCCCCATCTCCAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13292 Chironomidae sp. water mite diet isolate 13292-BHL040517-GBD24443_11381-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGAAGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAAAAAAAAAATAAGGTTTTGATTACTTCCCCCGTCATTAACCTTATTATTATCCAGCTCGCTAGGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13294 Paratanytarsus sp. water mite diet isolate 13294-BHL040517-GBD12678_25954-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGCACTTCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAAATTTTTTTTATAGTTATACCTATTTTATTTGGGGGTTTTGGAAATTGATTTTTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGAATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTACTTCTATCAAGAAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13297 Chironomidae sp. water mite diet isolate 13297-BHL040517-GBD10761_27016-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATATTTATACCAATTTTAATTAGAGGATTTGGTAATTGACTCTTGCCATTAATACTAAGATCCCCAGATATAGCTTTTCCTCGCATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATGATTACTATCAAGAAGTATTGTAGAAAATGGAGATGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13298 Paratanytarsus sp. water mite diet isolate 13298-BHL040517-GBD12044_10447-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCACGTATAAACAACATAAGATTTTGACTACTACCCCCATCTTAAACCCTTCTAGTATCAAGAAGAGTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13299 Chironomidae sp. water mite diet isolate 13299-BHL040517-GBD28678_12729-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTCGAATTAGGACACCCAGGCTCATTAATCGGAAACAATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTGGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTGCCGCGAATAAATAAAATAAGATTTTGATTATTACCCCCATCATTAACCTTACTTTTATCAAGATCAATAGTAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13300 Orthocladiinae sp. water mite diet isolate 13300-BHL040517-GBD11274_23243-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCAATGATCGGAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTATTTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCTTTTCTCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13304 Paratanytarsus sp. water mite diet isolate 13304-BHL040517-GBD5065_10056-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATCTTTTATTTTCGGAGCTTGGTCAGGAATAATCGAAACATCCTTAAGTCTACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGACATAGCGTGTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13308 Chironomidae sp. water mite diet isolate 13308-BHL040517-GBD15900_23093-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCTCGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAACGTATTTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATTCCAATTTTAATTGGAGGATTTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTCTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13309 invertebra sp. water mite diet isolate 13309-BHL040517-GBD21937_15020-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAA-TCATAAAGATATTGGTTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTACTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTTACTTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.7% identical to accession ID GU070927, identified in GenBank as invertebrate environmental sample. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13316 Paratanytarsus sp. water mite diet isolate 13316-BHL040517-GBD20599_25881-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCTGAACATCCTTAAGTATACTAATTCGAGTAGAATTAGGGCACCCTGGATCATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATACTTTTATTATAATTTTTTTTTATAGTTATACCTAGTTTAATTGGGGGTTTTGGGAATTGACTCCTTCCTTTAATATTAGGAGCTCCTGATATATCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAAAAGATTAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13318 Chironomidae sp. water mite diet isolate 13318-BHL040517-GBD21696_11147-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATTTTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGAAGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTCATTATAAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTCTTGCCATTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTTTAACATTATTACTATCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13319 Chironomidae sp. water mite diet isolate 13319-BHL040517-GBD3286_10933-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTGGATTCGAGCAAAACTAGGTCACGCTTGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTTGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGTGAGCCCCTGATATAGCATTCCCTCGACTAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13320 Chironomidae sp. water mite diet isolate 13320-BHL040517-GBD18771_9662-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGATTATTAATCGGAGACGAACAAATTTATAATGTAATTGTTACAGCACATGCTTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCATCATTAACCTTACTTTTATCAAAAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13322 Chironomidae sp. water mite diet isolate 13322-BHL040517-GBD20658_4338-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAACGTAATTGTTACTGCACATGCTTCCATTATAATTTTTTTTATAGTTATACCAATTTAAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGTAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13323 Paratanytarsus sp. water mite diet isolate 13323-BHL040517-GBD9736_16656-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATTAAATCTATAATATTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTGCATCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13326 Chironomidae sp. water mite diet isolate 13326-BHL040517-GBD22887_9929-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAAATGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGTAGCTCCCGACATAGCATTCCCTCGAATAAACAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13327 Chironomidae sp. water mite diet isolate 13327-BHL040517-GBD10476_26317-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCTAGCTGAATTAGGTCATCCTGGTACTTTTATTTGAGATGATTAAATTTATACTGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAAATGGAGGATTAGGTAATTGACTCTTGCCATTAATACTATGAGACCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTAGTACTTTCAAGAAGTATTGTAGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13331 Chironomidae sp. water mite diet isolate 13331-BHL040517-GBD20495_21196-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGTAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAACGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCATATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCCATCCCTGACATTATTACAATCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13334 Chironomidae sp. water mite diet isolate 13334-BHL040517-GBD22559_25783-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGTCTGATCAGGAATAGTTGGAACTTCCTTATGAATATTAATTCGAGTTGAATTAGGACATCCTGGTACTTTTATTAGAGATGATTAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCATTTCCTCGAAAAAATAATATAAGTTTTTGATTATTACCCCCAACTCTAACATAATTACCTTCAAGAAGTATTGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13340 Chironomidae sp. water mite diet isolate 13340-BHL040517-GBD19521_21901-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGACTATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATAAAATTTATAATGTAATTGTTACTGCACATGCTTTGATTATAATTATTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGATTCTTGCCATTAATACTAGGGGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13342 Paratanytarsus sp. water mite diet isolate 13342-BHL040517-GBD21488_8561-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATACTTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAAGAGTTCCCGAAATAACCTTTCCCCGTAAAAATAACATAAAGTTTTGAATAACACCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13344 Paratanytarsus sp. water mite diet isolate 13344-BHL040517-GBD27654_10834-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGCATAGTAGGAACTTCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGATCATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTACTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGAATAAATAACATAAGTTTTTGATTACTTCCCCCGTCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13347 Chironomidae sp. water mite diet isolate 13347-BHL040517-GBD6221_8692-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATTCTAATTCGAGCAGAATTAGGACACGCAGGGTCATTAATTGGAGACGAACAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCAAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13349 Paratanytarsus sp. water mite diet isolate 13349-BHL040517-GBD22665_7701-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGTGCCTGGTAAGGAATAATCGGAACTTCCTTAAGTATACTAATTCGAGCTGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGTTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGATTTTGACTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13354 Chironomidae sp. water mite diet isolate 13354-BHL040517-GBD4705_15604-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAATTTCCTTAAGAATATTATTTCGAGCTGAATTAGGACATCCTGGTAATTTTATTGGAGATGTTCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTTTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTTGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13355 Paratanytarsus sp. water mite diet isolate 13355-BHL040517-GBD5174_16216-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTTGGAGCTTGGTCAGGTATAATCGGAACTTCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGGTTTGGGAATTGACTTCTTCCTTTAATATTAGGAAGCTCCCGATATAGCTTTTCCACGAATAAATAACATAAGATTTTGATTACTACCCCCATCTCTAACCCTACTTCTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13360 Paratanytarsus sp. water mite diet isolate 13360-BHL040517-GBD25812_24181-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATTTATATTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTTAAACATTTATTGGAGATGACTAAATCTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGTGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCGTCTTTAACCCTTCTCCTATCAAGAAGATTAGTGTAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13361 Orthocladiinae sp. water mite diet isolate 13361-BHL040517-GBD6589_18229-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTGATCGGAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGACCCTGATATAGGTTTTCCCCGAATAAATAATACAAGATTTTGATTATTACCAACAGCATAAACCTTACTTTTATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13362 Paratanytarsus sp. water mite diet isolate 13362-BHL040517-GBD28531_20689-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTCGGAGCTTGGTCAGGAATAATAGGAACATCCTTAAGTATACTAGTCCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTATAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTGCCCCGTATAAATAACATAAGTTTTTGATTACTTTCCCCATCTTTAACCCGTCTTCTATCAAAAAGATGAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13366 Chironomidae sp. water mite diet isolate 13366-BHL040517-GBD9936_26845-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGTTCATTAATAGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCCCCAATAAATAATATAAGATTTTTATTATTACCCCCCTTCATTAACCTTACTTTTATCAAGATCATTAGTAGAAAATGAAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13371 Chironomidae sp. water mite diet isolate 13371-BHL040517-GBD24238_8568-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAAATAGGACATCCTGGAACTTTTATTGGAGATGATTAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATATTAGGAGCCCCAGACATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13372 Chironomidae sp. water mite diet isolate 13372-BHL040517-GBD13714_9223-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGTACTTCCTCAAGAATATTAATTCGAGCTGAATTAGGACATCCTGATACTTTTACTGGAGATGAACAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13376 Chironomidae sp. water mite diet isolate 13376-BHL040517-GBD13792_5657-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGTTACTTTTATTGGATATAATCAAATTTATAATGTAATTGTTACTTCACATTCTTTCATTATAATTTTTTTTTATAGTTATTCCAATTTTAATTGGAGGATTTGCTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13377 Chironomidae sp. water mite diet isolate 13377-BHL040517-GBD7931_20369-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGACCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATGATATAAGATTTTGATTATTACCCCCATCTTTAACATTATTACTATCAAAAAGTAGAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13380 Chironomidae sp. water mite diet isolate 13380-BHL040517-GBD17593_26932-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGACCAGGTATAGTAGGTCTATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGTTTCTTTATTCGGAGACGATCAAATTTATAATGTAATTGTTACCGATCTCGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGTTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13384 Chironomidae sp. water mite diet isolate 13384-BHL040517-GBD19489_18586-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATAGGAGGATTTGGCAATTGACTATTGCCATTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATGACCCCCATCTCTAGCATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13405 Paratanytarsus sp. water mite diet isolate 13405-BHL040517-GBD2752_10941-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACTTCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGATACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTTTTTTATTTGGGGGTTTTGAGAATTGACTTCTTCCTTTAATATTAGGAGGTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTTTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13406 Paratanytarsus sp. water mite diet isolate 13406-BHL040517-GBD25022_8892-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATTGGAACTTCCTTAAGTATATTAATTCGAGTAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCGACTTCTATCAAGAAGATTAGTGTAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13408 Paratanytarsus sp. water mite diet isolate 13408-BHL040517-GBD24734_19546-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAGGTATACTAATTCGAGCAGAATTAGGGCACACTGGAACATTTATTGGAGATGACCAAATCTAAAATGTAATTGTTACAGCTCATGCCTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTTGGGGTTTTGGGAATTGACTTCTTCCTTTAAAATTAGGAGCTCCCGATATAGCCATTCCCCTGCATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13411 Paratanytarsus sp. water mite diet isolate 13411-BHL040517-GBD20970_17625-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTTTACTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGGCACCATGGAACATTTATTGGAGATGATCAAAACTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATGCCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAACTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTGCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR672858, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13412 Chironomidae sp. water mite diet isolate 13412-BHL040517-GBD11913_28708-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGTCTGATCAGGAATAGTTGGAACTTCCTTTAGTATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCATTTTTAATTGGAGGATTTGATAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13414 Paratanytarsus sp. water mite diet isolate 13414-BHL040517-GBD8631_21582-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGAAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTACTTCGAGCAGAATTAGGGCACCCTGTAACATTTATTGGAGATGACCAAATCTATAATGTAATGGTTACAGCTCATTCTTTTATTATAATTTTTTTTATAGTTATTCCTATTTTAATTGGGGGTTTTGGTAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13417 Chironomidae sp. water mite diet isolate 13417-BHL040517-GBD23624_19381-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTGTATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGTACTTCCTTAAGACTATTAATTCGCGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCAGTAATACTAGGAGCCCCAAATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCAACTCTAACATTATTACTTTCAAGAAGTAGTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13425 Chironomidae sp. water mite diet isolate 13425-BHL040517-GBD7088_17527-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTTGGAGCCTGATCAGGATTAGTTGGAACTTTCTTAAGAATATTATTTCGAGCTGAATTAGGAAATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13428 Chironomidae sp. water mite diet isolate 13428-BHL040517-GBD10224_23093-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTTGGTACTTCCTTAAGAATATTAATTCGAGCTTAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAAAATAAGTTTTGGATTATGACCCCCATCTCTAACAGTATTGCTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13430 Chironomidae sp. water mite diet isolate 13430-BHL040517-GBD14689_2231-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAGTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTTGTACTTTTATTGGAGATGAGCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCGATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTATGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13436 Paratanytarsus sp. water mite diet isolate 13436-BHL040517-GBD26724_8263-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGTACATCCTTAAGTATACTAATTCGAGTAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACTAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGAGTTTTGGGAATTGACTTCTTCCATTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13437 Paratanytarsus sp. water mite diet isolate 13437-BHL040517-GBD21571_22499-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGACCATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAAATTTTTTTTATAGTTATACCTATTTTAATTAGGGGTTTTGGAAATTGACTTTTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGAATAAATAACATAAGATTTTGATTACTTCCCCCATCTTTAACCCTACTTCTATCAAGAAGAATAATGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13439 Paratanytarsus sp. water mite diet isolate 13439-BHL040517-GBD29136_11766-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTGTATTTCATTTTCGGAGCTTGGTAAGGTATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCATTTCCCCGAATAAATAACATAAGTTTTTGATTACTCCCCCCATCTTTAACCCTACTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13451 Chironomidae sp. water mite diet isolate 13451-BHL040517-GBD10186_22467-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTTAATTCGACTAGACTTAGTACACCCAGGATCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGCTATAGCATTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13452 Chironomidae sp. water mite diet isolate 13452-BHL040517-GBD15470_9756-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATTCGGTATAGTAGGTACCTCTTTAAGAATTTTAATTCGGGCAGCACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTGTGATTACTTCCCCCGTCATTAACATTATAATAATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13456 Paratanytarsus sp. water mite diet isolate 13456-BHL040517-GBD11475_10857-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTTTATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGACCGTCCTTACGTATACTAGTTCGAGCAGTATTAGTGCACCCTGGAACATTTATTGGAGATGACCAAATCTATCATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGTTTCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAAAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13457 Chironomidae sp. water mite diet isolate 13457-BHL040517-GBD16052_19130-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTTATTCGAGCTGAATTAGGACAATCTTGTACTTTTATTGGAGAAGATCAAATTTATTATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13459 Chironomidae sp. water mite diet isolate 13459-BHL040517-GBD6717_20184-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTTGGAGCCTGTTCAGGAATAGTTGGAACTTCCTTAAGAATATTATTCAGAGCTGAATAAGGACATCCTGGTACTTTTATTGGAGCTGATCAATTTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1346 Chironominae sp. water mite diet isolate 1346-BHL110116-GBD7153_11045-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGGACTTCTTTTAGTATGTTAATTCGAGCATAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTCACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR754526, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13461 Chironomidae sp. water mite diet isolate 13461-BHL040517-GBD13477_25967-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATGTTTATTCGAGCTGAATTAGGACAACCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGACTCTTGCCATTAATACTAGGAGCCCCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCACTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13470 Chironomidae sp. water mite diet isolate 13470-BHL040517-GBD29426_17393-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCAGGAACCGGACGGGGAGCAAGAGCAAGAGGAGAAAAGGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13473 Chironomidae sp. water mite diet isolate 13473-BHL040517-GBD25692_20283-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCCTTAAGAATACTAATTCGAGCTGAATTAGGACAACCTGGTACTTTATTTTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTAATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTCTTGCCTTTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTATCTAGAAGAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13477 Paratanytarsus sp. water mite diet isolate 13477-BHL040517-GBD24347_8727-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTTGGAGCTTGGTCAGGAATAATCGGTACTTCCTTAAGTATATTAATTCGAGCAGAATTCGGGCACCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCCTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTTTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCTAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13484 Chironomidae sp. water mite diet isolate 13484-BHL040517-GBD22876_5174-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTTGGAGCCTGCTCAGTAATAGTTGTGACTTCCTTAATAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCACAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATAATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13489 Chironomidae sp. water mite diet isolate 13489-BHL040517-GBD3959_22024-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTTGGAACTTACTTAAGAATATTAATTCGAGTTGAATTTAGACATCCTTGTACTTTTATTGGAGATGATCCAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTGTCCTCGAATAAATAATATAAGTTTTGGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13492 Paratanytarsus sp. water mite diet isolate 13492-BHL040517-GBD7461_14682-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCCTGGTCAGGAATAATCGGAACTTCCTTAAGTATACTAATTCGAGCTGAATTAGGGCACCCCGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGGGGGTTTGGGAATTGACTTCTTCCTTTAATATTAGGAACTCCCGATATAGCTTTACCCCGGAAAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGAATAGTGGAAGAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1350 Oligochaeta sp. water mite diet isolate 1350-BHL110116-GBD26651_8465-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGTATACTAATTAGAATTGAATTATCATAACCAGGAACATTCTTAGGAAGAGATTAATTATATAAAACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCGCCATCTCTAATCTTGCTAATATCTTCTACAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL13500 Chironomidae sp. water mite diet isolate 13500-BHL040517-GBD21449_26028-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGACTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAATTAGGACACCCAGGCTCATTAATCGGAGACAATCAAATTTATATTGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATCATTACCCCCTTCATTAACCTTACTTTTATCAAAATCAATAGTAGAGAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13508 Chironomidae sp. water mite diet isolate 13508-BHL040517-GBD5721_7595-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTGTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGTTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGTTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCTCTCACGCTTTTGTAATAATTTTTTTTTATACTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGAGAGCCCCTGATATAGCATTCCCTCGAATATACAATATAAGTTTTTGATTACTTCCCCCATCATTAACTTTATTATTATCTCGCTCTCTAGTTGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13511 Paratanytarsus sp. water mite diet isolate 13511-BHL040517-GBD27401_18498-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAAGGAAGCTTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13512 Paratanytarsus sp. water mite diet isolate 13512-BHL040517-GBD24987_23774-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGGGCTTGGTCAGGAATAATCGGAACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTAAATTGGAGGTTTTGGGAATTGACTTCTTCCTGTAATATTAGGAGCTCCCGATACAGCTTTTCCCCGAATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13516 Paratanytarsus sp. water mite diet isolate 13516-BHL040517-GBD13525_23401-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATATTCGGAACTTCCTTAAGTATTTTAATTCGAGTAGAATTAGGGCACCCTGGCACATTTATTGGAGAAGAACAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTACTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGATTTTGATTACTACCCCCATCTTTAACCCTTCTTCTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13523 Chironomidae sp. water mite diet isolate 13523-BHL040517-GBD11632_9865-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAGCTTCCTTAAGAATATTAATTCGATCGGAATTAGGACATCCTGGTTCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCTTTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATAATAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13532 Paratanytarsus sp. water mite diet isolate 13532-BHL040517-GBD16777_20364-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGTTCATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGAAATTGACTACTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGAATAAATAACATAAGTTTTTGATTACTTCCCCCATCATTAACCCTTCTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR742514, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13538 Chironomidae sp. water mite diet isolate 13538-BHL040517-GBD3945_9200-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTTAGAATTCTAGTTCGAGCAGAATTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTATTATTGGGAGTCCCATGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13539 Paratanytarsus sp. water mite diet isolate 13539-BHL040517-GBD21619_24762-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTACTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACGGCCCCCCACTTTAACCCATCATCAATCAAGAAGATGAGTGGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13540 Paratanytarsus sp. water mite diet isolate 13540-BHL040517-GBD7303_4853-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACTTCCTTAAGTATACTAATTCGAGCAGGATTAGGACACCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAACTGACTTCTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCCCGTATAAATAACATAAGACTTTGATTACTTCCCCCATCTTTAACCCTTCTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13543 Paratanytarsus sp. water mite diet isolate 13543-BHL040517-GBD11828_23985-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGAAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13544 Paratanytarsus sp. water mite diet isolate 13544-BHL040517-GBD11505_7759-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCCGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13545 Chironomus sp. water mite diet isolate 13545-BHL040517-GBD17256_3588-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCACGCATTTATTATAAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTAGGAAACTGACTTGTCCCCCTAATACTTGGAGTACCTGACATAGCTTTTCCCCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGATCTTTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13547 Chironomus riparius water mite diet isolate 13547-BHL040517-GBD12019_4209-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTCTACCAATTTTAATTGGAGGATTCGGAAACTGACTTATCACCCTAATACTGGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13548 Diptera sp. water mite diet isolate 13548-BHL040517-GBD14343_20162-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCCTTTACATCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.6% identical to accession ID KP702938, identified in GenBank as Lutzomyia umbratilis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13549 Chironomus sp. water mite diet isolate 13549-BHL040517-GBD26228_10271-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATATCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13550 Chironomus riparius water mite diet isolate 13550-BHL040517-GBD18263_27474-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGTAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCCCGAATAAATAATATAAGTTTCTGACTTTTTCCCCCCTCTCTTACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13551 Cricotopus sp. water mite diet isolate 13551-BHL040517-GBD8391_24958-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAACAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13552 Mucor sp. water mite diet isolate 13552-BHL040517-GBD20880_22942-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACTTTATATATCATCTTCTCTATTTTTGCCGGTATGATTGGTACTGCTTTTTCTATGTTAATTAGACTAGAATTAGCTGGCCCTGGAATTCAATATCTTCATGGTGATCATCAATTATCTAATGTACTTGTAACTGCTTACGCATTTGTAATGATTTTCTTCTTAGTAATGCCTGCAATGATTGGAGGTTTTGGTAACTGGTTTGTTCCTTTAATGATTGGAGCTCCTGATATGGCCTTCCCTCGATTAAATAATATTTCATTCTGGTTATTACCACCTTCTTTAATTCTATTAGTAGCTAGTGCCTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.7% identical to accession ID KR809877, identified in GenBank as Mucor circinelloides f. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13553 Psectrocladius sp. water mite diet isolate 13553-BHL040517-GBD18889_28965-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTGGGAGCCCCCGACATAGCAATCCCTCGAAAAAATAAAATAAGTTTTTGAATACTTCCCCCGTCATTAACTTTACTATTAACTAGCTCTCTAGTTGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13554 Chironomidae sp. water mite diet isolate 13554-BHL040517-GBD25388_16518-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13558 Chironomus riparius water mite diet isolate 13558-BHL040517-GBD11646_28282-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTATGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACGTGTTTTTATTATAATTTTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGCCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13559 Chironomus sp. water mite diet isolate 13559-BHL040517-GBD27108_10019-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGCGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATCTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13560 Mucor sp. water mite diet isolate 13560-BHL040517-GBD25408_22996-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACTTTATATATCATCTTCTCTATTTTTTGCGGGTTTGCTTGGTACTGCTTTTTCTTTGTTAATTAGACTGGAATTAGCTGGTCCTGGAATTCAATATCTTCATGGTGATCATCAATTATAGAATGTAATTGTAACTGCTCACGCATTTGTAATTATTTTCTTCTTAGTAATTCCTGCAATGATTGGAGGTTTTGGTATCTGGTTTGTTCCTTTAATGATTGGAGCTCCTGATATGGCCTTCCCTCGAATAAATAATATTTCATTCTGGTTATTACCACCTTCTTTAATTCTTTTAGTAGCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID KR809877, identified in GenBank as Mucor circinelloides f. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13562 Chironomus riparius water mite diet isolate 13562-BHL040517-GBD22274_3317-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTATTTGGGACTTGCTCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCATTTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCGTTCTAGTTCTTTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13563 Chironomidae sp. water mite diet isolate 13563-BHL040517-GBD13980_17284-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATCGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAACATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAATAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13564 Chironomus sp. water mite diet isolate 13564-BHL040517-GBD28054_20079-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTAATTGGAGATGACCAAATTTATAATCTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATCGGAGGGTTCGGAAACTGACTTTTCCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTCTACCCCCCTCTCTTACTCTTCTTCTTTCTAGAACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13565 Chironominae sp. water mite diet isolate 13565-BHL040517-GBD16015_25785-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCCCTTAGTATATTAATTCGAGCATAACTTGGACACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR286005, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13566 Chironomidae sp. water mite diet isolate 13566-BHL040517-GBD4002_15371-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGCTCAAATTTATAATGTAATTGTTACCGCTCACGCTTCTGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCGTTAATATTAGGAGCCCCCGACAGAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13568 Chironomus riparius water mite diet isolate 13568-BHL040517-GBD21343_8185-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACAAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATCTTTTTCATAGTTATACCAATTTTAATTGGAGGTTTCTGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCATCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13569 Chironomidae sp. water mite diet isolate 13569-BHL040517-GBD26366_14985-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGGCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13570 Psectrocladius sp. water mite diet isolate 13570-BHL040517-GBD15052_27241-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13572 Paratanytarsus sp. water mite diet isolate 13572-BHL040517-GBD2471_17204-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTTTATTTTATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCTTTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGATCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTT-ATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTACCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13573 Chironomus riparius water mite diet isolate 13573-BHL040517-GBD20418_17870-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTACGAATGCTTATTCGTGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTACAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACACTACTTCATTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13574 Psectrocladius sp. water mite diet isolate 13574-BHL040517-GBD28327_18612-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAAAAAAAAATATAAGTTTTTGATTTCTTTCCCCCGTCATTAACTCTACTATTATCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13576 Chironomidae sp. water mite diet isolate 13576-BHL040517-GBD20139_3207-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGATTAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAAGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTTCAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGGATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACGTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13578 Psectrocladius sp. water mite diet isolate 13578-BHL040517-GBD17680_19438-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGTAGAATTAGGTCATCCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13579 Chironomus riparius water mite diet isolate 13579-BHL040517-GBD8072_24052-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAAATAGGACGACCCGGAACTTTCATTGGAGATGACCATATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTTTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACCCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13582 Chironomus sp. water mite diet isolate 13582-BHL040517-GBD2961_13681-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTTATTCGAGCAGAATTAGGACGACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13584 Paratanytarsus sp. water mite diet isolate 13584-BHL040517-GBD13911_10443-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGGATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAATTGATACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCGTCCCCCCTCTTTAACTCTTTAAATATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13586 Psectrocladius sp. water mite diet isolate 13586-BHL040517-GBD4875_11218-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGGCATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTCGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGATCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13587 Chironomus riparius water mite diet isolate 13587-BHL040517-GBD7804_14986-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTATGAATGCTTACTTGAGCAGAATTAGTACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTGGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTGTACCAATTTTAATTGGAGGATTGGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13590 Paratanytarsus sp. water mite diet isolate 13590-BHL040517-GBD20976_25175-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATAATTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGCATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAA-TTTTTTCATAGTTATACCTATTTTAATTGGAGTATTTGGGAACTGATTATTGCCTTTAAAATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCACCTCTTTAACTCTTTTACTACCAAGTAGAATAGCGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13591 Psectrocladius sp. water mite diet isolate 13591-BHL040517-GBD19144_20027-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCCCTAAGAATCTTAATTCGAGCTGAATTAGGTCAGGCCTGGTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACCGCTCACGCCTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13593 Chironomus riparius water mite diet isolate 13593-BHL040517-GBD14778_16483-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAACACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCATCTTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13596 Paratanytarsus sp. water mite diet isolate 13596-BHL040517-GBD11882_28127-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAGCTTTATACATTATTTTTTGGGGCTTCCTCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGATCTGAATTAGGAGGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTCTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.1% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13598 Psectrocladius sp. water mite diet isolate 13598-BHL040517-GBD16741_2344-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGTTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGCTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTCGTTCAAAATGGCGCTGGACCAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13599 Psectrocladius sp. water mite diet isolate 13599-BHL040517-GBD14076_4444-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATGTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13600 Chironomus riparius water mite diet isolate 13600-BHL040517-GBD5739_10887-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATAGGAGGATTCGGAAACTGACTTGTCCCCCTAATACATGGAGCCCCTGACATAGCTTTTCCCCGAATAAATAACATAAGTTTCTGACTTTTACCCCCCCTCTCTTACCCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13603 Dicrotendipes sp. water mite diet isolate 13603-BHL040517-GBD4693_12950-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGGTATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCAATCTAGAGCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13604 Paratanytarsus sp. water mite diet isolate 13604-BHL040517-GBD23231_26372-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGAGCCTGATCAGGAATAGTGTGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAA-TTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGTACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCCATCTTTAACTCTTTTACTTCCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13605 Chironomus riparius water mite diet isolate 13605-BHL040517-GBD8062_3766-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13606 Paratanytarsus sp. water mite diet isolate 13606-BHL040517-GBD22497_5272-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCACTTTTGGTGCCTGATAAGGAATAGTAGTTACTTCCCTTAGAATATTAATTCGAGCTGATCTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCTTGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTTGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13614 Psectrocladius sp. water mite diet isolate 13614-BHL040517-GBD3669_18712-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATATTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGCTGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATCATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAAGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTTTTATCTAGCTCTCTACTTGAAAAGGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13615 Chironomus riparius water mite diet isolate 13615-BHL040517-GBD5993_18208-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACGTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTAGAGCAGTATTAGGACGACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTTAATGGGAGGATGCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13616 Chironomus riparius water mite diet isolate 13616-BHL040517-GBD8602_21929-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGGTGAACAAACTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTATCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13617 Chironomus riparius water mite diet isolate 13617-BHL040517-GBD21984_23708-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCATAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13621 Psectrocladius sp. water mite diet isolate 13621-BHL040517-GBD18969_22247-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCTACCGAAATAGCATTCCCTCGAATAAATAATAAAAGTTTTTGATTACTTCCCCCGTCATTAACATAACTATTATCTAGGTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13623 Chironomus sp. water mite diet isolate 13623-BHL040517-GBD9398_16788-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGCTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCATAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTTTCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13624 Chironomus riparius water mite diet isolate 13624-BHL040517-GBD24592_22126-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGTACGACCCGGAACTTTCATTGGAGATGACCAATTTTATAATGTTGTAGTTAATGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTATTTGGAGGATTCGGAAACTGACCTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTCTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13625 Chironomidae sp. water mite diet isolate 13625-BHL040517-GBD14925_10959-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTTGGGGCCTGATCGGGGATAGTAGGGTCATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACAACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTATGATTACTTCCTCCTTCTCTATCACTTTAACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13626 Chironomus sp. water mite diet isolate 13626-BHL040517-GBD26067_10171-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTTATCCGGTATAGTGGGTACTTCATTAAAAATTCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACTAAATTTATAATGTTATAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGATGATTCGGAAACTGACTTGTCCCCCTAATACTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGATCTTTAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13627 Psectrocladius sp. water mite diet isolate 13627-BHL040517-GBD19616_22304-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATATTGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTAATTTAATTGGAGGATTTGGAAATTGATTATTCCCGTTATTATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAAAATAAGTTTTTGATTACTTCCCCCGTCATTCACTTTACTATAATCTAACTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13628 Chironomus sp. water mite diet isolate 13628-BHL040517-GBD9290_21004-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTAGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCAGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTCAGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTGCTTCTGTCGAATTCTTTCGTAGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13629 Psectrocladius sp. water mite diet isolate 13629-BHL040517-GBD18287_25507-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCAGAACTCGGACCAGCTGGTTCCTTCATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTAACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13630 Chironomus sp. water mite diet isolate 13630-BHL040517-GBD16590_26734-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATAGATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACAACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTCAATGGAGGATTCAGAAAAATGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTATACCCCCCTCTCTTACTCTTCTTCTTTTTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13632 Chironomus sp. water mite diet isolate 13632-BHL040517-GBD16509_12001-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGCGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGTTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTCGGTAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGAGCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13633 Paratanytarsus sp. water mite diet isolate 13633-BHL040517-GBD24491_8485-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAAATTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAGTAAATAATATAAGATTTTGACGTCGTCCCCCCTCTTTAACACTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACCGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13634 Chironomus sp. water mite diet isolate 13634-BHL040517-GBD19133_15061-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGCTCCGGTATAGTGTGTACTTCATTAAAAAATGCTTATTCGAGCAGAATTAGGACGACCCGGTACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGATACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACATGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCGTCTTCTTTCTAGAGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13636 Chironomus riparius water mite diet isolate 13636-BHL040517-GBD9888_3109-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCTCCTAATACTTGGAGCACCTGACATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTTTATCCCCCTCTCTTACTCTTCTTCTTTCGAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13639 Chironomus sp. water mite diet isolate 13639-BHL040517-GBD27573_14546-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCCCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATAATTGGAGCACCTGACATAGCCTTTCCCCGAAAAAATAATATAAGTTTCTGACTTTTACCCCCCTCCCTTACCCTTCTTCTTTTCTAGATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13642 Chironomus riparius water mite diet isolate 13642-BHL040517-GBD20967_22872-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTATGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAGCTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAACAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTTACTCGTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13645 Paratanytarsus sp. water mite diet isolate 13645-BHL040517-GBD27020_12721-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGAGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACAACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTCATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTTATTTTTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATCGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13647 Paratanytarsus sp. water mite diet isolate 13647-BHL040517-GBD18471_19550-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGCTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATACCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAA-TTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGATCTCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13649 Mucor sp. water mite diet isolate 13649-BHL040517-GBD18876_26109-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACTTTATATATCATCTTCTCTATTTTTGCGGGTATGATTGGTACTGCTTTTTCTATGTTAATTAGACTAGAATTAGCTGATCCTGGAATTCAATATCTTCATGGTGATCATCAATTACTTAATGTAATTGTAACTGCTCACGCATTTGTAATGATTTTCTTATTAGTAATGCCTGCAATGATTGGAGGTTTTGGTAACTGGTTTGTTCCTGTAATGATTGGAGCTCCTGATATGGCCTTCCCTCGATTAAATAATATTTCATTCTGGTTATTACCACCTTCTTTAATTCTTTTAGTAGCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR809877, identified in GenBank as Mucor circinelloides f. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13653 Chironomidae sp. water mite diet isolate 13653-BHL040517-GBD5266_18434-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCCCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCAAGCTTTTGTAATAATTTTTTTTCATAGTTATACCAATTTAAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13656 Cricotopus sp. water mite diet isolate 13656-BHL040517-GBD21378_15791-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13658 Chironomus sp. water mite diet isolate 13658-BHL040517-GBD15332_14536-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTCGGTGCCTGATTAGGAATAGTGGGAACTTCCCTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTGCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCAACTTACATACCTTTTCCTCGAATAAATAATATAAGTTTTTTACTTTTACCCCCCTCTCTTACGCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13662 Chironomidae sp. water mite diet isolate 13662-BHL040517-GBD10698_14875-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTTGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTTATAATTTTTTTCATAGTTATACCAATTTTATTTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCAGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13663 Psectrocladius sp. water mite diet isolate 13663-BHL040517-GBD18188_18936-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGTCACGCTGGTTCTTTAATTGGAGATGAACAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTAAATTGGAGGATTGGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13667 Paratanytarsus sp. water mite diet isolate 13667-BHL040517-GBD21511_3997-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTGTACTTCATTTTCGGTGCCTGATCAGGTATAGTGTGAACTTCCCCTGAGAATATTAATTCGAGCTGAACTAGGACCTCCCGGAACCTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13669 Paratanytarsus sp. water mite diet isolate 13669-BHL040517-GBD25661_17191-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATACGAGCTGAACTAGGACATCCCGGGTCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGAATTTGACTTCTTCCCCCCGCTTTAACTCTATTACTACCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13671 Chironomus sp. water mite diet isolate 13671-BHL040517-GBD17455_20778-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTTGGGGGCTTGATCCGGATTAGTGGGAACTTCATTAAAAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGATCTTTCGTAGAAAATGGAGCTGTAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13673 Paratanytarsus sp. water mite diet isolate 13673-BHL040517-GBD22195_24689-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATGGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGGTCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCCTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGGAGAATAGTGGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13674 Psectrocladius sp. water mite diet isolate 13674-BHL040517-GBD21600_14015-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATCTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCATTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACATTACTATTATCAAGCACTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13676 Chironomidae sp. water mite diet isolate 13676-BHL040517-GBD13838_4250-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13678 Chironomus riparius water mite diet isolate 13678-BHL040517-GBD11519_12438-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTTGGGGCTTGATCCGTAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAATCTTCATTGGAGATGACCAATTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTCCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13680 Psectrocladius sp. water mite diet isolate 13680-BHL040517-GBD16904_5727-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCGTTAAGAATTTTAATTCGAGCAGAACTCGGTCAAGCTGTTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACTCTTTTGTAATAATGTTTTTTTATAGTAATAACTATTTTAATTGGAGGATTTGGAAATTGATTAGTCACGTGAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13684 Paratanytarsus sp. water mite diet isolate 13684-BHL040517-GBD7651_15974-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATCCTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTTGAGATGACTAAATTTATAATGTAATTGTTACAGCGCATGCATTTATTATAA-TTTTTTCATAGTTATACCTATTTTAACTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCTCCCTCTTTAACTCTGTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13686 Psectrocladius sp. water mite diet isolate 13686-BHL040517-GBD24810_6276-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTCGGTGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGCGCGGAACTCGGTCATGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAGTAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATCACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13688 Chironomus sp. water mite diet isolate 13688-BHL040517-GBD9212_15332-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGATTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCTCGCCTACACCTCATCAATCTAGAGCTTGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13691 Chironominae sp. water mite diet isolate 13691-BHL040517-GBD9081_16466-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGCCCTGGTACTTTTATTGGAGATGACCAAATTTACACTGTAATTATCACAGCATACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13696 Paratanytarsus sp. water mite diet isolate 13696-BHL040517-GBD16937_2572-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCTGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTGTTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGACACAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279360, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13697 Paratanytarsus sp. water mite diet isolate 13697-BHL040517-GBD28435_12753-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACCTCATTTTCGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAA-TTTTTTCATTGTTATTCCTATTTTTATTGGAGGATTTGGGAACTGAATATTGCCCTTAATAATAGGAGCCCCAGATATAGCTTTTCCTCGAAAAAATAATATAAGATTTTGACCTCTTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13700 Paratanytarsus sp. water mite diet isolate 13700-BHL040517-GBD24602_7459-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGCAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGCAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCGCTTTAACTCTTTTAGGGCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13703 Psectrocladius sp. water mite diet isolate 13703-BHL040517-GBD28163_14383-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATGTTAATTCGAGCAAAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTTATAATTTTTTTTTATAGTATTACCTATTTTAATTGGAGGTTTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGACATAGCATTCCCTTGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13704 Psectrocladius sp. water mite diet isolate 13704-BHL040517-GBD14369_6511-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTGATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACGTCCCCCGTCATTAACTTCACAAAAAGCTAGCGCTCGAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13705 Psectrocladius sp. water mite diet isolate 13705-BHL040517-GBD23173_23611-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGTGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTAGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTCCCGTTAATATTAGGAGCCTCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13707 Paratanytarsus sp. water mite diet isolate 13707-BHL040517-GBD22608_20289-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAGGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTAGTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGGTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCCTTTACGTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13708 Psectrocladius sp. water mite diet isolate 13708-BHL040517-GBD22144_26750-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGCGCTTGATCAGGCATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAAAACTAGGTCACGCTGATTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGTACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13710 Psectrocladius sp. water mite diet isolate 13710-BHL040517-GBD19710_26236-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGTCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCAAGCTGGTTCCTTAATTGTAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGATTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGATCCCCCGAGATAGCATTCTCTCGAATAAATAATAAAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAACGCTCTAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13714 Psectrocladius sp. water mite diet isolate 13714-BHL040517-GBD14949_28695-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTATCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTCCCGTTAATATTAGGCGCCCCCGACATAGCATTCCCCCGAAAAAAAAATATAAGGTTTCTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13715 Paratanytarsus sp. water mite diet isolate 13715-BHL040517-GBD9847_2756-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTATGAATATTAATTCGAGCCGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATGTAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCGTTAACACTTTTACAACCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13717 Paratanytarsus sp. water mite diet isolate 13717-BHL040517-GBD6674_17032-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACATTATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCAGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTATAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13720 Paratanytarsus sp. water mite diet isolate 13720-BHL040517-GBD24025_20193-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATACTTCGTTTTTCGGTGCCTGATCAGGATTAGTGGGAACTTCTCTAAGATTATTATTTCGAGCTGAACTAGGGCATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13727 Cricotopus sp. water mite diet isolate 13727-BHL040517-GBD6728_11204-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATACAGGGTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGGTATAGCTTTCCCTCGAATAAATAATATAAGTTTTTAATTATTACCTCCTTCTCTTACCTTATTACTATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13729 Chironomus sp. water mite diet isolate 13729-BHL040517-GBD16198_4512-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGAGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTAATTATTACCTCCTTCTCTTAC-CTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13730 Chironomus sp. water mite diet isolate 13730-BHL040517-GBD27653_11557-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGTGGCTTGATCCGGAATAGTGGGAACTTTATTAAAAATGCGTATTCGAGCAGAATTAGGATGACCCGGAATTTTTATTGGAGATGACCAAATTTATAAAGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAAGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCCCCTGACATAGCCTTTCCTCGAATAAAAAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13731 Paratanytarsus sp. water mite diet isolate 13731-BHL040517-GBD19464_4264-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAA-TTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGACTACTTCCCCCTTCTTTAACTTTATTACTACCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13733 Paratanytarsus sp. water mite diet isolate 13733-BHL040517-GBD3297_9045-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTATGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACATGCATTTATTATAA-TTTTTTCATAGTTATAACTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTATGAGCCCCAGATATAGCTTTTCCGCGAAGAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13735 Psectrocladius sp. water mite diet isolate 13735-BHL040517-GBD19269_26516-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGGGCTTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTATTAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGATCCCCCCACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13736 Paratanytarsus sp. water mite diet isolate 13736-BHL040517-GBD12726_28452-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATACTTCATTTTCGGTGCTTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTTATTCGAGCTGAACTAGGACATCCCGGAAATTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTT-ATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCATCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13737 Paratanytarsus sp. water mite diet isolate 13737-BHL040517-GBD23595_22564-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGGACTAAGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGTAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCATCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13741 Paratanytarsus sp. water mite diet isolate 13741-BHL040517-GBD17544_21422-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGAGCCAGATCAGGAATAGTGGGAACTTCCTTAAAAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTAATTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13748 Paratanytarsus sp. water mite diet isolate 13748-BHL040517-GBD28092_14423-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAA-TTTTTTCATAGTTACACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTTGGAGCCCCAGATATAGCTATTCCTCGAATAAATAATATATGATTTTGACTTCTTCCCCCCTCTGTAACTCTTTTACGACCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13752 Paratanytarsus sp. water mite diet isolate 13752-BHL040517-GBD11555_28281-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTACCTTAGAATATTAATTCGAGCTGAATTAGGACATCCCGGAACTTTTATTGGAGATGACCAACTTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATACAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCTCCCTCTTTAACTCTTTTACTTCCAAGTAGACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13754 Chironomus sp. water mite diet isolate 13754-BHL040517-GBD26375_7503-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACCTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATCGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGTGCACCTGACATAGCCTTTCCTCGAATAAAAAATATAAGTTTCTGACTGTAACCCCCCTCTCTTACTCTTCTACTTTCTAGAGCTTGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13755 Dicrotendipes sp. water mite diet isolate 13755-BHL040517-GBD26021_18867-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGGATTAGGACGACCCGGGACATTTATTGGAGATGATCAACTCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATGGTTATACCAATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCAAACTCTTCTCCATTCCAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13757 Paratanytarsus sp. water mite diet isolate 13757-BHL040517-GBD21898_23126-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCCAGCTGAACTAGTACATCCCGGATCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGATGATTTGTGTACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13758 Chironomus riparius water mite diet isolate 13758-BHL040517-GBD26175_17912-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGTGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTTGATGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGGTTCTGACTTTTACCCCCCCCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13759 Chironomus riparius water mite diet isolate 13759-BHL040517-GBD15172_3254-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGAAATAGGGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGTTACTTTCATTGGAGATGACCAGATTTATAACGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTGGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1376 Chironomidae sp. water mite diet isolate 1376-BHL110116-GBD28135_15447-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGTCACCCAGGCTCATTAATCGGACACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTATAAAATGGAGCTGAAACA	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13760 Chironomus sp. water mite diet isolate 13760-BHL040517-GBD21089_17242-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACCTGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGAATTGTCACCCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGGATAAATAATATAAGTTTTTGATTTTTACCCCCCTCACTAACTCTACTACTATCTAGTTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13762 Psectrocladius sp. water mite diet isolate 13762-BHL040517-GBD22522_19504-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGCATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTTGGTCAAGCTGGTTCCTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1377 Chironominae sp. water mite diet isolate 1377-BHL110116-GBD17685_4912-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGTAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTAGAATTTTTTTTATAGTTATACCTATTCTAATTGGTTGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCATGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCCTTCTAGCTCAATTGTATAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR754526, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13770 Paratanytarsus sp. water mite diet isolate 13770-BHL040517-GBD17985_2706-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAAATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAACTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGG	Using NCBI BLASTN in June 2018, this sequence was 98.4% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13772 Paratanytarsus sp. water mite diet isolate 13772-BHL040517-GBD19819_27656-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGTATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCATTAACGCGTTTACTTCCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13774 Paratanytarsus sp. water mite diet isolate 13774-BHL040517-GBD17786_28800-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGATCATTATACTTCATTTTCGGGGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAATTTTATAATGTAATTGTTACAGCTCATGTATTTATTATAATTTT-TTCATAGTTATTCCTATTTTAATTGGAGGATTTGGAAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13778 Paratanytarsus sp. water mite diet isolate 13778-BHL040517-GBD6254_20979-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAA-TTTTTTCATAGTTATACCTATTTTTAATTGGAGGATTTGGGAACCGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATAAAAGATATTGACTTCGTCCCCCCTCTTTAACTCGATTACTGCCAAGTAGACGAGTGGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13779 Chironomus riparius water mite diet isolate 13779-BHL040517-GBD22874_4647-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTGTACATTATTTTTGGGGCTTGATCCGGAATAGTGGGTACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGTATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATATGTTTCTGACTTTTACCCCCCTCGCTTACTCTTCCTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13783 Cricotopus sp. water mite diet isolate 13783-BHL040517-GBD16981_23259-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCCCTAAGAATCTTAATTCGAGCTAAATTAGATCATGCCGGGTCATTATTTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTCATTACTTTCAAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13786 Paratanytarsus sp. water mite diet isolate 13786-BHL040517-GBD26587_7759-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCTAAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCCCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCCTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13789 Psectrocladius sp. water mite diet isolate 13789-BHL040517-GBD25747_24059-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATCTTTGGAGCCTGAGCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCATGCTGGTTCCTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTCCCGTTAATATTAGGGGCCCCTGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13790 Paratanytarsus sp. water mite diet isolate 13790-BHL040517-GBD24163_14084-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGTATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAA-TTTTTTCATAGTTATACCTAATTTAATTGGAGGACTTGGGAACTGATTATTGCCTTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATGTTGACTTCTTCCCCCCTCTTTAACTCATTTACATCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13792 Paratanytarsus sp. water mite diet isolate 13792-BHL040517-GBD27067_17135-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTTATTTTCGGTGCTTGATCAGGAATAGTGGGAACTTCACTAAGAATATTAATTCGAGCTGAACTAGGACATACCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTTTTGCCTTTAATATTAGGAGCCCCAGATATAGCCTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCTTTTACTACCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13793 Paratanytarsus sp. water mite diet isolate 13793-BHL040517-GBD15875_26736-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGTTGAATTAGGACATCCTGTAACTTTTATTGGAGATGACAAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGTTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13797 Paratanytarsus sp. water mite diet isolate 13797-BHL040517-GBD19080_24365-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTAATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAAATAGTACATACCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATA-TTTTTTTCATAGTTACACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAGTATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13800 Paratanytarsus sp. water mite diet isolate 13800-BHL040517-GBD15462_16888-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTTAGAATATTAATTCGAGTTGAACTAGGACATCCCGGAACATTTATTGGAGATGACCAAATTTATAATGCAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTTGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTTTAACTCTTTTACTTCCGAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13801 Chironomus riparius water mite diet isolate 13801-BHL040517-GBD2526_14544-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGCATTAGGACGACCCGGAACTTTCAATGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGTGGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAGAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13809 Psectrocladius sp. water mite diet isolate 13809-BHL040517-GBD8404_7986-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGCATAGTAGGCATTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCATGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGATCTATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13816 Paratanytarsus sp. water mite diet isolate 13816-BHL040517-GBD13200_13795-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTATTGCCTTTAATATTAGGAGCCCCAGAGATAGCTTTGCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTATTACTGCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13819 Psectrocladius sp. water mite diet isolate 13819-BHL040517-GBD23906_5254-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCAAGCTGGTTCCTTAATTGGTGATGATCAAATTTATAATGTAATTGTTACCGGTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTTAATTGGAGGATTTGGAAATTGATTAGTTTCGTTAATATTAGGAGCACCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13822 Paratanytarsus sp. water mite diet isolate 13822-BHL040517-GBD7414_9960-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAAAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCCCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAAGTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGACTTTGACTTCTTCCCCCCTCTTTAACTCGTTTACATCCGAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13830 Paratanytarsus sp. water mite diet isolate 13830-BHL040517-GBD4349_18563-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCTGTGCTTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTT-CAAAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTTTTGCCTTCAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13832 Paratanytarsus sp. water mite diet isolate 13832-BHL040517-GBD15154_23484-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGAGTATTGCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279360, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13833 Psectrocladius sp. water mite diet isolate 13833-BHL040517-GBD22416_6711-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCATGCTGGTTCCTTTATTGGATATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCAGACATAGCATTCCCTCAAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAACACACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13836 Chironomus riparius water mite diet isolate 13836-BHL040517-GBD12553_8689-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTTTCCCCCTAATACTTGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCGCACTTACTCTTCTTCTTTCTAATTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13838 Chironomus sp. water mite diet isolate 13838-BHL040517-GBD26980_18651-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGTATCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCCCTTACACTACTACTATCTAGGTCTTTCGTAGTAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13840 Chironomidae sp. water mite diet isolate 13840-BHL040517-GBD5799_18281-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTAAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTCTGACTACTACCCCCGTCACTAACTTTATTACTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13841 Paratanytarsus sp. water mite diet isolate 13841-BHL040517-GBD14807_24970-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAA-TTTTTTCATTGTTATACCTATTTTAATTGGAGGATTTGGGTACTGATTATTGCCTTTAATATTAGGTGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTTGGATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13842 Paratanytarsus sp. water mite diet isolate 13842-BHL040517-GBD18977_5102-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTCGGGGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATGTTAATTCGAGCTGAACTAGGGCATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAA-TTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR282105, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13845 Paratanytarsus sp. water mite diet isolate 13845-BHL040517-GBD25641_15000-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTTATTTTTGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGTATATTAATTCGAGCTGAACTAGGACATCCCGGAACTCTTATTGGACATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTT-CATTGTTATACCTATTTTAATTTGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279360, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13849 Paratanytarsus sp. water mite diet isolate 13849-BHL040517-GBD18526_28712-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGATCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTCTAACTCGACTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13852 Psectrocladius sp. water mite diet isolate 13852-BHL040517-GBD24673_21635-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGACACGCTGGATCCTTAATTGGAGATGATTAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACAAAGCATTCCCTCGAATAAAAAATAAAAGTATTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13855 Chironomus riparius water mite diet isolate 13855-BHL040517-GBD26548_16658-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACCTTATTTTTGGTGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATTCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATCATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTACCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTGTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13857 Paratanytarsus sp. water mite diet isolate 13857-BHL040517-GBD26433_10266-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATCTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATTTTAATTCGAGTTGAACTAGGACATCCCGGATCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACTCTTTTACTACCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13859 Paratanytarsus sp. water mite diet isolate 13859-BHL040517-GBD24343_13335-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGTATAGTGGGTACTTCCTTAAGAATATTAATTTGAGCTGAACTAGGTCATCCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGTCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTACCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13862 Paratanytarsus sp. water mite diet isolate 13862-BHL040517-GBD7216_18536-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTGTAGTTCATTTTCGGTGCCTGATCAGGAATAGTGGGTACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTAGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGAGTTTGACTTCTTCCCCCCTCTTTAACTCAGGTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13863 Paratanytarsus sp. water mite diet isolate 13863-BHL040517-GBD12386_6566-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGTATATTAATTCGAGCTGAAGTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGTCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTCCCCCCCTCTCTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13867 Chironomidae sp. water mite diet isolate 13867-BHL040517-GBD28751_13900-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATTAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTCATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAAAAAAAAATAAAAGGTTTTGATTACTTCCCCCTTCATTAACTTTATTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13869 Paratanytarsus sp. water mite diet isolate 13869-BHL040517-GBD13250_26208-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGTCTGATCAGGAATAGTGGGAACTTCCCTATGAATTTTAATTCGAGTTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTT-ATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCAAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAATGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13870 Paratanytarsus sp. water mite diet isolate 13870-BHL040517-GBD15495_10546-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAA-TTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGTACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTGCCTCGAATAAATAATATAAGATATTGACTTCGTCCCCCCGCTTTAACACTAAAACTGCCAAGTAGAAGAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13874 Chironomus sp. water mite diet isolate 13874-BHL040517-GBD5193_14809-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGACCTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCATATTCGAGCGGAATTAGGACGATCCGGAACTTTCCTTGGAGAGTAACAAATTTATAATGGTGTAGTTACTGCACATGATTTTATTATAATTTTTTTCAGAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCGTCTTTCTAGATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13876 Paratanytarsus sp. water mite diet isolate 13876-BHL040517-GBD8034_16485-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAA-TTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTATGAGTCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCATCCACCCTCTTTAACTCTGTGACGACCAAGTAGAATAGTGGAAAATGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13882 Paratanytarsus sp. water mite diet isolate 13882-BHL040517-GBD12541_7512-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATAACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATAATAGGAGCCCCAGATATAGCTTTTCCTCGAATAAAAAATATAAGATTTTGAACTCTTCCCCCCTCTTTAACCCTTTTACCTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13884 Paratanytarsus sp. water mite diet isolate 13884-BHL040517-GBD17838_26643-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATACTTCATTTTTGGAGCCTGATCAGGAATAGTGGGAACTTACATAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTCGATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279360, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13885 Paratanytarsus sp. water mite diet isolate 13885-BHL040517-GBD12876_24055-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTGATTATACGTCATTTTCTGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGAAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATATTGACTTCTTCCCCCCTCTTTAACACTATTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13886 Psectrocladius sp. water mite diet isolate 13886-BHL040517-GBD23475_6950-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCGTAATTAACTCTACTACTACCTAGCACAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13890 Paratanytarsus sp. water mite diet isolate 13890-BHL040517-GBD17075_5652-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCTTAACTTTTATTGGAGATGACAAAATTTATAATGGAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGAGTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTTCTTCCAAGTAGAATAGTGGAAAATGGAGCTGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13895 Paratanytarsus sp. water mite diet isolate 13895-BHL040517-GBD22434_26006-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGAGCAGGAATAGTGGGAATTTCTCTAAGTATATTAATTCGAGCTGAACTATGACATCCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13897 Paratanytarsus sp. water mite diet isolate 13897-BHL040517-GBD12033_16752-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGCTCATTATATTTTATTTTCGGTGCCTGATCAGGTATAGTGGGAACTTCCCTAAGAATATTTATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAAATGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13899 Paratanytarsus sp. water mite diet isolate 13899-BHL040517-GBD14259_28620-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGAGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATGGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCGGTTACTACCAAGTAGACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13901 Paratanytarsus sp. water mite diet isolate 13901-BHL040517-GBD2801_20603-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCGGTATAGTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTTAACTAGGACATCCCGGAACTTTTATTGGAGATGACTTAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCATTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13902 Chironomidae sp. water mite diet isolate 13902-BHL040517-GBD29493_15494-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATAAGGCATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGACACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCTCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAAATGGAGGATTTGGAAATTGATTAGTACCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13903 Paratanytarsus sp. water mite diet isolate 13903-BHL040517-GBD14280_19607-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTACATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13905 Paratanytarsus sp. water mite diet isolate 13905-BHL040517-GBD28131_11962-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATCCTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGTCATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTAACTTCTTCCCCCCTCTTTAACTCATTTACTTCCAAGTAGAAGAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13906 Paratanytarsus sp. water mite diet isolate 13906-BHL040517-GBD9964_6726-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTTATTCGAGCAGAATTAGGACAACCCGGAACTTTCATTGGAGATGACCTAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13907 Paratanytarsus sp. water mite diet isolate 13907-BHL040517-GBD18527_24524-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTTATTTTCGGTGCCTGATCCGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTATTTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCCTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13908 Psectrocladius sp. water mite diet isolate 13908-BHL040517-GBD9844_20665-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATATTGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGAATAGTCCCGTTAATATTATGTGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGGGTTTGATTACTTCCCCCGACATTAACTTTACTATTAGCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13909 Paratanytarsus sp. water mite diet isolate 13909-BHL040517-GBD6568_6327-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTCGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTATTATACTTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCATTAACTCTATTACTAACAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13911 Chironomus sp. water mite diet isolate 13911-BHL040517-GBD18774_24688-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCACTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAAAGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCGCTCTTAAACGTCGACTATCTAGTTCTTTCGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13915 Paratanytarsus sp. water mite diet isolate 13915-BHL040517-GBD9722_23491-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTTATTTTCGGTGCCTGATCAGGAATAGTGGGCACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTT-ATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAACATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACTCTATTACTACCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13916 Paratanytarsus sp. water mite diet isolate 13916-BHL040517-GBD18055_13131-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATTCCTATTTTTATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGTCCCCGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAGGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13919 Paratanytarsus sp. water mite diet isolate 13919-BHL040517-GBD12612_2237-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCCTTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTAAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACGTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13924 Chymomyza sp. water mite diet isolate 13924-BHL040517-GBD13520_24590-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAGCACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTT-ATAGTTATACCTATTCTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACGCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.0% identical to accession ID EU493571, identified in GenBank as Chymomyza procnemis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13926 Paratanytarsus sp. water mite diet isolate 13926-BHL040517-GBD13587_21340-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTACTTTATACTTCATTTTCGGTGCCTGATCGGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTTATTGGAGAATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCCTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTATAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13927 Paratanytarsus sp. water mite diet isolate 13927-BHL040517-GBD8096_17280-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTAAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAA-TTTTTTCATAGTTATACCTATTTTAATTGAAGGATTTGGGAACTGATTATTGCCTTTAATATTAGAAGCCCCAGATATAGCTTCTCCTCGAATAAATAATATAAGATTTTGACTTCATACCCCCTCTTTAACACGTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13928 Psectrocladius sp. water mite diet isolate 13928-BHL040517-GBD12683_27360-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTTGAGCAGAACTCGGTCACGCGGTTTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTAACGCTTTTGTAATATTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTTCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13931 Paratanytarsus sp. water mite diet isolate 13931-BHL040517-GBD22177_22455-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATACTTTATTTTTGGTGCCTGATCAGGAATAGTGGGAACTTCATTAAGAATATTTATTCGAGCTGAACTGGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTT-CATTGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTTTTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13932 Cricotopus sp. water mite diet isolate 13932-BHL040517-GBD26942_19622-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACAGTATAGTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTGCTTACCTAGGAGTCTTAATTCGAGCTGAAGTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCCTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGCGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13937 Psectrocladius sp. water mite diet isolate 13937-BHL040517-GBD18107_12279-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGCACTTCTTTAAGTATTTTAATTCGAGCAGAACTCGGACACGCTGGTTCCTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACCGCTCACGCTTTTGTAATAAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13939 Chironomus sp. water mite diet isolate 13939-BHL040517-GBD9333_20027-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACAACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACCCTTCTTCTTGCTAAGGCTGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13946 Paratanytarsus sp. water mite diet isolate 13946-BHL040517-GBD29354_16776-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATAAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCTAATTTATAATGTAATTGTTACAGCTCATGCATTTATTAT-ACTTTTTTCATAGTTATACCTATTTTACTTGGAGGATTTGGGATCTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTGGAACGCGGGGACGGCCAAGGAGAAGAGGGGAAAAGGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13951 Paratanytarsus sp. water mite diet isolate 13951-BHL040517-GBD26407_15592-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATACTTCATTTTCGGTGCCTGATCAGGAATAGTTGGAACTTCCCTAAGAATATTAATTCGATCTGAACTAGGACATCCCTGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTTTTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTGCCCCCCTCTTTAACTCTATTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13958 Paratanytarsus sp. water mite diet isolate 13958-BHL040517-GBD10288_22959-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTTTACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTCCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTTGAAGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGTCCCAGATATAGCTTCTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTACCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13959 Paratanytarsus sp. water mite diet isolate 13959-BHL040517-GBD26279_19948-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATCCTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGCACTCAGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTGCTTCCCCCCTCTGTAACTCTTTTACTGCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13960 Chironomus riparius water mite diet isolate 13960-BHL040517-GBD20581_27844-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTTGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCAGAACTTTCATTGGAGATGACCAAATTTAAAATGTCGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCGCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13966 Paratanytarsus sp. water mite diet isolate 13966-BHL040517-GBD4809_13165-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTCATTTTCGGTGCATGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTT-TTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTTTTGCCTTTAATATTAGTAGCCCCAGATAAAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTTTTACTACCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13967 Chironomidae sp. water mite diet isolate 13967-BHL040517-GBD8677_18377-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13968 Chironomus riparius water mite diet isolate 13968-BHL040517-GBD7644_22181-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTCGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAAATTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCACTTACTCTACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13971 Chironomus riparius water mite diet isolate 13971-BHL040517-GBD20477_4886-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13972 Chironomidae sp. water mite diet isolate 13972-BHL040517-GBD19109_17077-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTTGGTCACCCATGCTCATTTATCGGAGACGATCAAATTTATAATGTTATTGTTACAGCTCAAGCTTTTGTTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAAATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13977 Chironomus riparius water mite diet isolate 13977-BHL040517-GBD25388_22755-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGAGGCTTGTTCCGTAATAGTGGGAACTTCATTAAGATTGCTTATTCGAGCAGAATTAGGACTACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTCGTTACTGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAATTATAATTGGAGGATTCGGAAACTGACTTGTCCTCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13978 Chironomidae sp. water mite diet isolate 13978-BHL040517-GBD21602_20157-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGAACAAATATATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13980 Diaphanosoma sp. water mite diet isolate 13980-BHL040517-GBD15380_22298-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTAATATGGCCTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13981 Chironomus sp. water mite diet isolate 13981-BHL040517-GBD15233_23577-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATATTTTATTTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTATTTCGAGCAGATTTAGGACGACCAGGAACTTTTATTGGAGACAACCAAATTTATAATGTAATTGTAACAACTCATGCTTTTATTATAATTTTTTTCATAATTATACCACTTATAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13983 Paratanytarsus sp. water mite diet isolate 13983-BHL040517-GBD6831_11318-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCCGAATTAGGGCACCCTGGAACATTTACTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTTGGGGTTTTGGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13984 Chironomus riparius water mite diet isolate 13984-BHL040517-GBD19222_21312-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTAGGGGCTTGATCCGGAATAGTGGGAATTTCTTTCAGAATGATTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13986 Chironomus riparius water mite diet isolate 13986-BHL040517-GBD24063_11309-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATCGTGGGAACTTCATTAAGAGTGCTTATCCGAGCAGAATTCGGACGACCCGGAACTTTCATTGGAGATGACCGAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTATCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTTCTTCGTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13987 Paratanytarsus sp. water mite diet isolate 13987-BHL040517-GBD8042_8365-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTAAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATACTAGGAGCCCCAGATATAGCTTTTTCCTCGAATAAATAATGTAAGACTTTGACTTCTTCCCCCCACTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13990 Chironomus sp. water mite diet isolate 13990-BHL040517-GBD9612_26366-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAAAACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAAAATAAGTTTCTGACTTTTACCCCCCTCCCTTACTCTTCTTCTTGCTAGTTCGTTCGCAGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13992 Chironomus riparius water mite diet isolate 13992-BHL040517-GBD15177_13994-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGATTGCTTTTCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTATCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTAACCCCCCTCTCTTACTCTTCTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL13994 Chironomus sp. water mite diet isolate 13994-BHL040517-GBD13511_1934-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTGGACCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTACAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACACTACTTCTATCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL13998 Chironomus riparius water mite diet isolate 13998-BHL040517-GBD23910_9538-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGCCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCATAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGAGATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTGCTGCATTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14005 Cryptochironomus sp. water mite diet isolate 14005-BHL040517-GBD19454_23168-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACAACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTCATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14007 Dicrotendipes sp. water mite diet isolate 14007-BHL040517-GBD8393_11054-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATTGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTGCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14009 Chironomus riparius water mite diet isolate 14009-BHL040517-GBD26564_19862-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTACTTTTGGGGCTTGATCCGGAATAGTGGGCACTTCATTAAGAATGCTTATTAGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14010 Chironomus sp. water mite diet isolate 14010-BHL040517-GBD13619_15778-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTGCCTCGAATAAATAATATAAGTTTCTGGCTTTGGCCCCCCACTCTTACACTTCATCTATCTAGTTCTTGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14012 Chironominae sp. water mite diet isolate 14012-BHL040517-GBD12296_2986-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATAATTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTTGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTGGATCACTTCTTCGGTCTAGCGCAATTGTATAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14014 Chironomus riparius water mite diet isolate 14014-BHL040517-GBD7275_15017-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTAATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAATTATACCAATTATAATTGGAGGATTCGGAAACTGACTTTTACCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTCACCCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14018 Chironomus riparius water mite diet isolate 14018-BHL040517-GBD23549_10878-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGTAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGCATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGTACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTCTAATTGGAGGATTCGGAAACTGACTTGTCACCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTTACCCCCCTCTCTTACTCTTCTGCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14019 Chironomus sp. water mite diet isolate 14019-BHL040517-GBD12026_27507-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCGTTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTCTTATTATAATTTTTTTCATGATTATACCAATTATAATTGGAGGATTCGGAAACTGACTTATCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACGCTTCTTCTTTCTAGTGCTTTCGTAGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14029 Chironomus sp. water mite diet isolate 14029-BHL040517-GBD24020_8198-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGAGCAGATTTAGGACGCCCCGGAACTTTCTTTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATATTTTTTTCATAATTATACCAATTATAATTGGAGGATTCGGAAAATGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAACAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTATCTAGTTCTTTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14039 Chironomus riparius water mite diet isolate 14039-BHL040517-GBD17030_12316-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTTATTGAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTATTGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAATTATAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCCTTATAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1404 Chironomidae sp. water mite diet isolate 1404-BHL110116-GBD27422_16810-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTCTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTGTCCGCGAAAAAATAATATAAGATTTTGATTATTACCCCCTGCATTAACCTTACTTTAATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14040 Orthocladiinae sp. water mite diet isolate 14040-BHL040517-GBD20949_11698-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTAATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGATCATTGATCGGAGACGACCAAATTTTTAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14044 Chironomus riparius water mite diet isolate 14044-BHL040517-GBD26445_17382-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCAATTCCGCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACGCTTCGTCTATTCTAGTTCGTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14050 Chironomidae sp. water mite diet isolate 14050-BHL040517-GBD23014_14609-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTTGGAGCCTGATCAGGAATAGTTGGGACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATAATCGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTAACCCCATCTCTAACATTATTACAATCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14052 Chironomus riparius water mite diet isolate 14052-BHL040517-GBD9396_12529-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATATTTTTTTTCATAATTATACCAATTATAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTCCAAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14057 Chironomus sp. water mite diet isolate 14057-BHL040517-GBD22095_22089-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGTCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAATTATACCAATTATAATTGGAGGATTCGGAAACTGACTTTTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTCTACCCCCCTCTCTTACTGTTCATCATTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14058 Chironomus sp. water mite diet isolate 14058-BHL040517-GBD5428_14148-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATATTTGGAGCACCTGACATAGCTTTTCCCCGAATAAATAATATAAGGTTCTGACTTTTACCCCCCCTCTCTTACTCTACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14060 Cryptochironomus sp. water mite diet isolate 14060-BHL040517-GBD22264_13564-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAGTTAGGACGACCAGGAACTTTTATTGGAGACAACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATCGCATTTCCCCGAATAAATAATATAAGAGTTTGACTTTTACCCCCATCCTTGACCCTACTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGATCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14065 Chironomus sp. water mite diet isolate 14065-BHL040517-GBD5440_14827-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCGTTGGAGATGACTAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCTTAGTTATACCAATTCTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCCGGCATTGCTTTTCCCCGAAAAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14068 Chironomus riparius water mite diet isolate 14068-BHL040517-GBD25534_20817-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATTAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTCTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCGCTAACTCTTCTTCTTTCTAGTACTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1407 Chironominae sp. water mite diet isolate 1407-BHL110116-GBD1984_13114-Lq45 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGGACACCACTTAGTATATTGATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAGTGTTATTGTATCAGCTCACGCTTTTATTATAATTTTTTTTTATAGTTATACCTATACTAATTGGTGGAATTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAACAATATGAGATTTTCATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR754526, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14070 Cryptochironomus sp. water mite diet isolate 14070-BHL040517-GBD11637_4386-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTCGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTAATTAGTACCTCTAATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGAGTTTGATTATTACCCCCATCCTTGACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14081 Chironomidae sp. water mite diet isolate 14081-BHL040517-GBD14659_26932-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTTCGACTAGAATTAGGACACCCAGGCTCATTAATCAGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGATTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAACATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTGTCAAAATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14087 Psectrocladius sp. water mite diet isolate 14087-BHL040517-GBD25698_15683-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATAAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCACACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAAGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCTTTAACTTTAGTATTATCTAGCACACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14093 Cryptochironomus sp. water mite diet isolate 14093-BHL040517-GBD13504_15642-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCCCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACAACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGAGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGAGTTTGACTTTAACCCCCATCCTGGACACTGCTTCTTTCAAGATCAATTGTAGAAAATGGCGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14107 Cricotopus sp. water mite diet isolate 14107-BHL040517-GBD20196_14275-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATTCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATACAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATAGTTGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14108 Chironomidae sp. water mite diet isolate 14108-BHL040517-GBD16969_23738-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATCCGAGCAGAATTAGGACACCCCGGTTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATATTTTTTTTTTATAGTGACACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14109 Chironomus riparius water mite diet isolate 14109-BHL040517-GBD11162_4469-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATCAAGGATGCTTATCCGAGCAGAATTAGGATGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGACTCAATAATATAAGTTTCTGTCCTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14111 Chironomus riparius water mite diet isolate 14111-BHL040517-GBD22998_6345-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATAGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCATAGCTTACTCTACTTCGTTCTAGTTCTGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14112 Chironomus riparius water mite diet isolate 14112-BHL040517-GBD25772_17752-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAATTATAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGAATTTTACCCCCCTCTCTTACTCGACATCTTTCTAGTTCTTGCGTATAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14115 Chironomus riparius water mite diet isolate 14115-BHL040517-GBD23532_14813-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGCGCAGAATTAGGACGACCCGGAACTTTCTTTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTTGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACGCGTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14116 Chironomidae sp. water mite diet isolate 14116-BHL040517-GBD11095_11971-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAAGAGCCCCAGATATAGCTTTTCCTCGAATAAAAAATATAAGTTTTTGATTATTACCCCCATCTCTAAAATTATAACTGTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14130 Chironomus sp. water mite diet isolate 14130-BHL040517-GBD4640_23666-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTATGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTATTGGAGATGACCGAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATCTTTTTTTTCATAATTATACCAATTATAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAACAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTGCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14131 Chironomus sp. water mite diet isolate 14131-BHL040517-GBD17484_28676-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATCCGAGCAGAATTAGGACGACCCGGAACTTTTATGGGAGATAACCAAATTTATAATGTTGTAGTTACTGCACATACTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTATCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14132 Chironomus sp. water mite diet isolate 14132-BHL040517-GBD9701_27758-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTCGTAGTTACTGCATATGCCTTTATTATAATTTTTTTCATAGTTATACCAATTTTAAATGGAGGATTCGGAAACTGAATTGTCCCCCATAATACTTGGAGCACCTGACATAGCTTTTTCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTGCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14145 Chironominae sp. water mite diet isolate 14145-BHL040517-GBD20040_4505-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTAGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14146 Chironominae sp. water mite diet isolate 14146-BHL040517-GBD11450_2281-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAACTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR166401, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14147 Paratanytarsus sp. water mite diet isolate 14147-BHL040517-GBD20046_2179-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTCGGAGCTTGATCAGGAATATTCAGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGTTCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR758568, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14148 Cricotopus sp. water mite diet isolate 14148-BHL040517-GBD11430_17454-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTATCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCATTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTGGATTACTTCCCCCTGCTTTATCTCGTCTTCTT-TCTAGCGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14149 Paratanytarsus sp. water mite diet isolate 14149-BHL040517-GBD9953_12872-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACTTCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATCTATTGGTGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGACATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCGTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14150 Cricotopus sp. water mite diet isolate 14150-BHL040517-GBD19117_16380-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTAGAGAAGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR160609, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14151 Chironomus sp. water mite diet isolate 14151-BHL040517-GBD5212_10308-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTACTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGACATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14152 Chironominae sp. water mite diet isolate 14152-BHL040517-GBD8626_6310-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGCACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGTATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAATAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR166401, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14153 Orthocladiinae sp. water mite diet isolate 14153-BHL040517-GBD24746_13355-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTGATCGGAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCATTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTAGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14154 Cricotopus sp. water mite diet isolate 14154-BHL040517-GBD27183_15866-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAAATTTTATTGGTTATGATCAAATTTACAATGTTATTGTAACAGCTCACGCGTTTATTATAAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCTCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14157 Paratanytarsus sp. water mite diet isolate 14157-BHL040517-GBD24236_6600-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATATTTTATTTTCGGAACTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAGCATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAATGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR758568, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14158 Paratanytarsus sp. water mite diet isolate 14158-BHL040517-GBD12158_25520-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCACTTTCGGTGCCTGATCAAGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1416 Oligochaeta sp. water mite diet isolate 1416-BHL110116-GBD8892_6022-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTACAGCAGTAGAAAATGGAGCCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL14160 Paratanytarsus sp. water mite diet isolate 14160-BHL040517-GBD20964_15192-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCACATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGTCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCATCATTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14162 Psectrocladius sp. water mite diet isolate 14162-BHL040517-GBD11058_6932-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTACTTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCCCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14163 Paratanytarsus sp. water mite diet isolate 14163-BHL040517-GBD16504_8471-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTGATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCACATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14164 Paratanytarsus sp. water mite diet isolate 14164-BHL040517-GBD16074_2190-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTCGGAGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGTAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTCATTTTAGGAGACCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14165 Orthocladiinae sp. water mite diet isolate 14165-BHL040517-GBD28817_16258-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTGATCGGAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATAAAGCTTTTCCCCGAACAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCGGACTATTAACAAGATCAAAAGTAGAAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14166 Orthocladiinae sp. water mite diet isolate 14166-BHL040517-GBD4462_12930-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTGATCGGAGACGACCAAGTTTATAATGTAATTGTTACAGCACAAGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCATGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAAC---TCTTTTACCTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14167 Chironominae sp. water mite diet isolate 14167-BHL040517-GBD5980_23677-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTAGAGTAGAATTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTAATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAAGAAAAAATATGAGATTTTGATTACTTCCCCCCTTCTTTAACTCTTCTTCTTTCTAGCGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR764241, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14168 Paratanytarsus sp. water mite diet isolate 14168-BHL040517-GBD28151_14091-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATACAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCGTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1417 Chironomidae sp. water mite diet isolate 1417-BHL110116-GBD23131_13504-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACCAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14170 Chironomus sp. water mite diet isolate 14170-BHL040517-GBD20897_18580-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACAAATCATAAAGATATTGGAACCCTTTACATTATTTTTTGGTGCTTGATCAGGAATGGTAGGGACTACTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.4% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14171 Chironominae sp. water mite diet isolate 14171-BHL040517-GBD19755_24224-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTCGGTGCCTGATCAAGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATATCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR286005, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14172 Chironomus sp. water mite diet isolate 14172-BHL040517-GBD11639_9034-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACCTTATATTTATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTACTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGTCGACGACCAGATTTATAATATAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATATTAGGGGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTTACATTACTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14173 Chironominae sp. water mite diet isolate 14173-BHL040517-GBD26539_23645-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCTTTTAGTATTTTAATTCGAGCAGAACTTGGTCACCCTGGTTCTTTTATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTCTACTACTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KM921023, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14174 Paratanytarsus sp. water mite diet isolate 14174-BHL040517-GBD7761_23061-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTTCATTATACTTCATTTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTCTATTGGAGATGACCAATTTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAACTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAAC---CTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR292109, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14175 Chironominae sp. water mite diet isolate 14175-BHL040517-GBD3622_9793-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCCTTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTTATAGTTATACCTATCTTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTAACCCTTCTTCTATCAAGCACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR286005, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14176 Chironominae sp. water mite diet isolate 14176-BHL040517-GBD19949_3460-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTCTTCCACGAATAAATAATACGAGATTTTGATAACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR286005, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14179 Chironomidae sp. water mite diet isolate 14179-BHL040517-GBD7580_24245-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCCGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGACTTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1418 Chironominae sp. water mite diet isolate 1418-BHL110116-GBD22348_14893-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR751061, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14180 Cricotopus sp. water mite diet isolate 14180-BHL040517-GBD14634_10058-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTACTCATGCTTTTGTAATAATTTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATGGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14181 Diptera sp. water mite diet isolate 14181-BHL040517-GBD17385_21986-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTTCTTTATATTTTATTTTCTGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.5% identical to accession ID JF966746, identified in GenBank as Anopheles maculipennis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14182 Chironominae sp. water mite diet isolate 14182-BHL040517-GBD4829_14451-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCATTTAGTATATTAATTCGAGCAGAACTTGGTCAACCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCAAGCTTTTATTATAAATTTTTTTTATAGTTATACCTATCCTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTGCTTCCCCCTTCATTATCTCTACTTCTATCTAGCTCAATTGTAGAAAATGAAGCTGGATCAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14183 Orthocladiinae sp. water mite diet isolate 14183-BHL040517-GBD20301_23614-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTATTTCGGCTAGAATTAGGACACCCAGGCTCATTGATCGGAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14184 Paratanytarsus sp. water mite diet isolate 14184-BHL040517-GBD26820_18704-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTATTTTCTGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACAATCTGGAACATTTATTGGAGATTATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATCATAATTTTTTTATATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR740890, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14186 Paratanytarsus sp. water mite diet isolate 14186-BHL040517-GBD27553_16548-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATTCTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTAGTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATTTTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAAAATAGTGGAAAAGGGAGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14187 Chironominae sp. water mite diet isolate 14187-BHL040517-GBD14308_10229-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTTCAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGAATACTTCCCCCATCACTTACATTACTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14188 Chironominae sp. water mite diet isolate 14188-BHL040517-GBD13294_15919-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAATAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGTTATAGCTTTTCCACGAATAAATAATATGAGATTTTGAATACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KT115418, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1419 Chaetogaster diastrophus water mite diet isolate 1419-BHL110116-GBD6008_7533-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAAGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCACTATTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAACTCTGCTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL14190 Chironomidae sp. water mite diet isolate 14190-BHL040517-GBD6224_20922-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14192 Chironominae sp. water mite diet isolate 14192-BHL040517-GBD16841_9155-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCCCTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGCTGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACGTCCCCCTGCCTTATCACTTCATCTTGCTAGCTCAATTGTAGGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR657518, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14193 Cricotopus sp. water mite diet isolate 14193-BHL040517-GBD20458_5120-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCAGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATAGCTTCTCCACGAATAAATAATATGAGATTTTGATTCCTTCCCCCCTTCTTCATCTCTTCTTCTT-TCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14194 Diptera sp. water mite diet isolate 14194-BHL040517-GBD23103_21565-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACTTTATATTTTATATTTGGAGCTTGAGCGGGAATAGTAGGAACTTCTCTTAGTATTTTAATTCGAGCAGAATTAGGACATCCAGGTGCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATATTTTTTTTTATAGTAATACCTATTATAATTGGAGGGTTTGGAAATTGATTGGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTATTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.5% identical to accession ID KJ522842, identified in GenBank as Anopheles sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14195 Paratanytarsus sp. water mite diet isolate 14195-BHL040517-GBD27093_13226-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACTTCCTTAAGTTTATTAGTTCGAGCGGAATTAGGAAACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATATTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14196 Cricotopus sp. water mite diet isolate 14196-BHL040517-GBD8826_15922-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTGTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTCAGAGTTTTAATTCGAGCAGATTTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAAAATAAGATTTTAATTATTACCACCTTCTTCAACATTATTATTATCAAGAGCTATTGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14197 Paratanytarsus sp. water mite diet isolate 14197-BHL040517-GBD11487_14414-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCTGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATCATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATCGACTTTTTCCTTTAATATTAGGAGCCCCCGACATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCCATCAAGAAGACTAGTGGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14201 Chironominae sp. water mite diet isolate 14201-BHL040517-GBD25552_18607-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATTAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCACTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTACCCCCTTCTTTAACTCTACTACTTTCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM988908, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14202 Paratanytarsus sp. water mite diet isolate 14202-BHL040517-GBD6969_7481-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTCGGTGCCTGATCAGGAATATTGGGAACTTCTCTAAGAATATTATTTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAATACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14203 Diaphanosoma sp. water mite diet isolate 14203-BHL040517-GBD23141_3696-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCTTTAGTATATTTATTCGAGCTGAATTAGGGCGGTGTGGCAGACTTATTGGTGATGACCCAATTTATAGTGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTGTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTAGCTGGTGCCTTTAATACTAGGTGCCCCTGATATAGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14204 Cricotopus sp. water mite diet isolate 14204-BHL040517-GBD27521_10406-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGTTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAAATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14206 Chironominae sp. water mite diet isolate 14206-BHL040517-GBD17582_13255-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTGTTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTACCAAGATTAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14210 Orthocladiinae sp. water mite diet isolate 14210-BHL040517-GBD28755_18363-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGTATTAGGACACCCTGGAACATTTATTGGAGATGATCAAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGACCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14211 Paratanytarsus sp. water mite diet isolate 14211-BHL040517-GBD18375_22849-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTCGGAGCCTGATCAGGAATAATCGGAACTTCCTTAAGTATATTAATTCGAGCTGAATTAGGACACCCTGGAACTTTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTTTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGATTTTGATTACTTCCCCCATCTTTAACCCTTCTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14213 Dicrotendipes sp. water mite diet isolate 14213-BHL040517-GBD16829_11874-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTTGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATCCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAAGATAAGTTTCTGACTATTACCTCCTTCTCTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14214 Mamiellaceae sp. water mite diet isolate 14214-BHL040517-GBD9292_9938-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACCTTATAT-TTATTATTCGGTGCATTTGCTGGGGTATTAGGGACGTGTTTTTCCTTAGTTATTCGAATGGACTTAGCACACCCTGGACAACAGATTTTAAATGGAAACCACCAATTATATAATGTCATTATTACAGCCCACGCATTCCTGATGATCTTCTTCATGGTAATGCCAG-TCTTAATCGGAGGTTTTGGTAACTGGTTTGTACCAGTCATAATTGGTGCACCGGACATGGCGTTTCCACGACTAAACAACATTAGTTTTTGGTTACTTCCCCCTTCTTTATCTCTTCT	Using NCBI BLASTN in June 2018, this sequence was 80.9% identical to accession ID FJ859351, identified in GenBank as Micromonas sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14216 Chironomidae sp. water mite diet isolate 14216-BHL040517-GBD27858_10279-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCTGGAATAGTTGGAACTTCCTTAAGGATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTTTACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATCATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1422 Chironomidae sp. water mite diet isolate 1422-BHL110116-GBD11147_18978-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTCATCGGAGACGATCAAATTTATAATGTTATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCAATTTTAATTGGAGGCTTAGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTCTTCCGCGAATAAATAATATAAGATTTTGATCATTACCCCCTTCATTGACCTTACTTTTATCAAAATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14221 Paratanytarsus sp. water mite diet isolate 14221-BHL040517-GBD26198_13947-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGCTCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATCATAATTTTTTTTATAGTTCTACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCAGCTTTAACCCTGCTGCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14225 Paratanytarsus sp. water mite diet isolate 14225-BHL040517-GBD6396_25120-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATATTCGGAACATCCTTAAGTATATTAATTCGAGTTGAATTAGGTCACCCTGGAACATTTAATGGAGATGATCAAATCTATAATGCTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCAACTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14232 Chironominae sp. water mite diet isolate 14232-BHL040517-GBD6315_10087-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAACATGAGATTTTGATTACTTCCCCCTTGTTTAAC-ATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14237 Chironominae sp. water mite diet isolate 14237-BHL040517-GBD25966_13916-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCATTTAGTATATTAATTCGAGCAGAATTTGGTCACCCTGGAACTTTTATTGGTAATGAACAAATTTACAATGTTATTGTAACAGCTCATGCTTTTATTATATATTTTTTTTATAGTTATACCTATCCTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGACTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR166401, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14239 Chironominae sp. water mite diet isolate 14239-BHL040517-GBD4794_11274-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTCGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATCTTAATTGGTGGATTTGGAAATTAATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAAAAAATAATATGAGATTTTGATTACTTCCCCCCTTCTTTATCTCGTCTTCTATCGAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL1424 Lebertia quinquemaculosa water mite diet isolate 1424-BHL110116-GBD4659_9765-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATACTTCGCTTTTGGGGCTTGATCAGGAATGGTGGGAGCAAGACTAAGAACTTTAATCCGTTTAGAATTAGGACAACCAGGAACTCTCCTAGGAAGAGACCAAATTTATAATACTATCGTAACAGCTCACGCCTTCATTATAATTTTCTTTATAGTTATGCCAATAATAATTGGAGGATTCGGAAATTGGCTAGTCCCATTGATAATTAGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGACTTTTACCCCCCCTCTTTAACTCTTCTACTATCTAGTTCTTTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID MG773261, identified in GenBank as Lebertia quinquemaculosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14240 Paratanytarsus sp. water mite diet isolate 14240-BHL040517-GBD6093_19904-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATCATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGACATAGCTTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTTACATTACTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14243 Cricotopus sp. water mite diet isolate 14243-BHL040517-GBD23627_7401-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATATTTGGAGCTTGAGCGGGAATAGTAGGAACTTCTCTTAGTATTTTAATTCGAGCAGAATTAGGACATCCAGGTGCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTATAATTGGAGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14244 Paratanytarsus sp. water mite diet isolate 14244-BHL040517-GBD27642_12457-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCTCTAAGTATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAAATGATTATTGCCTTTAATTATAGGAGCCCCAGATATAGCCTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCGTTAACTCTTTTACTTTCAAGTAGAATAGTGGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14246 Chironomus sp. water mite diet isolate 14246-BHL040517-GBD2932_14402-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACATTATTTTTTGGTGCTTGATCAGGAATGGTAGGGGCTACTTTAAGTATGCTTATTCGATCAGAGTTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGTGGCCCCTGACATAGCTTTCCCCCGAATAAATAATAAAAGTTTCTGATTACTTCCCCCATCACTTACAGTACTCCTTTCAAGTTCATTTGTAGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14248 Paratanytarsus sp. water mite diet isolate 14248-BHL040517-GBD19828_27493-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACGCCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGATACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCCTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCATTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR758568, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14249 Chironominae sp. water mite diet isolate 14249-BHL040517-GBD17934_17728-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCTTTTAGTATATTAATTCGAGCAGAACTTGGTCATCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCACCTTCTTTAACTCTACTTCTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR654792, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14250 Paratanytarsus sp. water mite diet isolate 14250-BHL040517-GBD10448_5526-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATCTTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACCTCCTTAAGTATCTTAATTCGAGCAGCATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCACCGTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14252 Paratanytarsus sp. water mite diet isolate 14252-BHL040517-GBD21671_27161-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTCTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGAAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTTCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14253 Paratanytarsus sp. water mite diet isolate 14253-BHL040517-GBD9122_6106-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACATCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCCTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14256 Cricotopus sp. water mite diet isolate 14256-BHL040517-GBD10539_17842-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCTGGAATAGTGGGTACTTCTCTTAGAATTTTAATTCGAGCAGAATTCGGTCATGCAGGTTCTTTAATTGGAGATGATCAAATTTCTAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14257 Orthocladiinae sp. water mite diet isolate 14257-BHL040517-GBD15307_11405-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTCGGTGCCTGATCAAGAATAGTAGGAACTTCCCTAAGAATTTTAATTCGACCAGAATTAGGACACCCAGGCTCATTGATCGGAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14259 Chironominae sp. water mite diet isolate 14259-BHL040517-GBD7734_10668-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAACAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGATTACTTCCCCATTCTTTAACTCTTCTACTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1426 Chironominae sp. water mite diet isolate 1426-BHL110116-GBD18949_2771-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14261 Orthocladiinae sp. water mite diet isolate 14261-BHL040517-GBD15282_4431-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTGATCGTCTACGTCCTAATTTATAATGTAATTGTTACAGCACATGCTTTTGTCATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGCGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14263 Paratanytarsus sp. water mite diet isolate 14263-BHL040517-GBD29123_12071-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGCTGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAGTATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGGTTTTGTTTACTTCCCCCATCATTAACCCTTCCTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14264 Cricotopus sp. water mite diet isolate 14264-BHL040517-GBD3558_18705-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATCAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14265 Paratanytarsus sp. water mite diet isolate 14265-BHL040517-GBD9628_9055-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATGAGGAATAATCGGAACATCCTTAAGTATTTTAATTCGAGCAAAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCCATAATGTTATTGTTACAGCTCATGCCTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGATTTTTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTACTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14270 Paratanytarsus sp. water mite diet isolate 14270-BHL040517-GBD13665_19026-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGGATAATCGGAACTTCCTTAAGTATATTAATTCGAGCAGAATTAGGACGCCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCCTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14271 Paratanytarsus sp. water mite diet isolate 14271-BHL040517-GBD23027_16888-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTAGGAGCTTGATCAGGAATAATCGGAGCATCCTTAAGTATACTAATTAGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14273 Orthocladiinae sp. water mite diet isolate 14273-BHL040517-GBD6953_13209-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCTTGATCTGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTATGACACCCAGGCTCATTGATCGGAGACGAACAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGACATAGCTTTTCCCCGAATAAATAATATAAGATTTTGAATATTACCCCCTTCATTAACCTTACTTTTATCAAAAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14276 Paratanytarsus sp. water mite diet isolate 14276-BHL040517-GBD25286_8364-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCCCGTATAAATAATATAAGTTATTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAACATTAATTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14279 Chironominae sp. water mite diet isolate 14279-BHL040517-GBD12823_10030-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGGACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14280 Paratanytarsus sp. water mite diet isolate 14280-BHL040517-GBD5692_6149-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGAGCCTGATCAAGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTATGACATCCCGGAACTTTTATTGGAGATGAACAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTTGGAGCCACTGATATAGCTTTTCCTCGAAAAAATAATATAAGATTTTGACTTCTTCCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14284 Paratanytarsus sp. water mite diet isolate 14284-BHL040517-GBD9218_6041-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGATACCCTGGAACATTTATTGGAGATGATCAAATCTGTAATGTTATTGTTACAGCTCATGCTTTTATCATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCACCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTAATTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14287 Chironomidae sp. water mite diet isolate 14287-BHL040517-GBD8209_25089-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTACTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGTAACTTTTGTTGGCGACGAACATATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAACTGATTATTGCCTTTAATTTTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAATAGAATAGTGGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID KR747869, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14294 Paratanytarsus sp. water mite diet isolate 14294-BHL040517-GBD24285_22650-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTATTTTTGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGATCAGAATTAGGACACCCTGGTTCATTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTTTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTACTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR758568, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14297 Paratanytarsus sp. water mite diet isolate 14297-BHL040517-GBD14487_25724-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAACTTGATCAGGAATAATCGGAACATCCTTAAGTATATTTATTCGAGCAGAATTAGGACACCCCGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCTCGTATAAATAATATAAGTTTCTGATTACTACCCCCATCTTTAACCCTTCTTCTATCCAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14299 Chironominae sp. water mite diet isolate 14299-BHL040517-GBD6920_22836-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCCTGATCTGGAATAGTAGGAACTTCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTATTTCCTTTAATATTAGGAGTCCCAGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCCTCTTTAACTCTTCTTCTTTCTAGCACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14300 Cricotopus sp. water mite diet isolate 14300-BHL040517-GBD10982_11508-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCCCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACCTTCAAGTACAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14302 Cricotopus sp. water mite diet isolate 14302-BHL040517-GBD26780_18742-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATTTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGTATTTTAATTCGAGCAGAATTAGGTCATGCTGGATCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTATAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGAATAGTCCCTTTAATACTAGGAGTCCCAGATATAGCATTCCCTCGAATAAAAAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATGATCAAGATCTAGTGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14303 Chironominae sp. water mite diet isolate 14303-BHL040517-GBD10689_21958-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGGCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTGCCCCCCTCCGTTAACACTTCATCAATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14304 Cricotopus sp. water mite diet isolate 14304-BHL040517-GBD22531_24632-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGTGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTATTAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14310 Chironominae sp. water mite diet isolate 14310-BHL040517-GBD26049_21285-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGTGCTTGATCTGGAATAGTAGGAACTTCCCTTAGTATATTAATTCGAGCTGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGATGGATTTGGAAATTGATTAGTGCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTACTTTCTAGCACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR286005, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14313 Paratanytarsus sp. water mite diet isolate 14313-BHL040517-GBD25167_7542-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTAGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATTTTAATTCGAGCAGAATTCGGACAACCTGGAACATTTATTGGAGATGATCAAATCTTTAATGTTATTGTTACAGCTCATGTTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14316 Paratanytarsus sp. water mite diet isolate 14316-BHL040517-GBD15538_25654-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATGCTTTATTTTCGGGGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATGTTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGATGATTTGGGAACTGATTATTGCCTTTAATTTTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTAAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR282105, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14319 Paratanytarsus sp. water mite diet isolate 14319-BHL040517-GBD4952_22249-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTATTACACCCTGGAACATTTATTGGAGATGATTAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACGTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1432 Chironomus riparius water mite diet isolate 1432-BHL110116-GBD5353_13205-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGAGGACCCGGAACTTTCATTGGATATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACAAATTTAAATTGGAGGATTCGGAAACTGACTTGTCCATCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14320 Chironominae sp. water mite diet isolate 14320-BHL040517-GBD26466_14250-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACCTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCTCTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAGTTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTCCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCATTAACTCTACTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14325 Chironominae sp. water mite diet isolate 14325-BHL040517-GBD27043_18602-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCATTTAGTATATTAATTCGAGCTAAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGTGTCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14329 Chironominae sp. water mite diet isolate 14329-BHL040517-GBD10555_26664-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACAGTATATTTTATTTACGGAGCTTGATCTGGAATAGTAGGAGGATCACTTAGTATATTAATTCGAGCAGAACGCGGTCACCCTGGAACTTTTATTGGTTATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTCGCTCAATTGTATAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14332 Paratanytarsus sp. water mite diet isolate 14332-BHL040517-GBD4252_13021-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTAGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATTAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCTTTTCCCCGATTAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCGAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14334 Chironomus sp. water mite diet isolate 14334-BHL040517-GBD22084_20443-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTATACATTATTTT-GGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACACGGAACTTTCATTAGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTAATATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCCAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1434 Chaetogaster diastrophus water mite diet isolate 1434-BHL110116-GBD16842_22345-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGGCTAACTATATCATACTCTTGTAACTGCCCACCCATTTCTAATAATTTTCTTTTTAGTTATACCATTATTTATTGGTGGATTTGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL14348 Paratanytarsus sp. water mite diet isolate 14348-BHL040517-GBD25432_21283-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTCATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATTAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGTTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR758568, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14350 Chironominae sp. water mite diet isolate 14350-BHL040517-GBD11307_21460-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTATGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATCTATTTTTTACTGATCATACTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGACTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14351 Chironominae sp. water mite diet isolate 14351-BHL040517-GBD15769_21998-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGGGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGTAGAATTTGGTCAACCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTTCCACGAATAAATAATATGAGATTTTGATTACTACCCCCTTCTTTAACTCTACTTCTTTCTAGCGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR764241, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14354 Cricotopus sp. water mite diet isolate 14354-BHL040517-GBD21761_12618-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCACAGATATAGCATTCCCTCGAATAAATAACACAAGATTTTGATTATTACCACCTGCTTAAACAGGATCAGTATCAAGATCTATTGTAGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14356 Paratanytarsus sp. water mite diet isolate 14356-BHL040517-GBD23361_20051-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATCAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATTAGATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCCCGAATAAATAATATAAGTTTTTGACTACTTCCCCCATCTTTAACCCTTCGTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14361 Paratanytarsus sp. water mite diet isolate 14361-BHL040517-GBD28290_11550-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGGCTACTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCAAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCCTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID KR747869, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14365 Paratanytarsus sp. water mite diet isolate 14365-BHL040517-GBD25390_14296-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGCACTTGATCAGGAATAATCGGAACATCCTTAGGTATATTAATTCGAGCAGTCTTAGGACACCCTGGAACATTTATTGGAGATGATTAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATAAAAGTTTTTGACTACTTCCCCCAACTTTAACCCTTCTTCTAACAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14369 Chironomidae sp. water mite diet isolate 14369-BHL040517-GBD25860_18973-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGGAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCACCTGATATAGCCTTTCCGCGAATAAATAATATAAGATTTTGATAATTACCCCCTTCACTAACCTTACTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14371 Paratanytarsus sp. water mite diet isolate 14371-BHL040517-GBD22376_7525-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGAGACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTTTTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGTAATTTACTTTTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATCACTTCCCCCATCTTTAACCCTTCGTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14373 Paratanytarsus sp. water mite diet isolate 14373-BHL040517-GBD3995_13121-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACAACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTAATTATTGCCTTTAATATTAGGATCCCCAGATATAGCCTTTCCTCGAATAAATAATAAAAGAATTTGACTTCTTCCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14375 Chironomus sp. water mite diet isolate 14375-BHL040517-GBD25322_10077-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTT-GGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGGATTAGGACGACAAGGATCTTTCATTATAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTTTTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTAGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14376 Paratanytarsus sp. water mite diet isolate 14376-BHL040517-GBD19123_4619-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTGTATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGATCTGAATTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATTGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACGTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14382 Paratanytarsus sp. water mite diet isolate 14382-BHL040517-GBD11670_4823-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTACGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGTCACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGATTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGGCTTTTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGACGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14383 Orthocladiinae sp. water mite diet isolate 14383-BHL040517-GBD15156_12134-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGCAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTGATCGGAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTAACATTGATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAAAAAGAAAAGATTTTGATTATTACCCCCTTCATTAACCTTGCCTTTATAAAGATCAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14386 Paratanytarsus sp. water mite diet isolate 14386-BHL040517-GBD25910_21556-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATACTTAAGTATATTAATGTGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAAAGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGTAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14389 Paratanytarsus sp. water mite diet isolate 14389-BHL040517-GBD27615_12010-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGCGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGACCATTTATTGGAGATGACAAAATCTATAATGCTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCCATTTTAATTGTATGTTTTGGGAATTAACTTCTTCCTTTAATATTAGGATCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGATTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL1439 Chaetogaster diastrophus water mite diet isolate 1439-BHL110116-GBD26930_15475-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAGTTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCTACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTGTAGTTATACCAGTATTTATTGGTGGATTCGGAAATTGAATTCCACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTTCCACCTACACTAATTCTACTAATTTCATCTGCAGCAGTATAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.1% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL14398 Paratanytarsus sp. water mite diet isolate 14398-BHL040517-GBD17395_23515-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGATCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATGGACTTCTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCCCATATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR758568, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14399 Orthocladiinae sp. water mite diet isolate 14399-BHL040517-GBD25227_12324-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATCGTGGGCACTTCTTTAAGAATTTTAATTCGACTAAAATTAGGACACCCAGGCTCATTGATCGGAAACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTAATACCCATTTTAATTAGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCAGATATAGCTTATCCCCGAATAAATAATATAAGATTTTGATTATTACTCCCTTCATTAACCTTACATTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14405 Chironomus riparius water mite diet isolate 14405-BHL040517-GBD26765_21266-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGCGCTTGATCAGGAATAGTGGGCACTTCATTAAGAATGCTTATTCGAGCATAATTAGGACGACACGGAACTTTCATTAGAGATGACCAAATTTATACTGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14406 Chironomidae sp. water mite diet isolate 14406-BHL040517-GBD15499_5767-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGTAACTTTTATTGGAGATTACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGTGGCTTTGGGAATTGATTAGTTACCCTAATATTAGGAGCACCAGATACGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTACTTTCTAGATCAATTGTCTAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.2% identical to accession ID JF412118, identified in GenBank as Glyptotendipes tokunagai. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14407 Dicrotendipes sp. water mite diet isolate 14407-BHL040517-GBD26189_17616-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTAAAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCGTCTCTAACCCTTCTGCTTTCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14409 Diptera sp. water mite diet isolate 14409-BHL040517-GBD18395_25859-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACATTTTATTTTATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTTAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCACCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.1% identical to accession ID KX372558, identified in GenBank as Celyphus obtectus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14413 Diaphanosoma sp. water mite diet isolate 14413-BHL040517-GBD18830_12065-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGATGTTGGTCCGGGATAGTTGGTACAGCCCTATGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACTAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATCCTCATTGGTGGCTTTGGTAATTGTCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGGTTTGAATATTACCCCCTTCTTTAACTCTTCTCTTGGTTGGAAGGGCAGTTGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14418 Cricotopus sp. water mite diet isolate 14418-BHL040517-GBD27863_14323-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATACTTCATTTTCGGTGCCTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAAATGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATAATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14425 Paratanytarsus sp. water mite diet isolate 14425-BHL040517-GBD22743_16036-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAAAATTAGGACACCCTGGAACATTTATTGGAGATGATTAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGATTTTTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTACTCCCCCCATCTTTAACCCTTCTTCTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14430 Cricotopus sp. water mite diet isolate 14430-BHL040517-GBD4359_14916-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGTTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATGTTTTTATTGTAATACCAAATTCTAATTGAAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAAAATAAGATTTTGATTATTACCACCTGCTTTAACATTATTATTATCAAGATCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14437 Chironominae sp. water mite diet isolate 14437-BHL040517-GBD18956_15474-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACCTCTCTTAGTATATTAATTCGAGCAGAACTAGGTCATCCTGGTTCTTTTATTGGTGATGATCAAATTTACAATGTTATTGTTACAGCTCACGCTTTTATTATAATTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTTCCACGAATAAATAACATGAGATTTTGATTACTTCCCCCTTCTTTAACACTACTTCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14452 Cricotopus sp. water mite diet isolate 14452-BHL040517-GBD9988_5603-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACACAAGATTTTGATTATTACCACCTTCGTTAACAAAATAAAAATCAAGAGCTAGAGTAGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14453 Chironominae sp. water mite diet isolate 14453-BHL040517-GBD19352_8048-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTACTTTAAGTATGCTTATTCGAGCAGAACTAGGTCACCCATGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGATCAATTATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR746550, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14454 Chironominae sp. water mite diet isolate 14454-BHL040517-GBD17593_13349-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTGTCGGAACTTGATCTGGAATAGTAGGAACTTCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGTGGATTTGGAAATTGAATAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTGCCCCCCTTCTTTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14459 Chironominae sp. water mite diet isolate 14459-BHL040517-GBD24976_22100-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACATGGTCACCCTGGAACTTTTATTGGTGATGATCGAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTATAGTTATACCTATACTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCAGGATATAGCTTTTCCACGAATAAATAAAATGAAATTTTAATTACTTCCCCCTTCTTTATCTCTACTTCTTTCTAGCTCAATAGTAGAAAATGGAGATGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14482 Chironominae sp. water mite diet isolate 14482-BHL040517-GBD13900_28316-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCATTTAGTATATTAATTCGCGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAATTTTACAATGTTATCGTAACAGATCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTGTAACAAAATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID KM960768, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14487 Paratanytarsus sp. water mite diet isolate 14487-BHL040517-GBD16618_4847-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTATATGTTAATTTCGGAGCTTGATAAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR758568, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14498 Paratanytarsus sp. water mite diet isolate 14498-BHL040517-GBD17424_4026-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTTTTGGAGATGACCAATTTTAGAATGTAATTGTTACGGCCCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATTTTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14501 Paratanytarsus sp. water mite diet isolate 14501-BHL040517-GBD16163_4294-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTATATTTTATTTTCGGAGCTTAATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGTAACATTTATTGGAGATGATTAAATCTACAATGTTATTGTTACAGATCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.1% identical to accession ID KR758568, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14502 Chironominae sp. water mite diet isolate 14502-BHL040517-GBD22935_6281-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCTCTTAGTATTTTAATTCGAGCAGAACTTGGTCACCCGGGTTCTTTTATTGGTGATGATCAAATTTACAATGTTATTGTTACCACTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14505 Cricotopus sp. water mite diet isolate 14505-BHL040517-GBD2773_16833-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGCTCTTTATTTGGAGTTGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATT-GGAAATTGATTAGTCCCTTTAATACTAGGATCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAAATCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14513 Chironomidae sp. water mite diet isolate 14513-BHL040517-GBD17747_20178-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCACTTAGTATATTTATTCGAGCAGAACTTGGTCAACCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTCGATTACTCCCCCCTTCTCTAACTCTTCTTCTTTCTAACTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR636712, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14518 Paratanytarsus sp. water mite diet isolate 14518-BHL040517-GBD19994_12858-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCAGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGAAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGGTATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCTCCATCTTTAACCCTTCGTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14519 Chironomus sp. water mite diet isolate 14519-BHL040517-GBD11698_26220-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTT-GGGGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATACTTATTCGAGCAGAATTAGGACGACACGGAACTTTCATTAGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTAGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14520 Paratanytarsus sp. water mite diet isolate 14520-BHL040517-GBD14648_24005-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTACTTTTGGTGCTTGATCAGGAATGGTAGGGACTACTTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAATGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.6% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14524 Paratanytarsus sp. water mite diet isolate 14524-BHL040517-GBD22261_22053-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGTACATCCTTATGTATATTAATTCGAGTAGAATTAGGACACCCTGGAACATCTATTGGAGATGATTAAATCTATAATGTTATTGTTACTGCTCATGCTTTTATTATGATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAATGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14525 Chironomus sp. water mite diet isolate 14525-BHL040517-GBD21627_8985-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTT-GGGGCTTGATCCGGAATTGTGGGAACTTCCTTAAGAATGCTTCTTCGAGCAGAATTTGGACGACACGGAACTTTCATTAGAGAAGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATATTTATACCAATTTTAATTGGAGGATTAGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14528 Chironomus sp. water mite diet isolate 14528-BHL040517-GBD17746_24992-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACATTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCATAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACGTCCCCCATCACTTACATTACTCCTTTCAAGTTTATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14530 Chironominae sp. water mite diet isolate 14530-BHL040517-GBD22926_23985-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTCGGAGCATGATCTGGAATAGTAGGAACATCACTTAGTATACTAATTCGAGCAGAATTAGGTCACCCTGGAACATTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCCTTAACTCTTCTTCTATCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM988908, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14533 Paratanytarsus sp. water mite diet isolate 14533-BHL040517-GBD29565_17166-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGCACATCCTTAAGTATATTAATTCGAGCAGAATTAGGCCACCCTGGAACATTTATTGGCGATGATTAAATCTATAATGTTATTTTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTTCCCCAGCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14536 Paratanytarsus sp. water mite diet isolate 14536-BHL040517-GBD6334_17933-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGCACTTCCTTAAGTATATTAATTCGAGCAGAATTCGGACACCCTGGAACATTTATTGGAGATGATTAAATCTATAATGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTCTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGAATAAATAATATAAGTTTTTGATTACTTCCCCCATCATTAACCCTACTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14539 Paratanytarsus sp. water mite diet isolate 14539-BHL040517-GBD23421_9723-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTCATTTTTCGGGGCCTGATCGGGATTAGTGGGAACTTCCCTAAGATTATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAGCTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTGTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14540 Paratanytarsus sp. water mite diet isolate 14540-BHL040517-GBD12155_3921-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTGGG-GCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACACGGAACTTTCATTAGAGATGACCAAATTTATAATGTTGTAGTTACTGGACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATTTTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.7% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14541 Chironomus sp. water mite diet isolate 14541-BHL040517-GBD15517_26251-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTACTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGCTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGGTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGACATAGCCTTTCCCACGAATAAATAATATAAGATTCTGATTATTTCCCCCATCACTTACATTACTCCTTTCAAGTACATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14544 Paratanytarsus sp. water mite diet isolate 14544-BHL040517-GBD27827_15425-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTCGGTGACTGATCAAGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTCGAGATGACCGAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTTATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR282105, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14546 Cricotopus trifasciatus water mite diet isolate 14546-BHL040517-GBD2564_16424-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGAAGCTTGATAAGGAATCGTAGGGACATCTCTAAGAATATTAATCCGGGCCGAATTAGGACATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTTACATTATTACTTACAAGTTCAATTGTAGAAACTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM933933, identified in GenBank as Cricotopus trifasciatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14547 Chironominae sp. water mite diet isolate 14547-BHL040517-GBD20510_12340-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTTGTCACCCTGGATCTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGGTATACCTGTCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGCGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR746550, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14550 Paratanytarsus sp. water mite diet isolate 14550-BHL040517-GBD16089_25323-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCATGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTAGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAGTATTAGGAGCCCCCGTTATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTACCCCCATCTTTAACCCATCTTCTATCAAGAAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14553 Orthocladiinae sp. water mite diet isolate 14553-BHL040517-GBD9465_21885-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTATGACACCCAGGCTCATTCTTCGGAGACGACCAAATTTATAATATAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTAATACCGATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGTCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14554 Chironominae sp. water mite diet isolate 14554-BHL040517-GBD9008_23092-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTAGGAACTTCATTTAGTATATTTATTCGAGCAGAATTTGGTCAACCTGGAACTTTCATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTGCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM989605, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14563 Diptera sp. water mite diet isolate 14563-BHL040517-GBD29267_12380-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATCTTTGAAGCATAAGCAGGAATAGTCGGAACTTCTCTAAGAATTCTAATTCGTGCTGAATTAGGACCCCCAGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGATCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCACCTTCACTTACACTATTATTAGTAAAAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.9% identical to accession ID KT272843, identified in GenBank as Archisepsis discolor. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14564 Chironomus riparius water mite diet isolate 14564-BHL040517-GBD11889_20381-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGCAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCGGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14565 Psectrocladius sp. water mite diet isolate 14565-BHL040517-GBD18997_24415-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAGTTTTTTTTACAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAGTAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14566 Chironomidae sp. water mite diet isolate 14566-BHL040517-GBD18325_18294-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTATAATAATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGGTATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGAACATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14570 Toxonevra sp. water mite diet isolate 14570-BHL040517-GBD16385_13745-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACACTATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.0% identical to accession ID KR262681, identified in GenBank as Toxonevra carterosoma. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14571 Chironomidae sp. water mite diet isolate 14571-BHL040517-GBD19172_25111-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14572 Psectrocladius sp. water mite diet isolate 14572-BHL040517-GBD5014_11399-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGTAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCAAATAAATAATATAAGTTTCTGACTTTTAC--CCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14573 Psectrocladius sp. water mite diet isolate 14573-BHL040517-GBD18630_18648-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTTATTCGAGCAGAACTCAGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14574 Chironomus sp. water mite diet isolate 14574-BHL040517-GBD27059_14136-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATTCATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGGTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGTTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATCGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14575 Dicrotendipes sp. water mite diet isolate 14575-BHL040517-GBD3048_11810-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATACTTTTTTTTATGGTTATACCTTTTCTAATTGGAGGATACGGAAATTGATTAGTCCCTTTAATATTAGGTGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14576 Chironomus sp. water mite diet isolate 14576-BHL040517-GBD13858_9875-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACACAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14577 Paratanytarsus sp. water mite diet isolate 14577-BHL040517-GBD13780_13792-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACTTTATATTTTATTTTTGGAGCCTGATCTGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14579 Psectrocladius sp. water mite diet isolate 14579-BHL040517-GBD23559_4205-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTGTATTTTATTTTTGGAGCCTGACCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCATGCCGGTTCCTTAATTGGAGATGATTAAATTTATATTGTAATTGTTACCGCTCACGAGTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAAAAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14580 Psectrocladius sp. water mite diet isolate 14580-BHL040517-GBD13929_12482-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACCCCGGTTCCTTAATTGGAGATGTTCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCAGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGTTCTATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14581 Psectrocladius sp. water mite diet isolate 14581-BHL040517-GBD17106_27275-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTCTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATATTTTTTTTATAGTAATACCTCTTTTATTTGGAGGATTTGGAAATTGATTAGTACCGTTAATATTAGGAGCCCCCGACATAGCATTCCCCCGAAAAAATAATATAAGTTTTTGATTACTCCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14582 Psectrocladius sp. water mite diet isolate 14582-BHL040517-GBD22878_21425-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCGTACGATTTTGTAATAATTTTTTTTAGAGTAATACCTATTTTAATTGGAGGATTTAGAAATTGATTAGTCCTGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCATTAACTTTACTATTATCTAGCTCTCTAGGTGAAAATAGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14583 Chironomus riparius water mite diet isolate 14583-BHL040517-GBD22657_17138-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAGTTAGGACGACCCGGAACTTTCATTGGAGGTGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCATTTTTAATTGGAGGATTCGGAAACTGACTTATCCCCCTAA-ACTTGGAGCACCTGACATGGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14584 Chironomus riparius water mite diet isolate 14584-BHL040517-GBD25032_10039-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCCTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAA-ACTTGGAGCACCTGACATAGCCTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTCCTTCTTTCCAGTTCTTTCGTAGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14585 Psectrocladius sp. water mite diet isolate 14585-BHL040517-GBD24098_11326-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTCCCTTTAATACTAGGAGCCCCCGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14586 Diptera sp. water mite diet isolate 14586-BHL040517-GBD5316_14797-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATACTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAACTAGGACACCCTGGAGCATTAATTGGAGAAGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTTTAATAATTTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGAGATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTACCTCCTTCACTTACACTATTATTAGCAAAAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.0% identical to accession ID KJ496572, identified in GenBank as Diptera environmental sample. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14587 Psectrocladius sp. water mite diet isolate 14587-BHL040517-GBD11954_14347-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCAAGCCGGTTCCTTCATTGGAGATGATCAAATTTATAATGTCCTTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACGTTACTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14588 Chironomus riparius water mite diet isolate 14588-BHL040517-GBD29514_13283-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGCGTAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACAGAGCTTTTCCTCGAAAAAAATAAGATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTATTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14589 Psectrocladius sp. water mite diet isolate 14589-BHL040517-GBD26770_16437-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCATGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTTGGTCACGCCGGTTCCTTAATTGGAGATGATTAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGATGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGTCCCCGACATAGCATTCCCTCGAATAAATAATATAAATTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14590 Diptera sp. water mite diet isolate 14590-BHL040517-GBD11143_3701-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGAGCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATGTAGCCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID MF381608, identified in GenBank as Anopheles darlingi. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14591 Psectrocladius sp. water mite diet isolate 14591-BHL040517-GBD11518_22435-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCAAGCAAAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATAAGTCCCGTTAATATTAGGAGCCCCCCCACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCGTCGTTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14592 Chironomus riparius water mite diet isolate 14592-BHL040517-GBD23953_6411-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGTATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCACGAATAAATAATATAAGTTTCTGACGTTTACCCCCCCCGCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14593 Paratanytarsus sp. water mite diet isolate 14593-BHL040517-GBD11232_10994-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACATCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTATTTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14594 Dicrotendipes sp. water mite diet isolate 14594-BHL040517-GBD16212_11663-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATATTTATTCGAGCCGAATTAGGACGACCCGGAACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTATTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCTACGAATAAATAATATAAGTTTCTGACTATTATCTCCTTCTCTAACCCTTCTTCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14596 Dicrotendipes sp. water mite diet isolate 14596-BHL040517-GBD4598_17665-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCATTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14598 Chironomus sp. water mite diet isolate 14598-BHL040517-GBD4841_19291-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATATTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTGCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14599 Paratanytarsus sp. water mite diet isolate 14599-BHL040517-GBD8290_21660-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGGAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID KR757714, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1460 Chironomidae sp. water mite diet isolate 1460-BHL110116-GBD16666_12986-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTTGGACATGCAAGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATACAAGTTTTTGATTGTTGCCCCCCTCATTAACTTAATAGTAATCTAGTTCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14602 Psectrocladius sp. water mite diet isolate 14602-BHL040517-GBD3903_9937-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGACTTTTAATTCGAGCAGAACTCGGTCACGCCGTTTCCTTAATGGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTGGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14603 Chironomus sp. water mite diet isolate 14603-BHL040517-GBD23961_10434-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGAAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGATGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14604 Chironomidae sp. water mite diet isolate 14604-BHL040517-GBD18068_9231-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGTGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14608 Psectrocladius sp. water mite diet isolate 14608-BHL040517-GBD22062_7780-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGAAGATGATCAAATTTATAATGTAATTGTTACCACTCACGATTTTGAAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATGCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAAATCTCGAGTTGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14610 Paratanytarsus sp. water mite diet isolate 14610-BHL040517-GBD3589_14638-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCCTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14611 Psectrocladius sp. water mite diet isolate 14611-BHL040517-GBD2720_19844-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGTATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14612 Chironomus riparius water mite diet isolate 14612-BHL040517-GBD9765_3195-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCATTTTTAATTGGAGGATTCGGAAACTGATTTGTCCACCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCGCTTACTCTTCTTCGTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14613 Stegana sp. water mite diet isolate 14613-BHL040517-GBD21554_13325-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATTCATTTGTAATAATTTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACTCTATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.0% identical to accession ID KF670983, identified in GenBank as Stegana sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14614 Psectrocladius sp. water mite diet isolate 14614-BHL040517-GBD24583_6707-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGATCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCACACGCTTTTGTAATAATTTTTTTAATAGTAATGCCTATTTTAATTGGAGGATTTGGAAATTGATTATTCCCGTTAATATTAGGAGCCCCAGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTGACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14615 Psectrocladius sp. water mite diet isolate 14615-BHL040517-GBD16378_2702-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATGATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGGTTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14616 Psectrocladius sp. water mite diet isolate 14616-BHL040517-GBD9014_16333-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGAAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCAGTCCCTCGAATAAATAATATAAGGTTTTGATTTCTTCCCCCGTCATTAACTTTGCTATTATCTAGCACGCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14617 Chironomidae sp. water mite diet isolate 14617-BHL040517-GBD15121_10822-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAATTTTATAATGTTGTAGTTACTGCACATGCTTTTGTACTAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCGTTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14618 Dicrotendipes sp. water mite diet isolate 14618-BHL040517-GBD5699_9498-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATTTTTGGGGCTTGATCCGGAATAGTAGGAACTTCCTTAAGTATATTTATTCGAGCCGAATTAGGACGACCCGGTACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGTTTTTATTATAATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTATCTCCTTCTCTAATCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14619 Psectrocladius sp. water mite diet isolate 14619-BHL040517-GBD21552_15887-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCTGAACTCGGTCACGCCGGTTCCTTAATTGGATATGATTAAATTTATAATGTAATTGTTACCGCTCATGCTTTTATAATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCATCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14620 Chironomus riparius water mite diet isolate 14620-BHL040517-GBD3486_14084-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGGCTTGACCCGGATTAGCGGGAACTTCATTAGGAATGCTTATTCGAGCAGAATTGGGACGACCCGGAACTTTCATGGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14621 Chironominae sp. water mite diet isolate 14621-BHL040517-GBD6496_21610-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCATGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14622 Dicrotendipes sp. water mite diet isolate 14622-BHL040517-GBD27605_11390-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCATTCCCACGAATAAATAATATAAGTTTCTGATTATTACCTCCTTCTCTAACCCTTTTACTATCTAAATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14624 Psectrocladius sp. water mite diet isolate 14624-BHL040517-GBD22939_14129-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGTTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAAAATAAGTTATTGATTACTTCCCCCGGCATTAACATTACTATTATCTAGCGCTCGAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14625 Psectrocladius sp. water mite diet isolate 14625-BHL040517-GBD16744_28964-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTACTTGATTGGAGATGCTCAAATTTATAATGTAAATGTTACCGCTCACGCTTTTTTAATAATTTTTTTTATAATAATTCCTATTTTTATTGGAGGATTTGGAAATTGATTCGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATAAAAGTTTTTGATTACTTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14627 Chironomus riparius water mite diet isolate 14627-BHL040517-GBD12905_21231-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACAACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACAAAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACACTACTTCTTTCTAGTATTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14628 Diptera sp. water mite diet isolate 14628-BHL040517-GBD6655_8802-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAACAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGAACAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATATTTTTTTTTTATAGTGATACCAATTTTAATTGGTGGATTCGGAAAATGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTCCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACTTTATTATTAGGAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.0% identical to accession ID KJ496572, identified in GenBank as Diptera environmental sample. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14629 Diptera sp. water mite diet isolate 14629-BHL040517-GBD19379_15811-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAACATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTCTGACTATTATCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.8% identical to accession ID KF137556, identified in GenBank as Phlebotomus wui. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14630 Dicrotendipes sp. water mite diet isolate 14630-BHL040517-GBD18920_26460-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTAATTCGAGCCAAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTCTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTACTACTTTCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14631 Chironomus riparius water mite diet isolate 14631-BHL040517-GBD5921_17878-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAACTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATAAAAGTTTCTGGCTTTTGCCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14633 Dicrotendipes sp. water mite diet isolate 14633-BHL040517-GBD13196_9951-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCCTGATCAGGAATAATAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGAACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAATCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14634 Chironomus riparius water mite diet isolate 14634-BHL040517-GBD23599_4776-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGTACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTTTCCCCCTAATACTTGGATCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTACTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14637 Psectrocladius sp. water mite diet isolate 14637-BHL040517-GBD24868_18838-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGACACGCCGGTGCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTATGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCGTTAATATTAGGAGCTCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14639 Psectrocladius sp. water mite diet isolate 14639-BHL040517-GBD14842_3390-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCTTTTCCTTAATTGGTGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCAGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAATTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGCGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14640 Chironomus riparius water mite diet isolate 14640-BHL040517-GBD23523_20387-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGATGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCATCTACTTTCTAGTACTTTCGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14642 Psectrocladius sp. water mite diet isolate 14642-BHL040517-GBD23597_22261-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGTATTTTAGTTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAAAACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAAAATTAGGTGCCCCCGACATAGCATTCCCTTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14644 Diaphanosoma sp. water mite diet isolate 14644-BHL040517-GBD12477_18617-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGGTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTACTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14645 Dicrotendipes sp. water mite diet isolate 14645-BHL040517-GBD5501_15453-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATATTTATTCGAGCCGAATTAGGACGACCCGGGTCATTTATTGGAGATGATCAAATCTACAATGTATTTGTTACAGCTCATGTTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTATCTCCTTCTCTAACCATTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14646 Psectrocladius sp. water mite diet isolate 14646-BHL040517-GBD13428_20096-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATGTAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14647 Chironomus riparius water mite diet isolate 14647-BHL040517-GBD23379_22094-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGATGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATCGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTATCCCCCTCGCTTACTCTTCTTCTTGCTAGTTTTGTTCGTTGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14648 Chironomus sp. water mite diet isolate 14648-BHL040517-GBD13246_11299-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTATCTGACCTTTACCCCCCCTCTCTTACCCTACTTCCATCTAGTTTTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14649 Psectrocladius sp. water mite diet isolate 14649-BHL040517-GBD25580_14834-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTGCTTTAAGAATTTTAATTCGAGCAGAACTCTGTCACGCAGGTTCCTTATTTGGAGATGATCAAATTTATAATGTACTTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14650 Psectrocladius sp. water mite diet isolate 14650-BHL040517-GBD2858_11985-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTTACGCCGATTCCTGAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14651 Psectrocladius sp. water mite diet isolate 14651-BHL040517-GBD20770_27742-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCATGATCAGGCATAGTATGCACTGCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGTTACCTTAATTGGAAATGATCACATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGTGTCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14652 Chironomidae sp. water mite diet isolate 14652-BHL040517-GBD4410_14580-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGGTCACGCTTTTGTAATAATTTTTTTTATAGAAATACCTATTTTAATTGGAGGTTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATGATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14653 Psectrocladius sp. water mite diet isolate 14653-BHL040517-GBD25977_9769-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAGCTCGGTCACGCCGGTTCCTTGATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTTATAAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14654 Psectrocladius sp. water mite diet isolate 14654-BHL040517-GBD14548_19391-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTATTTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAAAAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14658 Psectrocladius sp. water mite diet isolate 14658-BHL040517-GBD16548_16347-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTCTAATTCGAGCAAAACTCGGACACGCCGGTTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTGGAAAATGGAGATGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1466 Oligochaeta sp. water mite diet isolate 1466-BHL110116-GBD26975_7095-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAGGATATTGGCACTCTATACTTAATCTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTCCTACCACCATCTCTAATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.1% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL14660 Psectrocladius sp. water mite diet isolate 14660-BHL040517-GBD23343_15994-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGTTTCCTTAATTGGAGATGATCAAATTTCTAATGTAATTGTTACCGCTCACGCTTTTGTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTTGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCGTCATTAACTTTACAATAATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14663 Psectrocladius sp. water mite diet isolate 14663-BHL040517-GBD24052_16405-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGTAGAATTCGGTCACGCCGGTTTATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCACCGACATAGCATTCCCGCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14664 Chironomidae sp. water mite diet isolate 14664-BHL040517-GBD5399_20282-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTTATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGTGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGGTTTTGATTACTACCCCCGTCATTAACTTTATTATTATCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14665 Psectrocladius sp. water mite diet isolate 14665-BHL040517-GBD2909_20292-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGTAAAACTCGGTCACCCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGCAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCTACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTAGCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14668 Psectrocladius sp. water mite diet isolate 14668-BHL040517-GBD25963_9792-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGAAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGATTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTGATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCACCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACGTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAGTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14669 Psectrocladius sp. water mite diet isolate 14669-BHL040517-GBD24950_12253-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGGTGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTAATACCGATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCAGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACGTCCCCCGTCATTAACTTTACTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14672 Chironomidae sp. water mite diet isolate 14672-BHL040517-GBD13336_17529-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGATCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGCTTCCTTAATTGGAGATGACCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCACGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTATCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14673 Dicrotendipes sp. water mite diet isolate 14673-BHL040517-GBD26912_11516-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCAAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTAGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGGTATAGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACAC-TATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14676 Dicrotendipes sp. water mite diet isolate 14676-BHL040517-GBD18489_17777-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14677 Chironomus sp. water mite diet isolate 14677-BHL040517-GBD21752_13002-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAAATTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTACCCCTAATACTTGGAGCACCTGACATAGCCTTTCCCCGAATAAAAAATATAAGTATCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14678 Dicrotendipes sp. water mite diet isolate 14678-BHL040517-GBD16205_9279-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTACCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTCATTGGAGATGATCAAATCTACATTGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCAATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14683 Psectrocladius sp. water mite diet isolate 14683-BHL040517-GBD19326_21741-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGAGCTTGATCAGGCATAGTTGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCATGCCGGTTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCAAATAAATAATATAAGTTTTTGATTACTGCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14685 Psectrocladius sp. water mite diet isolate 14685-BHL040517-GBD14428_22589-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGATCACGCCAGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAAGAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14691 Dicrotendipes sp. water mite diet isolate 14691-BHL040517-GBD22456_10313-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATATTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACTGCTCATGTTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTATTATCTCCTTTTCTAACCCTACTACTTTCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14692 Psectrocladius sp. water mite diet isolate 14692-BHL040517-GBD11815_27345-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTGATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATCCCTAATTTATTTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGACCCCCCGACATAGCATTCCCTCGAAAAAAAAAAATAAGTTTTTGATTACTTCCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14693 Dicrotendipes sp. water mite diet isolate 14693-BHL040517-GBD7821_5274-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTTGGAGCTTGATCTGGAATAGTATGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGTGATGATCAAATCTACAATGTAATTGTTACTGCTCATGCTTTTATTATAAATTTTTTTATGGTTATACCTATTTTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCACCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14694 Psectrocladius sp. water mite diet isolate 14694-BHL040517-GBD23452_11641-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGGTCAGGCATAGTAGGCACTTCTTTAAGTATTTTAATTCGAGCAGAACTCGGTCACGCTGTTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTACAATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14695 Psectrocladius sp. water mite diet isolate 14695-BHL040517-GBD27791_21436-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGTGCAGAACTAGGTCAAGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCGTCATTAACTTTACTACTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14696 Chironomus sp. water mite diet isolate 14696-BHL040517-GBD21399_9062-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTTAATTGGAGGATTCGGAAACTGACTTTTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCATCTCTAACCCTTCTTCTATCTAGTTTATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14698 Chironomidae sp. water mite diet isolate 14698-BHL040517-GBD19104_26634-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCAACCAGCAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAATTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14699 Psectrocladius sp. water mite diet isolate 14699-BHL040517-GBD16227_19433-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAATAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAAATCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTAGTCCCGTTAATATTAGGAGCCTCAAACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14701 Psectrocladius sp. water mite diet isolate 14701-BHL040517-GBD10243_11436-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTTATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACCCCGGTTCCTTATTTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGATCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCGCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14703 Chironomus riparius water mite diet isolate 14703-BHL040517-GBD6831_15167-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAA-ACTTGGAGCACCTGACATAGCTTCTCCTCGAATAAAAAATATAAGTTTCTGGCTTTCACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCCGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14704 Psectrocladius sp. water mite diet isolate 14704-BHL040517-GBD17234_13143-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATATTTGGAGCATGAGCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAAATTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14705 Psectrocladius sp. water mite diet isolate 14705-BHL040517-GBD16833_2857-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGTTTCCTTAATTGGTGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATGTGGAAATTGATTAGTCACGTTAATATTAGGAGTCCCCGACATAGCATTCCCTCGAATAAATAATATATGTTTTTGATTACTTCCCCCGTCATTAACTTTCCTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14707 Psectrocladius sp. water mite diet isolate 14707-BHL040517-GBD17080_19028-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATGCCTATTTTAATTGGAGGATTTGGAAATTGATTGGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAAAATAAATATTTGATTACTTCCCACCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14709 Chironomus riparius water mite diet isolate 14709-BHL040517-GBD3944_14501-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTTGGGGCTTGATCCGGATTAGTGGGAACTTCATTAAGATTGCTTATTCGAGCAGATTTAGTACGACCCGGAACTTTCATTGGAGATGACCAATTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14712 Archisepsis sp. water mite diet isolate 14712-BHL040517-GBD23771_21626-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATCTTTGGAGCTTGAGCAGGAATAGTCGGAACTTCTATAAGAATTCTAATTCGTGCTGAATTAGGACAACCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTAATACCAATTATAATTGGTGGATTGGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTACTTCCTCCTTCACTTACACTATTATTAGTAAGAAGTATAGTAGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID EU435775, identified in GenBank as Archisepsis excavata. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14713 Chironomidae sp. water mite diet isolate 14713-BHL040517-GBD9991_16541-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATAATTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTGACCCCCCTCTCGTACTCTTCTTCTTTCCAGTTCTGTCGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.6% identical to accession ID GU565715, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14715 Psectrocladius sp. water mite diet isolate 14715-BHL040517-GBD13240_28245-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTGTATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCAAGCAGGTTCCTTAATTGGATATGATCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTCAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14718 Chironomus riparius water mite diet isolate 14718-BHL040517-GBD15859_7382-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGCATGCTTATTCGAGCATAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATCATTTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGTCATAGCTCTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14723 Paratanytarsus sp. water mite diet isolate 14723-BHL040517-GBD22299_16686-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGATCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATAATAGGAGCCCCAGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14726 Chironomidae sp. water mite diet isolate 14726-BHL040517-GBD24788_9948-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGTATTTTAATTCGAGTAGAACTCGGTCACGCTGGTTACTTAATTGGAGATGATCAAATTTATAATGTAACTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCTCGTCATTAACTTTATTATTATCTAGTTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14728 Chironomus riparius water mite diet isolate 14728-BHL040517-GBD7326_20700-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGGGTGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGAGGTAACGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14729 Dicrotendipes sp. water mite diet isolate 14729-BHL040517-GBD22241_9568-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14730 Psectrocladius sp. water mite diet isolate 14730-BHL040517-GBD13575_15675-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAAAACTAGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTACCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGTTCACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14731 Drosophila sp. water mite diet isolate 14731-BHL040517-GBD19640_21841-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATGTTGGCACACTTTATTTTATTTTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGAGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCTTCACTTACCTTATTATTAGTAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID EU493627, identified in GenBank as Drosophila malerkotliana. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14732 Dicrotendipes sp. water mite diet isolate 14732-BHL040517-GBD17484_28733-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTATGAACTTCCTTAAGTATACTTATTCGAGTCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGTGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCACTAACCCTTCTTCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14734 Psectrocladius sp. water mite diet isolate 14734-BHL040517-GBD27913_22123-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGTAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCCGAACTCGTTCACGCCGGTTCCTTAATTGGAGATGCTCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCTACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14735 Chironomus riparius water mite diet isolate 14735-BHL040517-GBD12381_10732-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGATGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTTTAGTTTTTTTCATAGTTATCCCAATTTTAATTGGAGGATTCGGACACTGACTTGTCCCCCTAATACTTGGTGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14736 Diptera sp. water mite diet isolate 14736-BHL040517-GBD9726_2780-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGATTTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID KF670983, identified in GenBank as Stegana sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14738 Chironomus riparius water mite diet isolate 14738-BHL040517-GBD23515_4934-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGTACCGGAACTTTCATTGGAGATGACCAACTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATATCGATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAA-ACTTGGAGCACCTGACATAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1474 Oligochaeta sp. water mite diet isolate 1474-BHL110116-GBD16618_2999-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACACTGTACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATGCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCATCTATAGAACACCCTAGTTACTGCTCATGCATTCTTAATAATTGTCTTTCTTGTAATACCAGTATTTAGTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACTAATTTCTTCTGCAGCAGTAGAAAATGGCGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL14742 Psectrocladius sp. water mite diet isolate 14742-BHL040517-GBD28198_9425-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGACTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCGTTAATATTAGGAGCCCCCGACATAGCATTTCCCCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14743 Orthocladiinae sp. water mite diet isolate 14743-BHL040517-GBD19582_20380-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTGATCGGAGACGACCAAATTTATAATGTAATTGTTACTGCACATGCCTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCACTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14744 Ceratitis sp. water mite diet isolate 14744-BHL040517-GBD24341_15241-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATTTTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAACGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTCATATTTATACCAATCATAATTGGTGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCTCCTGATATAGCATTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACACTATTATTAGCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.0% identical to accession ID AY788423, identified in GenBank as Ceratitis curvata. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14745 Psectrocladius sp. water mite diet isolate 14745-BHL040517-GBD22723_7763-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCTTAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAAAACTCGGACACGCCGGTTACTTAATTGGCGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTGGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCGTCATCAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14746 Dicrotendipes sp. water mite diet isolate 14746-BHL040517-GBD21005_9415-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTTGGCACTTTATCTGGAATAGTATGAACTTCCTTAAGTATACATATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGAAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14748 Psectrocladius sp. water mite diet isolate 14748-BHL040517-GBD22829_9184-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGACTTTTACTTCGAGCCGAACTCGGTCGCGCCGGTTCCTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGACCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14749 Chironomus riparius water mite diet isolate 14749-BHL040517-GBD8795_11940-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTT-GGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTTGAGCAGGATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATTATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCGGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14752 Drosophila sp. water mite diet isolate 14752-BHL040517-GBD4598_10797-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATTTTTGGAGCATGAGCAGGAATAGTCGGAACTTCTTTAAGAATTTTAATTCGTGCTGAATTAGGACATCCTGGAGCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACCAACACTAGTATTAGTAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID KJ463787, identified in GenBank as Drosophila melanogaster. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14753 Chironomus sp. water mite diet isolate 14753-BHL040517-GBD13456_13960-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTACAATCTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCACGAATAAATAATATAAGATTCTGACTTTTATCCCCCTCTCTTACCCTACTACTTTCTAGTGCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14756 Psectrocladius sp. water mite diet isolate 14756-BHL040517-GBD22583_15327-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTTAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCTTTAACTTTACTATTATCTAGCTCACCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14759 Psectrocladius sp. water mite diet isolate 14759-BHL040517-GBD15952_28844-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTCCTTGGAGATGATCAACTTTATAATGTAATTGTTACCGCCCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTCCCGCTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14761 Psectrocladius sp. water mite diet isolate 14761-BHL040517-GBD17847_6326-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTAGAGCAGAACTCGGTCACGCCGATTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTACAGTAATACCTATTTTAATTGAAGGATTTGGAAATTGATTAGTCCCGTTAATAATAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAACTCTCTAGTTGAAAATGGAGCTGGACCAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14762 Diptera sp. water mite diet isolate 14762-BHL040517-GBD21732_23543-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGTAAATTGGTTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAAAAATATAAGTATATAACTTCGTCCTCCTTCACTTACACTATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.6% identical to accession ID AY788423, identified in GenBank as Ceratitis curvata. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14763 Psectrocladius sp. water mite diet isolate 14763-BHL040517-GBD16337_4438-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCATGAGCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATGCGAGCAGAACTCGGTCACGCCGTTTCCTTAATTGGAGATGATCAAATTTAGAATGTAATTGTGACCGCGCACGCTTTTGTAATAATTTTTTTTATAGTAACACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGCTGAAACTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14765 Psectrocladius sp. water mite diet isolate 14765-BHL040517-GBD13455_28281-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCAGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGTGCCCCCGACATAGCATTCCCGCGAATAAATAATATAAGATTTTGATAACTACCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14767 Psectrocladius sp. water mite diet isolate 14767-BHL040517-GBD5293_18175-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTAAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTAATAATGTAATTGTTACCGCACACGCTTTTGTAATAATTTTTTTTATAGTAATAACTATTTTAATTGGAGGATTTGGAAATTGATTAGTCACGTTAATATTAGGAGCCCCTCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14768 Chironomus riparius water mite diet isolate 14768-BHL040517-GBD14808_3210-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCTGAACTTTCATTGGAGATGACCAAATTTATACTGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTGGTCCCCCT-ACACTTGGAGCACCTGACATAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGC	Using NCBI BLASTN in June 2018, this sequence was 98.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1477 Chironomus riparius water mite diet isolate 1477-BHL110116-GBD13337_19412-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTAGCTTACTCTTTGTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14771 Psectrocladius sp. water mite diet isolate 14771-BHL040517-GBD28172_11426-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTGTATTTTATTTTTGGAGCATGATCAGGTATATTAGTCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGCTCACGCCGGTTCCTTAATTGGAGATGATAAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14772 Psectrocladius sp. water mite diet isolate 14772-BHL040517-GBD5598_19394-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGAAGCCTGATCAGGCATAGAAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCTGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGTAGGATTTGGAAATTGATTATTCCCGTTAATATTAGGATGCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14774 Psectrocladius sp. water mite diet isolate 14774-BHL040517-GBD28645_12401-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTCGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTACTTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGATATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTCTAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTGTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCGCTAGTTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14775 Chironomidae sp. water mite diet isolate 14775-BHL040517-GBD9727_24594-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTAGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCAGTTACACTATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14776 Psectrocladius sp. water mite diet isolate 14776-BHL040517-GBD5302_18219-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTAAATTCGAGCAGAACTCGGGCACGCCGTGTCCTTAATTGGAGATGATCAAATTCATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCTCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14777 Psectrocladius sp. water mite diet isolate 14777-BHL040517-GBD22338_22907-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGACCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCGGAACTCGGTCACGCCGGTTCCTTAATAGGAGATGATCAAATTTCTAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCTGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTAGCTAGCACTCTAGTTGAAAATGGACCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14781 Psectrocladius sp. water mite diet isolate 14781-BHL040517-GBD9455_7820-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGATCCTGATCAGGCATAGTAGTCACTTCTTTAAGAATTTTAGTTCGAGCAGAACTCGGTCACGCCGATTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATCACTTCCCCCGTCATTAACTTTACTATAATCTAACTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14783 Psectrocladius sp. water mite diet isolate 14783-BHL040517-GBD23461_15408-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTCGGAGCCTGATCAGGCATAGTAGGCACTTCCTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTACCTTAATTGGAGATGAACAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATATTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACTCTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14785 Psectrocladius sp. water mite diet isolate 14785-BHL040517-GBD12581_20591-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCGTAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGACACCCCGGTACCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTACTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTGCTATTATCTAGCTCTCTAGTTGAATAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14786 Chironomus riparius water mite diet isolate 14786-BHL040517-GBD19233_21465-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATACGGAATAGTGGGAACTTCATTAAGAATGCTTATTAGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTTTTACTCTTCATCAATCTAGTGCTTTCGTATAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14788 Psectrocladius sp. water mite diet isolate 14788-BHL040517-GBD29114_17678-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGCCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCAGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTCCCGCTCACGCTTTTGTAATAATTTCTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTGTGATGACGTCCCCCGTCATTAACTTTACTATGATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14789 Psectrocladius sp. water mite diet isolate 14789-BHL040517-GBD23480_10764-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATCTTTTATTTTTGGAGCCTGATCAGGCCTAGTAGGCCCTTCTTTAAGAATTTTACTTCGAGCAGAACTCGTTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1479 Cricotopus sp. water mite diet isolate 1479-BHL110116-GBD18723_22192-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCTGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTTATAGTATTACCAATTCTAATTGGAGGATTTGGAAATTGATTATTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCATTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14790 Psectrocladius sp. water mite diet isolate 14790-BHL040517-GBD3266_21108-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATAACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGTTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14791 Chironomus riparius water mite diet isolate 14791-BHL040517-GBD16493_27769-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGCGGGAACTTCGTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAAT-CTTGGAGCACCTGACATAGCTTCTCCCCGAATAAATCATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14792 Paratanytarsus sp. water mite diet isolate 14792-BHL040517-GBD14228_3274-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACACCCCCTAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTAATGCATTGATTATAATTTTTTTCATAGTTATACATATTTTAATTGGAGGATTTGGGGCACTGATTATTGCCTTTAATATTAGGAGGCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCGTTTACTTTCAAGTAGAATAGTGGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14793 Chironomidae sp. water mite diet isolate 14793-BHL040517-GBD22941_8881-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGTAATAGTTGTTACTTCTTTAAGAATTCTAATTCGGGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGATCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCGCATCATTAACTTTATCATTATCTAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14802 Chironomus riparius water mite diet isolate 14802-BHL040517-GBD9988_23805-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGCCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGGTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTATTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTTCCCCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTTTTTCGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14803 Psectrocladius sp. water mite diet isolate 14803-BHL040517-GBD13114_8691-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGTTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGAAGGATTTGGAAATTGAATAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGATCTATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14807 Psectrocladius sp. water mite diet isolate 14807-BHL040517-GBD3940_14236-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTACTTAATTGGAGATGTTCAAATTTATAATTTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCGTTAATATTAGGTGCCCCCGACATAGCATTCCCTCGATTAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14808 Psectrocladius sp. water mite diet isolate 14808-BHL040517-GBD21650_22543-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTTGGAGCCTGGTCAGGCATAGTAGGTACTTCTTTAAGAATTTAAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTTACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCTCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14818 Psectrocladius sp. water mite diet isolate 14818-BHL040517-GBD11325_23362-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATCTTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTATGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTCTAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTAATACCTACTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTCTGATTACTTCCCCCGTCATTAACTTAACTATTATCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14819 Psectrocladius sp. water mite diet isolate 14819-BHL040517-GBD26866_16394-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTATGAAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGTATTTGGAAATTGATTAATCTCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTTAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14822 Chironomus riparius water mite diet isolate 14822-BHL040517-GBD22981_23762-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGTTTGTTCGGGAATAGTGGGAACTTCATTAAGAATGGTTATTCGAGCGGACTTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTTTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14825 Drosophila sp. water mite diet isolate 14825-BHL040517-GBD24458_19712-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACATCCTGGAGCATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTGGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGATTTTGACTTCTACCTCCTTCACTTACGCTATTATTAGTAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID KJ463787, identified in GenBank as Drosophila melanogaster. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14827 Psectrocladius sp. water mite diet isolate 14827-BHL040517-GBD20184_3653-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAACTGATTAGTACCGTTAATATTAGGAGCCCCCGGCATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14828 Chironomus sp. water mite diet isolate 14828-BHL040517-GBD10621_23172-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGGATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAACTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACACGCCTTTATTATAATTTTTTTTCTTAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCTCC-AAAACTTGGAGCACCTGACATAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14830 Psectrocladius sp. water mite diet isolate 14830-BHL040517-GBD19817_20688-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTATCGCCGGTTCCTTAATTGGAGATGATCAAATTTATATTGTAATTGTTACCACTCACGCTTTTGTAATATTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCTGTTAATATTAGGAGCTCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14831 Psectrocladius sp. water mite diet isolate 14831-BHL040517-GBD8503_4184-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCATTAATTGGCGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATATTAATTGGAGGATTTGGAAATTGATTAGTCACGTTAATATCAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTGCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14834 Psectrocladius sp. water mite diet isolate 14834-BHL040517-GBD11650_21330-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGTATGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAACTTTATAATGTCATTGTTACCGCTCACGCTTTTTTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGCGCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14835 Cricotopus trifasciatus water mite diet isolate 14835-BHL040517-GBD23512_9656-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATGGTAGGGACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGACATGCTGGCTCATTAATTGGTGATGATCAAATTTATAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTTACATTATTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KM933933, identified in GenBank as Cricotopus trifasciatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14836 Psectrocladius sp. water mite diet isolate 14836-BHL040517-GBD11179_16696-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTATTTCGAGCAGAATTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATATTTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCACTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14838 Psectrocladius sp. water mite diet isolate 14838-BHL040517-GBD2290_14427-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATCTTTTATTTTTGTAGCCTGATCAGGCATAGTAGTCACTTCTTTAAGAATTTTAATTCGAGTAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGATCACGCTTTTGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGACCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTATCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14839 Psectrocladius sp. water mite diet isolate 14839-BHL040517-GBD16444_10350-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACTTTATTTTTGGAGCTTGATCCGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTGTAATAAATTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14841 Paratanytarsus sp. water mite diet isolate 14841-BHL040517-GBD27477_10934-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATAGTTCATTTTAGGTGCCTGATAAGGAATAGTGGGAACTTACCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCTTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATAAAAGATTTTGACTTCTTCCCCCCTCTTTAACACTTTTACTTTCAAGTAAAATAGTGTAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14845 Psectrocladius sp. water mite diet isolate 14845-BHL040517-GBD19865_3688-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATAAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCAAGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCTCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTTGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTATGATTTCTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTTTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14846 Psectrocladius sp. water mite diet isolate 14846-BHL040517-GBD28243_19851-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGCATGTTAATTCGAGCAGAACTAGGTCATGCCGGTTCTTTCATTGGAGATGATCAAATTTCTAATGTCATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14847 Chironomus riparius water mite diet isolate 14847-BHL040517-GBD8527_3874-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGACCCGGAATAGTGGGAACTTCATTAAGAAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCGAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTACACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAA-AATTGGAGCACCTGACATAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTATCTAGTTCTTTCGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14850 Paratanytarsus sp. water mite diet isolate 14850-BHL040517-GBD27462_10923-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTGTAGTTCATTTTCGGTGCCTGATCAGGAATAGTGGGTACTTCCCTATGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCTTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGCATAAAGAATATAAGATTTTGACTACTTCCCCCCTCGTTAACTCTTTTACTTTCAAGTAAAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14852 Chironomidae sp. water mite diet isolate 14852-BHL040517-GBD13005_2813-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTAATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAACTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCACCCGACATAGCATTCCCTCGAATAAACAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGCTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14853 Psectrocladius sp. water mite diet isolate 14853-BHL040517-GBD20563_13240-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGTTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCACACGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACGTTACGATGATCTAGCTCTCGAGTTGAAAATGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14854 Chironomus riparius water mite diet isolate 14854-BHL040517-GBD19305_13445-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTGTACATTATTTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCTTTAAGATTGCTTATTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTACATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTGCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14856 Chironomidae sp. water mite diet isolate 14856-BHL040517-GBD9852_14922-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCTAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTACCATTAATAATAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACATTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14858 Psectrocladius sp. water mite diet isolate 14858-BHL040517-GBD27633_21723-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCAGGCCGATTCATTAATTGGAGATGATCATATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGAAGGATTTGGAAATTGATTAGTTCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTTTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14861 Diptera sp. water mite diet isolate 14861-BHL040517-GBD19906_20259-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTAGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGAGATAGCCTTTCCACGAATAAAAAATATAAGTTAATGAATTCTTCCTCATTCACTTACACGAATAATAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.0% identical to accession ID KR262659, identified in GenBank as Prochyliza xanthostoma. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14862 Chironomus sp. water mite diet isolate 14862-BHL040517-GBD26524_23844-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGGTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATATATATTGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCCCCTGTCATAGCTTTTCCTCGAATAAAAAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTGCTTTCTAGTTTTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14863 Psectrocladius sp. water mite diet isolate 14863-BHL040517-GBD14838_5498-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATGCGAGCAGAACGCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGAAATTGGTACCGCTCTCGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTTGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14864 Diptera sp. water mite diet isolate 14864-BHL040517-GBD27596_16375-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACAGTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAAGTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAACAATATAAGTTTTTGACTTCTTCCTCCTTCACCTACACAATTATTAGTAAAAAGTATAGTAGAAAATGGCGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 89.1% identical to accession ID JX887648, identified in GenBank as Leucophenga sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14866 Psectrocladius sp. water mite diet isolate 14866-BHL040517-GBD23817_23369-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGCACTTGGTCACTCCGGTTCCTTAATTGGAGATGATCAAATTTATCATGTAATTGTTACCGCTCACGCTATTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGTAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14868 Psectrocladius sp. water mite diet isolate 14868-BHL040517-GBD6986_20102-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAATAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCTGTCACGCCAGTTCCTTAACTGGAGATGATCAAATTTATAATGTAATTGTTACCGCCCACGCTTTTGTATTAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14872 Psectrocladius sp. water mite diet isolate 14872-BHL040517-GBD29594_16375-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCAGTAACGGGACGAGGAGCGAGCGCGCGAGGGGAAAAGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14873 Psectrocladius sp. water mite diet isolate 14873-BHL040517-GBD2698_18523-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGCACTCGGGCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGTAGGATTTGGAAATTGATTAGTCTCGTTAATATTAGGCGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATCACTTCCCCCGTCATTAACGTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14878 Psectrocladius sp. water mite diet isolate 14878-BHL040517-GBD15754_23134-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTAAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGATAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTACTATTAGCTAGCCCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14885 Psectrocladius sp. water mite diet isolate 14885-BHL040517-GBD24067_23946-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAATAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTGGTCCCGTTAATATTAGGAGCCCCCGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTACTATAAAGCTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14893 Psectrocladius sp. water mite diet isolate 14893-BHL040517-GBD18022_27261-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATAGTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCTCTCACACTTTTGTAATCATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCTCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCTGTCATTAACTTGACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14895 Psectrocladius sp. water mite diet isolate 14895-BHL040517-GBD2560_13317-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCTTATTAGTCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTAACGCCGGTGCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCACCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14898 Psectrocladius sp. water mite diet isolate 14898-BHL040517-GBD5387_7399-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATAATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAGTTGTTACCGCACACGCTTTTGTAATAATTTTTTTTATAGTAATACCTGTTTTAATTGGAGGATGTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATAAACTTTACTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14899 Psectrocladius sp. water mite diet isolate 14899-BHL040517-GBD18734_28612-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAAGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATATAAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAAAATTAGTAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14900 Psectrocladius sp. water mite diet isolate 14900-BHL040517-GBD11720_2415-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGACATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCAGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTTGGAAATTGATTAGTCACGTTAATATTAGGAGCCCCCGACACAGCATTCCCCCGAATAAATAATATAAGTTCTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14904 Psectrocladius sp. water mite diet isolate 14904-BHL040517-GBD11970_5897-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTGTGTATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCGCTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTGCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGAATAGTCCCGTTAATATTAGGAGCCCCCGACACAGCATTCCCTCGAATAAACAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14905 Chironomus riparius water mite diet isolate 14905-BHL040517-GBD22523_19963-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGAGCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTGGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGGGGATTCGGAAACTGACTTGTCCCCCTAA-ACTTGGAACACCTGACATAGCTTCTACTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14907 Psectrocladius sp. water mite diet isolate 14907-BHL040517-GBD4176_18654-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGATCAGGCATAGTAGTCACTTCTTTAAGCATTTTCATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGTTCAAATTTATAATGTAATTGTTACCGATCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTAAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14909 Lucilia sp. water mite diet isolate 14909-BHL040517-GBD16507_2401-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACTTTATACATTATTTTGGG-GCTTGATCCGGAATAGTGGGAACTTCACTAAGAATTTTAAGTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTTATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACACTATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.1% identical to accession ID KX161608, identified in GenBank as Lucilia caesar. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14911 Psectrocladius sp. water mite diet isolate 14911-BHL040517-GBD22931_24475-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGTACTTCTTTAAGAATTTTAATTTGAGCATAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAACTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGTCGCCCCTGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14914 Dicrotendipes sp. water mite diet isolate 14914-BHL040517-GBD8435_4523-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGTGACATTTATTGGAGATGATAAAATCTACAATGTAATTGTTACAGTTCATGCTTTTATTATAATTTTTTTTTATGTTTATACCGATTTTATTTGGAGTATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGGTATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCGTTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14915 Chironomus riparius water mite diet isolate 14915-BHL040517-GBD13102_27965-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGTCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGTATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATCATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGAC-TTTATCCCCCTCTCTTACTCTTCTTCTTTCTAGATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14917 Psectrocladius sp. water mite diet isolate 14917-BHL040517-GBD23506_25811-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGTTCAGTCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAAGATTATGATCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTGTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14918 Psectrocladius sp. water mite diet isolate 14918-BHL040517-GBD15661_2127-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATAAAGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATACTTTTCTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGGCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCATCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14924 Diptera sp. water mite diet isolate 14924-BHL040517-GBD4727_13725-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCTGTACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACAACCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTAACTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAAAATAAGTTTTTGACTTCTTCCTCCTTCATTTACACTATAATTAGTAAGAAGTATAGTAGGAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.9% identical to accession ID KJ496572, identified in GenBank as Diptera environmental sample. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14927 Psectrocladius sp. water mite diet isolate 14927-BHL040517-GBD2895_16946-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATCTTTTATTTTTGGAGCTTGATCGGTAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGTTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTGATTGGAGGATTTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14941 Chironomus sp. water mite diet isolate 14941-BHL040517-GBD10051_26084-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTAATCCGGAATAGTGGGAACTTCATTAAGAATTTTTATTCGAGCAGAATTCGGACGACCCGGAACTTTCATCGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14945 Dicrotendipes sp. water mite diet isolate 14945-BHL040517-GBD17817_21917-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGTCGAATTAGGACGACCCGGGACATTGATTGGAGATGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATGGTTATACCCATTCTAATTGGAAGTTTCGGAAATTGATTAGTCCCTATAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTATCTAAATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14946 Chironomidae sp. water mite diet isolate 14946-BHL040517-GBD3601_11944-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGATTATTATTTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTATAATCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14947 Psectrocladius sp. water mite diet isolate 14947-BHL040517-GBD20098_26556-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGGCTGATCAGGCATAGTAGATACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGTTTCCTTAATTTGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTCAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTTAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14948 Psectrocladius sp. water mite diet isolate 14948-BHL040517-GBD7498_22591-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCTGAACTCTGTCACCCCGGTTCCTTAATTGGAGAAGATCAAATTTATAATGTAATTGTTACTGCTCACGCTTTCGTAATAATTTTTTTTTATTGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCCGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14949 Psectrocladius sp. water mite diet isolate 14949-BHL040517-GBD25285_16064-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGTCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTATTTGGAGATGATCAATTTTATAATGTAATTGTTACCGCTCACGATTTTGTAATAATTTTTTTTACAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14950 Psectrocladius sp. water mite diet isolate 14950-BHL040517-GBD20450_25867-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGAACTTCTTCAAGAATTTTAATTCGAGTAGAATTAGGTCACGCCGGTTCCTTCATTGGAGATGATCAAATTTATAATGCAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14951 Psectrocladius sp. water mite diet isolate 14951-BHL040517-GBD25552_16729-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCATAACTCGGTCACGCCGGGTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCCCGCTTTTGCAATAATTTTTTTTATAGTAATACCTATCTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCTAATAAATAATATAAGTTTTTGATTACTTCCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14952 Psectrocladius sp. water mite diet isolate 14952-BHL040517-GBD10371_19864-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGATATGATCAAATTTATAATGTAATTTTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGTTTAGTACCATTAATATTATGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14953 Ceratitis sp. water mite diet isolate 14953-BHL040517-GBD13444_12724-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATTTTTGGAGCATGAGCAGGAACAGTAGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGCGCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAGTAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGATTTTGACTACTACCTCCTTCACTAACCCTATTATTAGTAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID AY788423, identified in GenBank as Ceratitis curvata. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14954 Drosophila sp. water mite diet isolate 14954-BHL040517-GBD18586_21358-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATATTTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAAAATAAGTTTTTGACTACTTCCTCATACACCAACACAATAATTAGAAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.6% identical to accession ID DQ471533, identified in GenBank as Drosophila repleta. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14957 Cryptochironomus sp. water mite diet isolate 14957-BHL040517-GBD8164_16352-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATATCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGTCCCAGATATAGCTTTTCCCCGCACAAATAATATAAGATTTTTACTTTTACCACCATCCTTGAGCCTTCTTCGTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14962 Dicrotendipes sp. water mite diet isolate 14962-BHL040517-GBD16735_27156-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTATGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGAAATTTATTGGTGATGATCAAATCTATAATGCTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATGGTTATGCCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL14964 Psectrocladius sp. water mite diet isolate 14964-BHL040517-GBD20510_9069-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAGCTCGGTCACGCCGTTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAACTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATAACTTCCCCCGTCATTAACTTTACTACTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14965 Psectrocladius sp. water mite diet isolate 14965-BHL040517-GBD21951_13060-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATACGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAAATTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAAAAAAATAAGTTTTTGAATACCTCCCCCGTCATTTACCTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14977 Chironomidae sp. water mite diet isolate 14977-BHL040517-GBD18857_13168-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGTCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAACAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATATTGTAATTGTTACCGTTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTTGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGATTACTACCACCGTCATTATCTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14979 Chironomus riparius water mite diet isolate 14979-BHL040517-GBD27501_21461-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCAAGCAGAATTAGGACTACCCGGACCTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTTGAGGATTCGGAAACTGACTTGTCCACCTAA-ACTTGGAGCACCTGACATAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14990 Psectrocladius sp. water mite diet isolate 14990-BHL040517-GBD17868_15595-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAGTTCGAGCAGAACTCGGTCACGACGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATTCCTATTTTAATTGGAGGATTTGGAAATTGATTATTCCCGTTAATATTAGGTGCCCCCTACATAGCATTCCCTCGAATAAATAATATAAGGTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14996 Psectrocladius sp. water mite diet isolate 14996-BHL040517-GBD6712_23605-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGCCACTTCTTTAAGATTTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTATTTGGAGATGATCAAATTTATAATGTAATTGTTCCCGCTCACCCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL14997 Psectrocladius sp. water mite diet isolate 14997-BHL040517-GBD18312_13034-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTGTATTTTATTTTTGGAGTCTGATCAGGTATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGTTTCATTCATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGAATAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACATTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15001 Psectrocladius sp. water mite diet isolate 15001-BHL040517-GBD22462_17578-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGACACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCATGCCGGTTCCTTAATTGGAGATGTTCAAATTTATAATGTAATTGTTACCGCTCACGCTATTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAAATTGATTAGTCCCGTTAATATTATGAGTCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15003 Chironomus riparius water mite diet isolate 15003-BHL040517-GBD24578_14930-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTAACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTAATTTGTCCCCCTAA-ACTTGGAGCACCTGACATAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTATAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15004 Dicrotendipes sp. water mite diet isolate 15004-BHL040517-GBD14328_9745-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCTAAATTAGGACGACCCGGGACATTGATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATATTTTTTTTTATGGTTATACCCATTCTCATCGGAGGTTTCGGAAATTGATTAGTACCTATAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL15008 Chironomus riparius water mite diet isolate 15008-BHL040517-GBD16663_4421-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGGTGATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCATATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCACCCTAATACTTGGAGAACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTTTTTCGTAGAAAATGGAGCTGGTACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15011 Psectrocladius sp. water mite diet isolate 15011-BHL040517-GBD6079_24193-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTCTGGAGCCTGATCAGGCATAGTATGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGCCGGGTCCTTCATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCATCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15013 Psectrocladius sp. water mite diet isolate 15013-BHL040517-GBD21912_19787-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGACTTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATTATCCAATTTATAATGTAATTGTTACCTCTCAAGCTTTTTTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCATCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15015 Psectrocladius sp. water mite diet isolate 15015-BHL040517-GBD23944_25833-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGCAGTCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGTGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTGGGAGGCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACCATTATCTAGCTCGCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15018 Dicrotendipes sp. water mite diet isolate 15018-BHL040517-GBD12403_27824-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTGATTGAAAATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCCATTCTAATTGGAGGTTTCGGAAATTGATTAGTCCCTATAATATTAGGAGCCCTCGATATAGCTTTCCCACGAATAAATAAAATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAAAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15028 Psectrocladius sp. water mite diet isolate 15028-BHL040517-GBD29337_17532-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTGCCTTAATTGGAGATGATCAAATTTATAATGTTATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATCCCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATGAGGAGCCCCCGAAATAGCATTCCCCCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCAGTAACGGGACGAGTAGCTAACTCTCTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15031 Chironomus riparius water mite diet isolate 15031-BHL040517-GBD24880_9427-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGTCTTGATCCGGAATAGTGTGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGTACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGTATGCGGAAACTGACTTGTCCCCCTAA-ACTTGGAGCACCTGACATAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15036 Psectrocladius sp. water mite diet isolate 15036-BHL040517-GBD28970_13114-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCAGGCCATTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTCCCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCACGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACGGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15040 Psectrocladius sp. water mite diet isolate 15040-BHL040517-GBD10681_27245-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATAAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCAAGCCGGTTCCTTATTTGGAGTTGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCGTCATAAACTTTACTATTATCTAGCTCTCTAGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15041 Chironomus riparius water mite diet isolate 15041-BHL040517-GBD15022_28797-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAGGAATGCTTATTCTAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACTAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAA-ACTTGGAGCACCTGACATAGCTTCTCCTTGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCGTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL15045 Psectrocladius sp. water mite diet isolate 15045-BHL040517-GBD24157_21461-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGAGCAGGCATAGTAGGCACTTCTTTAAGAATTT-AATTCGAGCAGGACTCGGTCACGCCTGTTCCTTAATTGGAGATTATCAAATTTATAATGTAACTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGATGATTTGGAAATTGATTAGTTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15046 Chironomus sp. water mite diet isolate 15046-BHL040517-GBD23927_6151-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGATTTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCTCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTGCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15047 Psectrocladius sp. water mite diet isolate 15047-BHL040517-GBD3780_21797-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGCGCCTGATCAGGCATAGTAGGCACTTCTTAAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGATCCTTAATTGGTGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCAGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCTTTAACTTTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15048 Psectrocladius sp. water mite diet isolate 15048-BHL040517-GBD4399_18780-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCACTAAGACTATTAATTCGAGCTGAATTAGGACGTCCCGGAACTTTTATTGGAGATGACTAAATTTATAATGTTATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGGTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15049 Chironomus sp. water mite diet isolate 15049-BHL040517-GBD20558_28146-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGAAACTTTCATTGGAGGTGTCCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGAAAACTGACTTGTCCCCCTAA-ACTTGGAGCACCAGACATAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15050 Dicrotendipes sp. water mite diet isolate 15050-BHL040517-GBD23475_10556-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCAAATTAGGACGTCCCGGGACTTTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCACCCGATATAGCATTCCCACGAATAAATAATATAAGATTCTAACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15051 Psectrocladius sp. water mite diet isolate 15051-BHL040517-GBD25939_24041-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTGGAGCAGAACTAGGTCAAGCCGGTTACTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTATTACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15053 Chironomus riparius water mite diet isolate 15053-BHL040517-GBD9730_24908-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTCTTGGGGCCTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAATTTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTCATAGTTATACTAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAA-ACTTGGAGCACCTGACACAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15063 Dicrotendipes sp. water mite diet isolate 15063-BHL040517-GBD8669_16825-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTATGAACTTCCTTAAGTATACTTATTCGAGCCAAATTATGACGACCCGGGACATTTATTGGAGATGAACAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTATTCCCTTTAATATTATGAGCCCCCGATATAGCTTTCCCACGAATAAATGATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15064 Psectrocladius sp. water mite diet isolate 15064-BHL040517-GBD24311_17822-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGTTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCTCTCACGCTTTTGTAATCATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTCCCGTTAATATTAGGATCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL15071 Chironomus sp. water mite diet isolate 15071-BHL040517-GBD26385_21560-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTTGAGCAGAATTGTGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTCGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATCCTTGGGTCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCCTCTCTTACTCGTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15073 Chironomus riparius water mite diet isolate 15073-BHL040517-GBD12228_5279-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACCACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTTCATAGCTATACCAATTTTAATGGGAGGA-TCGGAAACTGAGTTGTCCCCCTAA-ACTTGGAGCACCTGACATAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15075 Chironomus riparius water mite diet isolate 15075-BHL040517-GBD21339_26071-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTAGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGGAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTACACATGCTTTTATTATAATTTTTTTCATCGTTATACCAATTTTAATTAGAGGATTCGGAAACTGACTTGTCCCCCTAA-ACTTGGAGCACCTGACATAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACGCTTCTTCTTTCTAGTTCTTTCGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15079 Chironomus riparius water mite diet isolate 15079-BHL040517-GBD26540_23810-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAACGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAA-ACTTGGAGCACCTGACATAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTGCTAGTGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15080 Chironomus riparius water mite diet isolate 15080-BHL040517-GBD2573_12563-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGAAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCTCCCTAATACTTGGAGCACCTGACATAGCTTTGCCACGAATAAATAATATAAGTTTCTGAC-TTTACCCCCCTCTCCTACTCTTCCTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15082 Dicrotendipes sp. water mite diet isolate 15082-BHL040517-GBD25443_12234-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCATGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTATAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15083 Psectrocladius sp. water mite diet isolate 15083-BHL040517-GBD26628_19542-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATTGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCTCCTGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATAACTTCCCCCGTCATTAACTTTACTATTATCTAGCGCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15084 Psectrocladius sp. water mite diet isolate 15084-BHL040517-GBD8141_13351-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTCGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACCTAGCCTTCCCTCGAATAAATAATATAAGTTTTTGATTTCCTCCCCCGTCATTAACTTTACTATTATCTAGCTCCCTAGTTGAAAATGGAGCTGTAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15085 Chironomus riparius water mite diet isolate 15085-BHL040517-GBD16114_14298-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTGGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTCGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTCCCCCGAATAAATAAAATAAGTTTCTGAC-TTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15094 Chironomus sp. water mite diet isolate 15094-BHL040517-GBD21360_17835-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTACTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTAAATTGATGGTTTTGGAAATTGACTTGTACCTTTAATACTATGGGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACTTACATTACACCATTCAAGTTCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL15102 Psectrocladius sp. water mite diet isolate 15102-BHL040517-GBD28083_12357-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCAGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAAAAAATAAAAAAAGTTTTTGATAACTCCCCCCGTCATTAACCTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15105 Chironomus sp. water mite diet isolate 15105-BHL040517-GBD17332_22730-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGTTTGATCCGGAATAGTGGGAACTTCATTTAGAATTCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGAAAACTGACTTGTCCCCCTAA-ACTTGGAGCACCTGACATAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACACTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15113 Chironomus riparius water mite diet isolate 15113-BHL040517-GBD11145_9788-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGATCCGGAACTTTCACTGGAGATGACCAAATTTATAAAGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGAATTCGGAAACTGACTTGTCCCCCTAA-ACTTGGAGCACCTGACATAGCTTCTCCTCGAATAGATAATATAAGTTTCTGACCTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15114 Chironomus riparius water mite diet isolate 15114-BHL040517-GBD6151_24046-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATCCGAGCAGAATTAGGATGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTTTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCTCCTAATACTTGGAGCACATGACATAGCTTTTCATCGAATAAATAATATAAGTTTCTGAC-TTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15115 Psectrocladius sp. water mite diet isolate 15115-BHL040517-GBD3216_13888-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATAAGGAATAGTAGGAACTTGTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGTCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTCTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15124 Chironomus sp. water mite diet isolate 15124-BHL040517-GBD22888_26920-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGTATAGAGGGAACTTCATTAAGAATTCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTGATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAAGACATGGAGCAACTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15133 Chironomus riparius water mite diet isolate 15133-BHL040517-GBD21760_3879-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGCTTGATCCGGAATAGTGAGAACTTCAGTAAGAATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTCACTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAA-ACTTGGAGCACCTTACATAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCGTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15136 Chironomus sp. water mite diet isolate 15136-BHL040517-GBD4830_11819-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGGTGACCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAAT-CTTGGATCACCTGACATAGCTTCTCCTCGAGTAAATAATATAAGTATCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15148 Psectrocladius sp. water mite diet isolate 15148-BHL040517-GBD9629_20225-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTTATTGAAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCACGTTAATATTAGGAGCCCCTAGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTAATTCCCCCGTCATTAACTTTACTATTATCTAGAACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15153 Psectrocladius sp. water mite diet isolate 15153-BHL040517-GBD29569_15258-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGTAGAACTAGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCGTTAATATTAGGAGCCCCTGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATAAACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL15158 Chironomus sp. water mite diet isolate 15158-BHL040517-GBD3279_20784-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGAGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTTGTCCCTCTAA-ACTTGGAGCCCCTGACATAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15161 Psectrocladius sp. water mite diet isolate 15161-BHL040517-GBD12169_22558-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCTGAACTCTGTCAAGCCGGTTCCTTAATTGGAGATAATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTGCTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCAGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15165 Dicrotendipes sp. water mite diet isolate 15165-BHL040517-GBD10792_11020-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATATTTGGAGCATAAGCAGGAATAGTCGGGACTTCTCTAAGAATTTTAATTCGTGCTGAACTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTACTTGTTACAGCTCATGCTTTTATTATAATTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15173 Paratanytarsus sp. water mite diet isolate 15173-BHL040517-GBD25297_21213-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATAGTTCATTTTCTGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGGATATTAATTCGAGCTGAACCAGGACATCCCAGAACTTTTATTGGAGATGACTAAATTTCTAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15180 Chironomus riparius water mite diet isolate 15180-BHL040517-GBD5403_19574-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATATTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGTAGGATTCGGAAACTGACTTGTCCCCCTAA-ACTTGGAGCACCTGACATAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15184 Chironomus riparius water mite diet isolate 15184-BHL040517-GBD28329_17095-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGCTCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAAGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGCAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTCTACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCGTTTCCTCGAATAGATAATATAAGTTTCTGAC-TTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15198 Chironomus sp. water mite diet isolate 15198-BHL040517-GBD11565_6257-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGACTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCCCCTGACATAGCTTTCCCCCAAAAAAAAAAAAAAAAGTTTCTGAC-TTTACCCCCCTCTCTTACCCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15199 Chironomus riparius water mite diet isolate 15199-BHL040517-GBD15301_7243-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGTAGGATTCGTAAACTGACTGGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCCCGAATAAATAATATAAGTTTCTGAC-TTTACCCCCCTCTCTTACTCTTCTTCTATCTAGTTCTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15208 Diptera sp. water mite diet isolate 15208-BHL040517-GBD26292_15764-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACACTTTATTTTATCTTTGGAGCATGAGCAGGAATAGTCGGTACTTCTCTAAGAATTTTAATTCGTGCTGATTTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCGCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTATTTGACTTCTTCCTCCTTCACTAACACGATTATTAGTAAGAAGTATAATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID KJ496572, identified in GenBank as Diptera environmental sample. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15220 Chironomus sp. water mite diet isolate 15220-BHL040517-GBD10041_6344-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGTACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTATTTGGAGGATTCGGAAACTGACTTGACCACCTAA-ACTTGGAGCACCTGACATAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCATCTCTGACTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL15234 Chironomus riparius water mite diet isolate 15234-BHL040517-GBD22933_26821-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACCTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCAGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGTTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAA-ACTTAGAGCACCTGACATAGCTTCTCCTCGAATAAATAAAATAAGTTTCTGACTTTTACCCCCCTCTCATACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15236 Psectrocladius sp. water mite diet isolate 15236-BHL040517-GBD24331_18891-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGTCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAAGACCTATTTTAATTGGAGGAATTGGAAATTGATTAGTCCCGTTAATATTAGTAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTGTTTGATTACTTCCCCCGTCATTAACTTAACTATTATCTAGCTCGCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15239 Dicrotendipes sp. water mite diet isolate 15239-BHL040517-GBD27812_21587-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGAACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAACTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15247 Dicrotendipes sp. water mite diet isolate 15247-BHL040517-GBD20883_26964-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTCCTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGGCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGATATACCTATTCTAATGGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGTGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15248 Psectrocladius sp. water mite diet isolate 15248-BHL040517-GBD24740_13257-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTGACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGTTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAAGATTAGGAGCCCCCGACATAGCATTCACTCGAATAAATAATATAAGTTTTTGATTACTTCCCTCGTCATTAACTTTACTATTATCTAGCTAACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15251 Psectrocladius sp. water mite diet isolate 15251-BHL040517-GBD2695_17299-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGAAGTAGCATTCCCACGAATAAAAAAAAAAAGTTTTTAATTACCCCCCCCGCCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15257 Psectrocladius sp. water mite diet isolate 15257-BHL040517-GBD9177_19438-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTTGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAACCCCCGACCAAGCATTCCCTCCAATAAAAAAAATAAGTTTTTGATTACCTCCCCCGTCATTAACTTTACTACTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15259 Diptera sp. water mite diet isolate 15259-BHL040517-GBD25558_8573-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATAAAGATATTGGAACACTTTATTTTATTTTTGGAGCATGAGCAGGAATAATCGGAACTTCTCTAAGAATTTTACTTCGTGCTGAATTAGGACACCCTGGAACATTAATTGGAGACGACAAAATTTATAATGTAATTGTTACCGTTCATACATTTGTAAAAATTTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACTTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACACTATTATTAGCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.5% identical to accession ID KM243502, identified in GenBank as Diachlorus curvipes. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1526 Oligochaeta sp. water mite diet isolate 1526-BHL110116-GBD19765_21772-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCCGGAATAATTGGAACAGGGACTAGAATACTCATTCGACTTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTTAAGATTCTGACTACGACCACCATCTCCAATCTAACTAAAAGCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL15271 Psectrocladius sp. water mite diet isolate 15271-BHL040517-GBD8005_15721-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGAGCAGGAATAGTAGGCACTTCTTTTAGAATTTTAATTCGAGTAGAACTCGGTCACCCCGGTTCCTTATTTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTCATGGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCGCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL15274 Chironomus sp. water mite diet isolate 15274-BHL040517-GBD20446_9146-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGGACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTCTCCTCGCATAAATAATATAAGTTTCTGACCTTTACCCCCCCGCTCTTACACTTCGTCTGTCTAGTTTTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15280 Psectrocladius sp. water mite diet isolate 15280-BHL040517-GBD16048_7654-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAAAACTCGGTCACGCCGGTTCCTTCATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTAAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGGTTTTGATTACTTCCCCCGTCATTAACTTTACTATTACCTAGCTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15282 Chironomidae sp. water mite diet isolate 15282-BHL040517-GBD19261_9323-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGCGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATCGGAAGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGACTTTCCCTCGAATAAATAATATAAGGTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.4% identical to accession ID KR961588, identified in GenBank as Chironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15283 Chironomidae sp. water mite diet isolate 15283-BHL040517-GBD3414_8755-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATATCCATTCTAATTGGAGGTTTCGGAAATTGATTAGTCCCTATAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KM900037, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15291 Paratanytarsus sp. water mite diet isolate 15291-BHL040517-GBD27738_9752-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAAGTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACGTTCATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGCATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACATCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATATTGTAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15293 Psectrocladius sp. water mite diet isolate 15293-BHL040517-GBD23472_11961-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGTATTTTAATTCGAGCGGAACTCGGTCACGCCTGTTCCTTAATTGGAGCTGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTAACAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTAATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL15295 Dicrotendipes sp. water mite diet isolate 15295-BHL040517-GBD23185_7083-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATCTTTAGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGATGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCCCCTTCTCTAACCCCTACTTCTTTCTAGGTCAATTGTAGAAAATGGAGCTGGAACCGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1535 Oligochaeta sp. water mite diet isolate 1535-BHL110116-GBD20011_27793-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTCTATACTTAATTCTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGACTTTCCCACGACTAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCTTACAAAAATCTTCTGCATCAGTATAAGGTGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 88.6% identical to accession ID MG423151, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL1632 Dero sp. water mite diet isolate 1632-BHL110116-GBD18284_22195-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCA-AAAGATATTGGCACTCTATACATCATCCTTGGAGTATGAGCAGGAATAGTAGGAACTGGAACAAGACTACTAATTCGAATAGAACTAGCTCAACCAGGATCATTTCTAGGCAGAGATCAACTATATAATACACTAGTAACAGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGCATTTATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGATTAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID MG423030, identified in GenBank as Dero obtusa. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL1636 Chaetogaster diastrophus water mite diet isolate 1636-BHL110116-GBD28212_14280-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATAAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGGGACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTATAGTTATACCAGTATTAATTGGTGGATTCGGAAATTGAATTCTACCTTTAATACTAGGAGCCCCAGATATGGCATTCCCACGAATAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATTCTACTAATTTCATCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL1641 Chaetogaster diastrophus water mite diet isolate 1641-BHL110116-GBD23773_9948-Lq46 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAATATTAATTCGAATTGAATTATCTCAACCAGGGTCATTCCTAGGTAGATACCAACTATATAATACTCTAGTAACTGCCCACGCATTTCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGTATTCGGAAATTGAATTCTACCTGTAATACGAGGAGCCCCAGATATGGCATTCCCACGATAAAACAATCTAAGATTTTGACTTCTTCCACCTTCACTAATTCTACTAATTTAATCTGCAGCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID GQ355367, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL1644 Chironomus riparius water mite diet isolate 1644-BHL110116-GBD10528_3657-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGAAACTTTCATTGGAGGTGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1645 Cricotopus sp. water mite diet isolate 1645-BHL110116-GBD12805_20224-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAAATGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1646 Lebertia sp. water mite diet isolate 1646-BHL110116-GBD17542_9664-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGGCTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1647 Lebertia sp. water mite diet isolate 1647-BHL110116-GBD24535_12145-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTGCTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTTGATTAAGAACCCTTATTCGACTTGAATTAGGACAACCAGGCACATTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGATTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCGGATATAGCCTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTGAACTCTACTTCTATTAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1648 Lebertia sp. water mite diet isolate 1648-BHL110116-GBD10538_4920-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTACTTTGTTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACCCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAAATTTTTTCATAGTAATACCAATAATAATTGGAGGGTTTGGAAACTGATTAGGTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCAAGAATAAATAATATAAGAATTTGACTTCTTCCCCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1650 Lebertia sp. water mite diet isolate 1650-BHL110116-GBD17031_11093-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGTATGAGCAGGAATAATTGGAGCTAGATTAAGAACACTAATTCGACTTGAATTATGACAACCAGGCTCACTCCTAGGAAGTGAACAAATTTACAATACAATTGTTACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACCTCTATCAAGCTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1651 Lebertia sp. water mite diet isolate 1651-BHL110116-GBD15678_14937-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCCCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGGTTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGAGTGTGACTTCTTACACCATCCTTAACGCTACTACTACCAAGTTCCATTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1652 Lebertia sp. water mite diet isolate 1652-BHL110116-GBD17730_4837-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACCTTGATTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATCATAATTGGCGGTTTTGGAAACTGATTAGTTCCACTAATCATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATCAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTCTCAAGTTCCTTTACCGGAAAATGGAGCTGAAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1653 Lebertia sp. water mite diet isolate 1653-BHL110116-GBD16011_27625-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTGATTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGTCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTACCTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGGTTTGGAGACTGATTAGTTCCACTAATAATCAGATACCCAGATATATCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL1654 Chironominae sp. water mite diet isolate 1654-BHL110116-GBD27530_14453-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTACGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1658 Lebertia sp. water mite diet isolate 1658-BHL110116-GBD25671_6115-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTTGATTAAGAACCCTAATTCGACTTAAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACCATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGAAATAGCCTTTCCACGAAAAAATAATATAAGATTTTGAATTCTTACTCCATCCTTAACCCTACTTCTATCAAGTTTCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1660 Oligochaeta sp. water mite diet isolate 1660-BHL110116-GBD13349_8077-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGTCTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCCCTAATACTTGGAGCTCCAGATATGGCTTTCCCACGAATAAATAATTTAAGATTCTGACTACTACCACCATCTCTAATCCTACTAATTACCTATGCAGAAGGAGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.4% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL1661 Lebertia sp. water mite diet isolate 1661-BHL110116-GBD3177_21143-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAATGAACAAATTTATAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCCATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCACAGATATAGCTTTTCCACCAATAAATAATATAAGATTTTTGCTTCTTCCTCCCTCCTTAACCCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1662 Lebertia sp. water mite diet isolate 1662-BHL110116-GBD4621_21052-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTGGATTAAGAACCCTAATTCGACTTTAATTAGGACAACCAGGCTCACTCCTAGGAAGTGATCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTCCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACGTCTGCCTCCATACTTAACACTGCTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1671 Lebertia sp. water mite diet isolate 1671-BHL110116-GBD15734_2017-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGGGCATGATCCGGAATAATTGGAGCTAGATTAAGAATCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTTACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATGATAATTGGTGGTTTTGGGAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTGACTCTGCTTCTGACAAGTTCCTTTACGGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1672 Lebertia sp. water mite diet isolate 1672-BHL110116-GBD11025_13796-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTTTACTTTGCTTTTGGAGCATGATCCGAAATAATTGGAGCTAGATTACGAATCCTACTTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTACTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTACTAACAAGTTCCTTTACAGGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1674 Oligochaeta sp. water mite diet isolate 1674-BHL110116-GBD13504_23791-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGGGTATGAGCCGGAATAATTGGAACAGGGACTAGAATATTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATTAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTCTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGAAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCCCGACTAAATAATTTAAGATTCTGACTACGACCACCATCTCTAAACGTACTAATTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 84.8% identical to accession ID KY633408, identified in GenBank as Stylaria fossularis. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL1677 Lebertia sp. water mite diet isolate 1677-BHL110116-GBD25364_9765-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTACTTTGTTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAATCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGATCAAATTTACAATACAATTGTATCTGCTCATGCTTTCGTTATAATTTTTTTTATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAACCTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCCTCCTTAACTCTACTTCTATCAAGTTCCTTTACAAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1683 Lebertia sp. water mite diet isolate 1683-BHL110116-GBD23592_13686-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTCACTGCTCATGCTTTTGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGAATAGTTCCACTAATAATCAGAGCCCCAGAAATAGCTTTTCCACGAAAAAATAAAAAAAAATTTTGACTTCTTCCCCCATCCTTAACCCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL1684 Lebertia sp. water mite diet isolate 1684-BHL110116-GBD3934_8212-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGTTTTTGGAGCCTGATCCGGAATAATTGGCGCTTGATTAAGAATTCTAATTCGACTTGAATTAGGACAACCCGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCACGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAAAAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTAACAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1690 Lebertia sp. water mite diet isolate 1690-BHL110116-GBD16654_12309-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTAAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGGTTTGGAAACTGATTAGTTCCACTAATAATCAGAACCCCAGAAAAAGCTTTTCCACGAATAAATAAAATAAGAATTTGACCTCTTCCCCCATCCTTAACTCTACTTCTATCAAGTTCCTGTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1693 Hydrachnidiae sp. water mite diet isolate 1693-BHL110116-GBD13650_22196-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATACTTAATTTTAGGAGTATGAGCAGGAATAATTGGAACAGGGACTAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACCATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAGTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.1% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1704 Lebertia sp. water mite diet isolate 1704-BHL110116-GBD14631_20431-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTATGAACCCTAATTCGACTTGGATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAAGATAAGATCATGACTTCTTCCTCCATCCTTACCACTCCTACTAACAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1706 Lebertia sp. water mite diet isolate 1706-BHL110116-GBD26740_22091-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTCGATTAAGAATCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTTACTGCTCATGCTTTCGTTATAAATTTTTTCATAGTAATACCAATAATAATTGGAGGGTTTGGAAACTGATTAGTTCCACTAATAATCAGAGTCCCAGATATAGCTTTTCCACGAATAAAAAAAATAAGATTTTGACTTCCTCCTCCATCCTTAACTCTACTTCTATCAAGGTCCATTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1714 Lebertia sp. water mite diet isolate 1714-BHL110116-GBD13045_25672-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAGGAACCCTAGTTCGACTTGAATTAGGACAACCAGACTCACTCCTAGGAAGTGACCAAATTTGCAATACAATTGTAACTGATCATGCTTTTGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTGGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAACATAAGATTTTGACTTCTTCCTCCATCCTTAACACTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1716 Lebertia sp. water mite diet isolate 1716-BHL110116-GBD21208_23570-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTTCTTTTGGAGCATGATCCGGAATAATTGTAGCTAGATTAAGAACCCTAATCCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTGTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGAGTTTGACTTCTTCCTCCATACTTAACTCTACGTCTATCAAGTTACGTTACAGGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1719 Lebertia sp. water mite diet isolate 1719-BHL110116-GBD16863_13176-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGTTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAATCTTAATTCGACTCGAATTAGGACAACCAGGCTCATTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATATTAACTGGAGGGTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTGTGACTTCTTCCTCCATCCTTAACTCTACTTCTAGCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1725 Oligochaeta sp. water mite diet isolate 1725-BHL110116-GBD9990_16284-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTTTACTTAATTTTAGAAGTATGAGAAGGAATAATTGGAACAGTGTATAGAATACTAATTCGAATTGAATTATCACAACCAGGATCATTCTTAGGAAGAGATCAACTATATAACACCCTAGTTACTGCACATGCATTCTTAATAATTTTCTTTCTTGTAATACCAGTATTTATTGGAGGATTTGGAAACTGATTAGTACCACTAATACTTGGAGCTCCAGATATGGCTTTCCCACGACTAAATAATTCAAGATTCTCACCACGACCACCATCTCTAATCTTACTAAAATCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.8% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL1738 Lebertia sp. water mite diet isolate 1738-BHL110116-GBD7024_23314-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAGCCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAGTAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATCAGATTTTGCCTCATTCCTCCATACTTAACCCTACTACTAACAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL1740 Lebertia sp. water mite diet isolate 1740-BHL110116-GBD19005_3309-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGGGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATGCGGCTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGAACAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAAAACCAATAATAAATGGAGGTTTTTGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGACTTCTTCCCCCATCCTTAACCCTACTTCTATCAAGTTCCTTTACTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1743 Lebertia sp. water mite diet isolate 1743-BHL110116-GBD21811_27828-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTTGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAAGGTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAAAAAAAAAAATAAGATTTTGACTTCTTCCGCCAACCTTAAATCTACTTCTAACAAGGTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1752 Lebertia sp. water mite diet isolate 1752-BHL110116-GBD27673_22195-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGGTACGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACCCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCCTTTCCACGAAAAAAAAAAAAAAGATTTTGACTTCTTCCCCCATCCTTAACTCTACTTCTATCAAGGACCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1754 Lebertia sp. water mite diet isolate 1754-BHL110116-GBD25806_21736-Lq47 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGCGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATAAAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAAATGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGATTTTCCACGAATAAATAAAATAAGATTTTGAATTATTCCTCCATCCTTAACTCTACTTCTAACGAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1759 Chironomidae sp. water mite diet isolate 1759-BHL110116-GBD4495_11888-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAACTTGATCGGGAATAGTAGGCACTCCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1760 Paratanytarsus sp. water mite diet isolate 1760-BHL110116-GBD22992_25976-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATGTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGACTTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTGCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1761 Psectrocladius sp. water mite diet isolate 1761-BHL110116-GBD27259_14825-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATATTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGATCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1763 Dicrotendipes sp. water mite diet isolate 1763-BHL110116-GBD14239_26324-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGGTATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1764 Chironomidae sp. water mite diet isolate 1764-BHL110116-GBD25755_24643-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGTAATAGTTGTAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTCCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATATTAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR287302, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1765 Cricotopus sp. water mite diet isolate 1765-BHL110116-GBD13704_27144-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTGTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCTGATCATTATTTGGAGATGATCAAATTTTTAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATCGCTTTCCCTCGAATAAATAATATAAGTTTTTGGTTATTACCCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL1772 Chironominae sp. water mite diet isolate 1772-BHL110116-GBD25433_17438-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTCATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGCATAAATAATATGAGATTTTGATTCCTTCCCCCTTCTATATCTCTTCTGCTTACTAGCTCAACTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1773 Paratanytarsus sp. water mite diet isolate 1773-BHL110116-GBD10108_20987-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCCTCATTAACTCTTTTACTTTCAAGTATAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1774 Chironominae sp. water mite diet isolate 1774-BHL110116-GBD13804_26963-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCCTGACCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTAAATTAGGACACCCAGGAACATTATTTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGACTAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTACTCTTTTACTTTCTAGTGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR670143, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1776 Chironominae sp. water mite diet isolate 1776-BHL110116-GBD9117_16469-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACACTGTAATTATCACAGCATATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1777 Chironomidae sp. water mite diet isolate 1777-BHL110116-GBD16871_18285-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTATGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATCATATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1778 Paratanytarsus sp. water mite diet isolate 1778-BHL110116-GBD18990_8867-Ldc71 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGCCACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTTTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGAATAAATAATATAAGTTTTTGACTACTACCCCCATCTTTAACCTTTCTTCTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1788 Chironomus riparius water mite diet isolate 1788-BHL101516-GBD12770_3937-Ldc85 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAGGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAAGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATACCTTTTCCTCGAATCAATACTATAACTTTCTGACTTTTATCCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1789 Paratanytarsus sp. water mite diet isolate 1789-BHL101516-GBD22264_21583-Ldc85 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTCTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATGCCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTGCCCCCATCTTTAACCCTACTTCTATCAAGGAGATTAGTGGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1791 Chironomus riparius water mite diet isolate 1791-BHL101516-GBD16084_13644-Ldc85 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCCTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTCTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1793 Chironomus riparius water mite diet isolate 1793-BHL101516-GBD18096_6513-Ldc86 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATAACCAAATTAATAATGTTGTAGTTACTGCAAATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTTAATTGGAGGAGTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL1794 Chironomus riparius water mite diet isolate 1794-BHL101516-GBD3313_14480-Ldc86 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTAATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTGGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCCAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTCTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1796 Paratanytarsus sp. water mite diet isolate 1796-BHL101516-GBD1857_17074-Ldc86 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTCGGAGCTTGTGCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAAAATTAGGTCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCACATCTTTAACCCTTCTTCAATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1797 Chironominae sp. water mite diet isolate 1797-BHL101516-GBD11025_12388-Ldc86 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACATTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTAATGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACGTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1799 Paratanytarsus sp. water mite diet isolate 1799-BHL101516-GBD11531_19120-Ldc86 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGAATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTACTACTATCAAAAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR672858, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1800 Chironomus riparius water mite diet isolate 1800-BHL101516-GBD23974_5393-Ldc86 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTCTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTATCCCCCTAATACTTGGAGCACCTGACATAGGTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCATCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1801 Chironomus riparius water mite diet isolate 1801-BHL101516-GBD22859_25481-Ldc86 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGCTCCGGAATAGTGGTAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTTTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTAGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTTTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1802 Chironomus maturus water mite diet isolate 1802-BHL101516-GBD16006_11232-Ldc86 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTCTTAGTATGCTTATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTAACTACCCACGCATTTATTATATTTTTTTTTCATAGTTATACCAATTCTAATTGGTGGTTTTGGTAATTGACTTGTACCCTTAATATTAGGAGCCCCAGATATGGCTTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTTACTCTTTTACTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR665396, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1805 Lebertia sp. water mite diet isolate 1805-BHL101516-GBD7771_21336-Ldc86 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAAGTTTTGGAAACTGATTAGTTCCCCTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAAATTTTTACTTCTTCCTCCATCCTTAACCCTACTTCTATCAAGATCCATTTCAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1810 Lebertia sp. water mite diet isolate 1810-BHL101516-GBD26554_17827-Ldc86 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTCGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATAGAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCGTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1823 Chironomus riparius water mite diet isolate 1823-BHL022317-GBD18499_20495-Ldc88 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGTGGATTCGGAAACTGACTTGTCCCCCTAATACATGGAACACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL1824 Podocopida sp. water mite diet isolate 1824-BHL022317-GBD14184_21557-Ldc88 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGGCCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTACCTTTAATAATAGGGGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTACCAACTGGAATACTAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1825 Chironomus riparius water mite diet isolate 1825-BHL022317-GBD7163_17774-Ldc88 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTAGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTATTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGTACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCATACTCTTCTTCTTTCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1829 Chironominae sp. water mite diet isolate 1829-BHL022317-GBD28000_9948-Ldc88 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTTACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTGACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1831 Psectrocladius sp. water mite diet isolate 1831-BHL072216-GBD4828_10618-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAAAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGTTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1832 Chironomidae sp. water mite diet isolate 1832-BHL072216-GBD13264_7131-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACAATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTATAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCTAATAAATAATATAAGTTTTCGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1833 Paratanytarsus sp. water mite diet isolate 1833-BHL072216-GBD8313_25513-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATACTTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCCCATATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1834 Chironomidae sp. water mite diet isolate 1834-BHL072216-GBD25899_10898-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTCTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1835 Chironomus riparius water mite diet isolate 1835-BHL072216-GBD11691_24212-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATCTTGTAGTTACTGCACATGCCTTTATTATAATTTTTTTTTCATAGATATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1838 Chironomidae sp. water mite diet isolate 1838-BHL072216-GBD8165_10114-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1840 Dicrotendipes sp. water mite diet isolate 1840-BHL072216-GBD23027_24319-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGATCATTTATTGGAGATGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATATCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCACGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL1842 Chironominae sp. water mite diet isolate 1842-BHL072216-GBD7671_21483-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCTCTAACTCGTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1845 Chironomus riparius water mite diet isolate 1845-BHL072216-GBD11704_12200-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAACGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGCTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCCCGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1846 Orthocladiinae sp. water mite diet isolate 1846-BHL072216-GBD13051_3623-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAAAATTAGGACACCCAGGCTCATTTATCGGAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTAATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTACTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1848 Chironominae sp. water mite diet isolate 1848-BHL072216-GBD25803_9021-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACATCATTTAGTATTTTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTTACAGCTCACGCTTTTGTTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTAACTCTACTACTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1854 Cryptochironomus sp. water mite diet isolate 1854-BHL072216-GBD27518_19557-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTTTTTTTGGAGTTTGAGCAGGGATGTTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATATCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTACACTGGGAGTCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1860 Chironominae sp. water mite diet isolate 1860-BHL072216-GBD21844_7115-Lunk72 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGTGCTTGATCTGGAATAGTAGGAACATCTCTTAGTATATTAATTCGAGCAGAATTTGGTCATCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTCATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1868 Chironomus riparius water mite diet isolate 1868-BHL022317-GBD7481_6795-Ldc89 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1872 Podocopida sp. water mite diet isolate 1872-BHL022317-GBD17348_21047-Ldc89 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACTGCCTTAAGAGTAATTATTCGGGCTGAGCTCGGTCAACCTGGGGCACTTATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAACTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGTGCACCAGATATAGCGTTTCTTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTCATCCTTATTAACAATTGGAATACTTACAGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1873 Lebertia sp. water mite diet isolate 1873-BHL022317-GBD24056_16261-Ldc89 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1874 Chironominae sp. water mite diet isolate 1874-BHL022317-GBD3289_14861-Ldc89 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCCGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGGACTTGGACGACCTGGTACTTTTAATGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTTCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL1875 Chironomus maturus water mite diet isolate 1875-BHL022317-GBD22166_22111-Ldc89 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTCTTAGTATGCTTATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTAACTACCCACGCATTTATTATATTTTTTTTCATAGTTATACCAATTCTAATTGGTGGTTTTGGTAATTGACTTGTACCCTTAATATTAGGAGCCCCAGATATGGCTTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTTACTCTTTTACTATCTAGTTCATTCGTAGAAAATGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR665396, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1881 Chironominae sp. water mite diet isolate 1881-BHL022317-GBD25364_5633-Ldc89 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATACTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTAATGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTGTCCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACGACTTCCCCCTTCATTAACTCTTTTACTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1882 Chironomus riparius water mite diet isolate 1882-BHL022317-GBD16518_24258-Ldc90 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATAACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCGTAGTTTTACCAATTTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1883 Podocopida sp. water mite diet isolate 1883-BHL022317-GBD20260_20406-Ldc90 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGGCCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTATCCTTATTAACAATTGGAATACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1884 Paratanytarsus sp. water mite diet isolate 1884-BHL022317-GBD24549_8805-Ldc90 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATCCCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1887 Chironomus maturus water mite diet isolate 1887-BHL022317-GBD15191_21362-Ldc90 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTCTTAGTATGCTTATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGCAGTAACTACCCACGCATTTATTATATTTTTTTTCATAGTTATACCAATTCTAATTGGTGGTTTTGGTAATTGACTTGTACCCTTAATATTAGGAGCCCCAGATATGGCTTTTCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTTACTCTGTTACTTTCTAGTACATTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR665396, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1889 Chironomidae sp. water mite diet isolate 1889-BHL022317-GBD14944_25943-Ldc90 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACTCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTACCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGAGTTAGATTACTTCCCCCATCCCTTACCCATCTTCTTTAAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.3% identical to accession ID KM991708, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1892 Chironomidae sp. water mite diet isolate 1892-BHL022317-GBD10290_7231-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTTGGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCTTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCATACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1894 Lebertia sp. water mite diet isolate 1894-BHL022317-GBD17967_19930-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACGACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCCCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAGTAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1895 Coelotanypus sp. water mite diet isolate 1895-BHL022317-GBD29566_14376-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTCATCTTTGGAGCTTGAGCTGGTATAGTAGGTACCTCCCTTAGTATCTTAGTTCGAGCTTAATTGGGTCATCCTGGTGCTCTAATTGGTGATGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTTGTAATAATTTTCTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATCGACTAGTTCCTTTAATATTAGGTGCCCCTGATATAGCCTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCATTAACATTATTATTAGCAAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR085247, identified in GenBank as Coelotanypus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL1897 Chironomus riparius water mite diet isolate 1897-BHL022317-GBD22913_8556-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTTGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTTCCCCCCCGCTCTTACTCTACTTCGTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1898 Paratanytarsus sp. water mite diet isolate 1898-BHL022317-GBD3221_15287-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGTAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCCTATAAATAACATAAGTTTTTGATTACTTCCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1900 Chironomidae sp. water mite diet isolate 1900-BHL022317-GBD6460_17489-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATTATATTTTATTTTTGGAACTTGATCTGGAATAGTAGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCACACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTTCTGCTTTCAAGATCAATTGTAGAAAATGGAGCCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.9% identical to accession ID JF412134, identified in GenBank as Paracladopelma camptolabis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1902 Chironomidae sp. water mite diet isolate 1902-BHL022317-GBD28703_19152-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCTTTAAGAATGTTTATTCGGGCAGAATTAGGACGACCTGGGACTTTTATTGGAGATGACCATATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.1% identical to accession ID KM991708, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1903 Amphichaeta raptisae water mite diet isolate 1903-BHL022317-GBD8370_18134-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGTGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATCTTTAATAATTTTTTTCTTAGTAATACCAGCTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGACTTTGACTATTACCCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL1906 Chironomidae sp. water mite diet isolate 1906-BHL022317-GBD17429_17501-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCTGGAGTAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATGCCCTCGAAGAAATAATAAAAGATATTGATTACTTCCCCCATCCCTTACCCGACATCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.1% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1907 Chironomidae sp. water mite diet isolate 1907-BHL022317-GBD24915_25364-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGTACATCTTTAAGTATGCTTATTCGGGCAGAATTAGGACGACCCTGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCTATCCCTTACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTTGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.3% identical to accession ID KR287333, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1911 Chironomidae sp. water mite diet isolate 1911-BHL022317-GBD17698_6814-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAGTGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAACACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCTTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.8% identical to accession ID KM991708, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1912 Lebertia sp. water mite diet isolate 1912-BHL022317-GBD20428_13453-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGGATTAGGACAACCAGGCTCACTTCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTATTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAAAAAATAATAAAAGAATTTGACTTCTTCCCCCATCCTTAACTCTACTTCTAACAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1914 Lebertia sp. water mite diet isolate 1914-BHL022317-GBD24416_16816-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTTGGAAGTGACTAAATTTATAATACAATTGTAACTGCTCATGCTTTTGTTATAATTTTTTTCATAGTAATACCAATATTAATTGGAGGTTTTGGAAACTGAATAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAAAATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGGTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL1915 Chironomidae sp. water mite diet isolate 1915-BHL022317-GBD25258_24094-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGGACTTGATCTGGAATAGTGGGACCATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGCCCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAAGTTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTCCGAAATTGATTAGTTCCTCTTATACTAGAGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.1% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1917 Lebertia sp. water mite diet isolate 1917-BHL022317-GBD10700_4275-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCCCGAAAAAATAATATAAGATTTTGACATATTACTCCATCCTTAAATCTAATTCTATCAAGTAACTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1919 Chironomidae sp. water mite diet isolate 1919-BHL022317-GBD5503_18253-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGGACTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCTGGCAGAATTAGGACAACCCGGGACTTTTATTGGAGCTGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCATCTTATACTAGGGTCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.8% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1921 Lebertia sp. water mite diet isolate 1921-BHL022317-GBD23083_5243-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAATCCTAATTCGACTTGAATTAGGACAACCAGGCTCATTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTTGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGGTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAAAAAAAGATTTTGACTTCTTCCCCCATCCTTAACCCTACTTCTAACAAGTTCCATTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1924 Chironomus maturus water mite diet isolate 1924-BHL022317-GBD20763_4576-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTCTTAGTATGCTTATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTAACTACCCACGCCTTTATTATATTTTTTTTCATAGTTATACCAATTCTAATTGGTGGTTTTGGTAATTGACTTGTACCCTTAATATTAGGAGCCCCAGATATAGCTTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTTACTCTTTTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR665396, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1925 Lebertia sp. water mite diet isolate 1925-BHL022317-GBD6509_7417-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAATCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAAATTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAACCCCAGATAAAGGTTTTCCACGAATAAATAAAATAAGATTTTGACTTCTTCCCCCATCCTTAACTCTTCTTCTATCAAGGTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1926 Lebertia sp. water mite diet isolate 1926-BHL022317-GBD26178_10150-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAGGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCCTTTCCACGAATAAAAAAAATAAGATTTTGACTTCTTCCTCCATCCTTAACCCTACTTATAACAAGGCCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1930 Lebertia sp. water mite diet isolate 1930-BHL022317-GBD24019_5413-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGACCCGGAATCATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAAATGGAGGTTTTGGAAACTGAATAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAAAAATATAAGATTTTGACTTCTTCCCCCATCCTTAACTCTACTTCTATCAAGGTCCATTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1931 Chironomidae sp. water mite diet isolate 1931-BHL022317-GBD13914_14622-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGATTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.1% identical to accession ID DQ648215, identified in GenBank as Kiefferulus brevibucca. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1933 Lebertia sp. water mite diet isolate 1933-BHL022317-GBD8924_23834-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTTGTTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTAGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCCCTAATAATCAGAGCCCCAGATAAAGCTTTTCCACGAAAAAATAAAATAAGATTTTGACTTCTTCCTCCATCCTTAACCCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL1936 Hydrachnidiae sp. water mite diet isolate 1936-BHL022317-GBD21604_24346-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1941 Lebertia sp. water mite diet isolate 1941-BHL022317-GBD28453_13137-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTTGATTAAGAACTCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTTGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGAAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAAAAAACAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTAACAAGGTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1942 Chironomus riparius water mite diet isolate 1942-BHL022317-GBD25367_20505-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGGTTGATCCGGAATACTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTATCCCCCTCTCCTACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1944 Lebertia sp. water mite diet isolate 1944-BHL022317-GBD19861_17629-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAGATGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCAAAGTAATACCAATAACAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAAAAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTTACTTCTTCCCCCATCCTTAACCCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1946 Lebertia sp. water mite diet isolate 1946-BHL022317-GBD19754_28680-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGGTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCCTTTCCACGAATAAATAAAATAAGAATTTGACTTCTTCCCCCAACCTTAACTTTACTTCTATCAAGATCCTTCACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1947 Lebertia sp. water mite diet isolate 1947-BHL022317-GBD13126_23678-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCCAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTTGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATACAGCTTTGCCACGAATAAATAATATAAGATTTTGACTTCTTCCTGCAACCTTAACGCTGCTTCTATCAAGTTCCTTTACAGGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1954 Lebertia sp. water mite diet isolate 1954-BHL022317-GBD11151_12446-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAGTTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATGCAATTGTAACTGCTCATGCTTTTGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTATTCCACGAATAAATAATATAAGATTTTGACTTCTTCCCCCAGCCTTAACCCTACTTCTAACAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1955 Chironominae sp. water mite diet isolate 1955-BHL022317-GBD11709_7179-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTCTTCTTTCTAGTTCACTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1958 Lebertia sp. water mite diet isolate 1958-BHL022317-GBD27153_10880-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACGTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTGGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGCCTTCTTCCTCCATACTTCACTCAACTTCTAACAAGTTCCTTTACAGGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1960 Lebertia sp. water mite diet isolate 1960-BHL022317-GBD16779_9220-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGTTTTCGTGATAATTTTTTTCATAGTAATACCAATAAAAAATGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCAAGATATAGCTTTTCCACGAATAAATAATATAAGAATTTGACTTCTTCCTCCATCCTTAACACTACTACTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL1961 Chironomidae sp. water mite diet isolate 1961-BHL022317-GBD4900_17030-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTTAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTCACATACCACGCATTTATTATAATTTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCAGTCCCTCGAATAAATAATATAAGAGTTTGATTACTTCCCCCATCCCTTACCCAGCTTCTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.8% identical to accession ID KR287333, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1973 Lebertia sp. water mite diet isolate 1973-BHL022317-GBD14742_28959-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATGGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGTAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCCTTTCCCCGAAAAAAAAAAATAAGATTTTGACGTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1977 Lebertia sp. water mite diet isolate 1977-BHL022317-GBD17228_6022-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTCTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGACCCAGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCCTTAACCCTTCTTCTATCCAGTTCCTTTACTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1978 Lebertia sp. water mite diet isolate 1978-BHL022317-GBD20280_12058-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTACTTTGCTTTTGGAGCATGGTCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAATGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCATTATAATTTTTTTCATAGTAATACCAATAAAAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTGCTAACAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1979 Lebertia sp. water mite diet isolate 1979-BHL022317-GBD14448_23976-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGTTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAATCCTAATTCGACTTGAATTAGGACAACCTGGCTCACTCCTAGGAAGTGACCAAATTTATAATACAATTGTAACTGCTCATGCTTTTGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGACTTCTTCCCCCATCCTTAACTCTACTTCTATCAAGTTCCTGTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1981 Lebertia sp. water mite diet isolate 1981-BHL022317-GBD2244_13250-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTCGGACAACCAGGCTCACTCCTAGGAAGTGAACAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGGTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCCTTTCCACGAAAAAATAATAAAAGATTTTGGCTTCTTCCTCCATCCTTAACCCTACCTCTAACAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1985 Lebertia sp. water mite diet isolate 1985-BHL022317-GBD13550_10350-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAAATTTTTTCATAGTAATACCAATAATAATTGGAAGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAAAATTTGACTTCTTCCTCCATCCTTAACCCTACTTCTAACCAGTTCCTTTACTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1987 Lebertia sp. water mite diet isolate 1987-BHL022317-GBD18523_27369-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTTGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTAAAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGCTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCATATATAGCATTTCCACGAATAAATAAAATAAGATTTTGTCTTCTTCCTCCATCCTTAACTCTACTTCTAACAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1989 Lebertia sp. water mite diet isolate 1989-BHL022317-GBD6477_9261-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGATCAAATTTACAATACAATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTCATAGTAATACCAATAATAAATGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAAAAAATAATAAAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTAACAAGTACCATTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL1993 Chironomidae sp. water mite diet isolate 1993-BHL022317-GBD11032_26146-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACCTTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTAAACTAGGGGCTCCTGAAATAGCATTCCCTCGAATAAATAAAAAAAGATTTGGATAACTTCCCCCATCCCTTACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.0% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2007 Lebertia sp. water mite diet isolate 2007-BHL022317-GBD23462_22801-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAGTTGTAACAGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGATCCCCAGATATAGCCTTTCCACGAATAAAAAATATAAGATTTTGAATTATTCCCCCATCCATAACTCTACTTCTAACAAGGTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2008 Oligochaeta sp. water mite diet isolate 2008-BHL022317-GBD8320_18311-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCGGGA--CTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.8% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL2019 Lebertia sp. water mite diet isolate 2019-BHL022317-GBD15556_23797-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATCGGAGCTAGATTAAGAATCCTAATTCGACTTGAATTAGGACAACCAGGCCCACTCCTAGGAAGTGAACAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAACTTTTCCACGAATAAAAAATAAAAGATTTTGACTTCTTCCTCCATCCTTAACCCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2021 Lebertia sp. water mite diet isolate 2021-BHL022317-GBD16863_12415-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCACACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTACACTAAAAATCAGAGCCCCAGATATAACCTTTCCACCAATAAATAATATAAGATTTTTACTTCTTCCCCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2023 Lebertia sp. water mite diet isolate 2023-BHL022317-GBD25491_13535-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTACTTTGTTTTTGGAGCATGATCCGGAATAATTGGAGCTTGATTAAGAATCCTAATTCGACTTGAATTAGGACAACCAGGCTCATTCCTAGGAAGTGACCAAATTTACAATACTATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCTGATATAGCTTTTCCACGAATAAAAAATATAAGATTTTGGCTTCTTCCCCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2027 Lebertia sp. water mite diet isolate 2027-BHL022317-GBD28329_17096-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCCTTTGGAGCATGATCCGGAATAATTGGAGCTCGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTACTCATGCTTTTGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAAGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCCCCATCCTTAACTCTACTTCTATCAAGGTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2031 Chironomidae sp. water mite diet isolate 2031-BHL022317-GBD17280_5155-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGTGACTTTTATTGGAGATGACCATATTTATAATGTGATGGTAACAGACCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTAAGGAAATTGATTAGTTCCTCTTATACTAGGTGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2036 Lebertia sp. water mite diet isolate 2036-BHL022317-GBD7011_9018-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAATCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTATAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATAAAGCCTTTCCACCAAAAAAAATATAAGATTTTGGCTTCTTCCTCCATCCCTAACCCTACTTCTAACAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2043 Chironomidae sp. water mite diet isolate 2043-BHL022317-GBD27344_16232-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGATCAAATTTATAATGTGATTGTAACAGCCCACGCTTTTGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACCAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAAATTTTGACTTCTTCCCCCAGCCTTAACTCTACCTCTATCAAGTTCCTTTACATGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.0% identical to accession ID DQ648215, identified in GenBank as Kiefferulus brevibucca. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2046 Chironomidae sp. water mite diet isolate 2046-BHL022317-GBD14572_11182-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTATGAATGTTTATTCGGGCAGAATTAGGACGACCCGGGACTTTTATTGGAGATGACTAACTTTATAATGTGATTGTCACAGCCAACTCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGCTTCGGAAATTGATTAGTTCCTCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.7% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2048 Lebertia sp. water mite diet isolate 2048-BHL022317-GBD29187_14850-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATAATCAGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTTATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAAAAAATAATATAAGTTTTTGACTTCTTCCTCCATCCTTAACCCTACTTCTATCAAGGTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2056 Lebertia sp. water mite diet isolate 2056-BHL022317-GBD16365_29094-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGTGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTATACCACGAAAAAAAAAAATAAGATTTTGACTGCTTCCACCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2058 Chironomidae sp. water mite diet isolate 2058-BHL022317-GBD29156_14357-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGAACATCTTTAAGAATGCTTATTCGGGCGGAATTAGGACGAGCCGGGACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTAACAGCCCACGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTCGGAAATTGATTAGTTCCGCTTATACTAGGGGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCCTTACCCAGCTTCTTTCAAGAACAATTGTATAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.0% identical to accession ID KR286010, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2059 Lebertia sp. water mite diet isolate 2059-BHL022317-GBD25418_20326-Ldc91 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGGATAATTGGAGCTAGATTAAGAACCCTAACTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAGCTGCCCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAAAAAAAAAAATAAGATTTTGGATTCTTCCCCCATCCTTAACCCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2062 Chironominae sp. water mite diet isolate 2062-BHL072216-GBD9420_11075-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTACCCCCCTTCTTTAACTCTTCTTCATTCTAGTTCGATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2063 Chironominae sp. water mite diet isolate 2063-BHL072216-GBD11813_27196-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2066 Chironomidae sp. water mite diet isolate 2066-BHL072216-GBD12982_22672-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGGGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTTTAACTCTCTTCTTCTTTCTAAATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.8% identical to accession ID JF412118, identified in GenBank as Glyptotendipes tokunagai. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2067 Chironominae sp. water mite diet isolate 2067-BHL072216-GBD17848_11585-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACGCCCAGGTACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTTATATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTTTACCACCCTCTTTAACCCTTTTACTTTCAAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR289362, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2068 Chironomidae sp. water mite diet isolate 2068-BHL072216-GBD11334_17727-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGCTTTAATTCGAGCTGAATTAGGGCATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2069 Chironomidae sp. water mite diet isolate 2069-BHL072216-GBD24209_24653-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGGCATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTATCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR285214, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2070 Tanytarsus sp. water mite diet isolate 2070-BHL072216-GBD24631_18209-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTATACTTTATTTTCGGAGCTTGATCTGGAATAGTCGGAACTTCTTTAAGTATATTAATCCGTGCAGAATTAGGACACCCGGGAACTTTAATCGGAGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGCTTTGGAAATTGATTATTGCCTCTTATACTCGGGGCTCCCGACATAGCCTTTCCTCGAATAAATAACATGAGATTCTGATTACTTCCCCCATCTATTTCTTTACTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KP043761, identified in GenBank as Tanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2072 Megaselia sp. water mite diet isolate 2072-BHL072216-GBD17022_17593-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTTTATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACATCTTTAAGTATACTTATTCGTGCAGAATTAGGTCATCCAGGCACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCCCATGCTTTTATCATAATTTTTTTTTATAGTTATACCTATCTTAATTGGGGGATTTGGAAATTGACTTTTACCATTAATGCTTGGAGCACCAGATATAGCTTTCCCCCGAATGAATAATATAAGTTTTTGACTTCTTCCCCCATCTCTAACCCTTCTTCTTTCTAATTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KX774883, identified in GenBank as Megaselia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2073 Chironominae sp. water mite diet isolate 2073-BHL072216-GBD23348_25398-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCCCTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCCTTCCAGCTCAATTGTAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR286005, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2074 Dicrotendipes modestus water mite diet isolate 2074-BHL072216-GBD14050_23516-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID MG449574, identified in GenBank as Dicrotendipes modestus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2076 Diaphanosoma sp. water mite diet isolate 2076-BHL072216-GBD26889_21369-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GACTTTATATTTTATTTTCGGAGTATGGTCTGGTATAGTAGGTACCGCTTTTAGTATATTAATTCGAGCAGAGTTAGGCCAATGTGGTAGCTTTATTAGGGGACGATCAATTTTACAATGTTATTGTAACTGCTCATGCTTTTGTTATAATTTTCTTTATGGTTATACCTATTCTTATTGGTGGGTTTGGAAATTGGTTGGTTCCTTTAATGTTAGGGGCTCCTGATATGGCCTTCCCTCGTTTAAATAATTTAAGATTTTGATTACTTCCTCCTTCTTTAACTTTACTTTTAGTTGGTAGGGCTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID MG449947, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2077 Chironominae sp. water mite diet isolate 2077-BHL072216-GBD15244_3806-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCGGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTAGGACACCCAGGAACATTTATTGGAGATGATCAAATTTTCAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR689936, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2078 Chironomidae sp. water mite diet isolate 2078-BHL072216-GBD14241_22649-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGGGCTTGATCTGGAATAGTGGGTACCTCCCTTAGTATCCTTATTCGTACAGAATTAGGTCACCCAGGAGCTTTAATTGGAGACGATCAAATCTATAATGTAATTGTAACGGCACATGCTTTTGTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGTGGATTTGGTAATTGACTAGTACCCCTTATACTAGGAGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTACTACCCCCTTCTTTAACCTTACTATTATCTAGCTCTATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KP043430, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2080 Lebertia quinquemaculosa water mite diet isolate 2080-BHL072216-GBD19700_26452-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATACTTCACTTTTGGGGCTTGATCAGGAATGGTGGGAGCAAGACTAAGAACTTTAATCCGTTGAGAATTAGGACAACCAGTAACTCTCCTAGGAAGAGACCAAATTTATAATACTATCGTAACAGCTCACGCCTTCGTTATAATTTTCTTTATAGTTATGCCAATAATAATTGGAGGATTCGGACATTGACTAGTCCCATTGATAATTAGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGACTTTTACCCCCCCTCTGTAACTCTTCTACTATCTAGTTCTTTCACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID MG773261, identified in GenBank as Lebertia quinquemaculosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2081 Chironominae sp. water mite diet isolate 2081-BHL072216-GBD15526_11736-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2082 Chironominae sp. water mite diet isolate 2082-BHL072216-GBD21925_11102-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTCTATTTTATTTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATGGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCCCTTCTTCTTTCTAGTTCTATTGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2083 Chironomidae sp. water mite diet isolate 2083-BHL072216-GBD9789_9024-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCATTGTGGCAGACTTATTGGTGATGATCAAATTTATAATGTTATTGTTACGGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTGCCACCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2084 Chironominae sp. water mite diet isolate 2084-BHL072216-GBD11072_15823-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTGCCACCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2085 Chironomidae sp. water mite diet isolate 2085-BHL072216-GBD9017_23349-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAGTTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGTGGCTTTGGTAATTGGCTGTTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGCTGGAAGGGCAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2086 Chironomidae sp. water mite diet isolate 2086-BHL072216-GBD2382_11485-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCCTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR647156, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2087 Chironomidae sp. water mite diet isolate 2087-BHL072216-GBD13871_19001-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACCTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTCCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2089 Sididae sp. water mite diet isolate 2089-BHL072216-GBD22699_17045-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGGATTAGGTCATCCTGGAACATTTATTGGTGATGACCAATTTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.7% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2090 Polyphemus sp. water mite diet isolate 2090-BHL072216-GBD19637_4896-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAAGAATTCTCATTCGTGCTGAATTAGGACAAGCAGGAAGATTAATTGGTGATGATCAAATTTATAACGTAATTGTAACTGCCCATGCTTTTGTTATAATTTTTTTTATAGTGACGCCTATTATAATTGGGGGGTTTGGTAATTGACTTGTTCCTCTAATGTTAGGAGCTCCTGATATGGCTTTTCCTCGGTTAAATAATTTAAGTTTCTGATTCCTTCCTCCTGCTTTAACTCTTCTCTTAGTTGGGGGGGGCTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID GQ406859, identified in GenBank as Polyphemus pediculus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2091 Chironominae sp. water mite diet isolate 2091-BHL072216-GBD10729_24530-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCTACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTCTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2092 Chironomidae sp. water mite diet isolate 2092-BHL072216-GBD22344_22090-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTG--GAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID KM993864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2094 Coenagrionidae sp. water mite diet isolate 2094-BHL072216-GBD17857_27667-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTATACCTAATGTTTGGTGCATGAGCAGGTATAGTAGGTACTGCACTAAGTATATTAATTCGAGTTGAGTTAGGCCAACCTGGATCATTAATTGGGGATCATCAAATTTACAACGTAGTAGTAACTGCACATGCGTTTGTAATAATTTTTTTTATAGTTATGCCAATTATAATTGGTGGTTTTGGAAATTGATTAGTACCTCTAATACTAGGAGCCCCAGATATAGCTTTCCCTCGATTAAATAACATAAGATTCTGACTTCTACCCCCATCGTTAACCCTTCTACTAGCAAGCAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR148702, identified in GenBank as Coenagrionidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2095 Tanytarsus sp. water mite diet isolate 2095-BHL072216-GBD4977_15579-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGACCGGAATTAGGTCATCCTGTAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTATTGTCTCTTATACTCGGGGCTCCCGACATAGCCTTTCCTCGAATAAATAACATGAGATTCTGATTGCTTCCCCCATCTATTTCTTTACTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR966081, identified in GenBank as Tanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2102 Chironominae sp. water mite diet isolate 2102-BHL072216-GBD11625_17018-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2103 Chironomidae sp. water mite diet isolate 2103-BHL072216-GBD4647_11419-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTCATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATTTTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTAGCCCCCATCATTAACTTTATAATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2107 Chironominae sp. water mite diet isolate 2107-BHL072216-GBD26117_15661-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATGATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2108 Chironomidae sp. water mite diet isolate 2108-BHL072216-GBD13559_12528-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR636712, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2110 Chironominae sp. water mite diet isolate 2110-BHL072216-GBD23820_21037-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTTGGCGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATACAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID KR286005, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2115 Chironominae sp. water mite diet isolate 2115-BHL072216-GBD14867_18124-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTTTACCACCCTCTTTAACTCTTTTACTTTCAAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID KR285347, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2116 Chironomidae sp. water mite diet isolate 2116-BHL072216-GBD14517_16073-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAAATAGTAGGCACTTCTTTAAGAATTTTATTTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTGCATTAACCTTACTTTTATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2119 Dicrotendipes sp. water mite diet isolate 2119-BHL072216-GBD4518_13823-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2120 Paratanytarsus sp. water mite diet isolate 2120-BHL072216-GBD15843_12447-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGTATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTTCCCCGTATAAATAACATAAGATTTTGATTACGTCCCCCATCTTTAACCCATCTTCAATCAAGAAGATTAGTGGAAAATGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2121 Chironomidae sp. water mite diet isolate 2121-BHL072216-GBD12757_16253-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCA---GTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2122 Diptera sp. water mite diet isolate 2122-BHL072216-GBD9509_14331-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCTTATACTTTATTTTCGGAGCTTGATCTGGAATAGTCGGAACTTCTTTAAGTATATTAATCCGTGCAGAATTAGGACACCCGGGAACTTTAATCGGAGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATAGCCACCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.9% identical to accession ID GQ409325, identified in GenBank as Eutrichota paratunicata. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2127 Diaphanosoma sp. water mite diet isolate 2127-BHL072216-GBD12729_18408-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGTACAGTCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCTTTTAATACTAGGTGCCCCTGATATGGCATTTCCTCGTTTAAACAATTTACGGTTTTGAATATTACACCCCTTCTTTAACACGGCGTTTGGTTGGAAGGGCAGTTGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2128 Chironominae sp. water mite diet isolate 2128-BHL072216-GBD22814_18056-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTTTACCACCCTCTTTAACTCTTTTACTTTCAAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KR285347, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2130 Psectrocladius sp. water mite diet isolate 2130-BHL072216-GBD19006_28072-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTCATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTAAATTGGAGGTTTTGGAAATTGATTAGTCCCATTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2132 Dicrotendipes sp. water mite diet isolate 2132-BHL072216-GBD13566_10803-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGCAGGAACTCCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR746632, identified in GenBank as Dicrotendipes modestus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2136 Dicrotendipes sp. water mite diet isolate 2136-BHL072216-GBD2244_12719-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTAAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTAATTGTAACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR746632, identified in GenBank as Dicrotendipes modestus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2141 Chironomidae sp. water mite diet isolate 2141-BHL072216-GBD25971_16078-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTTCTTCTTTCCAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2146 Chironominae sp. water mite diet isolate 2146-BHL072216-GBD8841_21993-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTACCACCATCTCT-TACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2147 Diaphanosoma sp. water mite diet isolate 2147-BHL072216-GBD17584_21994-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGGTCCGGGATAGTTGGAACATCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGATTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTTATAGTTATGCCTATTCTAATTGGTGGATTTGGAAATTGGCTGGTGCCTTTAATACTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2157 Dicrotendipes sp. water mite diet isolate 2157-BHL072216-GBD21930_4584-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAACATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2159 Chironominae sp. water mite diet isolate 2159-BHL072216-GBD11966_25238-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGTGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2171 Diaphanosoma sp. water mite diet isolate 2171-BHL072216-GBD18844_12048-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACTGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATCCTCATTGGTGGCTTTGGTAATTGGTTGGTGCCTTTAATACTAGTTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTAAAGGTTTTGAATATTACCCCCCTCTTTAACCCTTCTTTTGGTTGGAAGGGCAGGTGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2181 Dicrotendipes sp. water mite diet isolate 2181-BHL072216-GBD10386_5398-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTGTAATTGGAGGCTTTGGAAATTGATTATTGCCTCTTATACTCGGGGCTCCTGACATAGCCTTTCCTCGAATAGATAACATGAGAGTCTGATTGCTTCCCCCATCTATTCCTTTACTTCTTTCTAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID KR282179, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2184 Chironominae sp. water mite diet isolate 2184-BHL072216-GBD4877_10743-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCGGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGATTATGCCTATTTTAATTGGAGGATTTGGAAATTGTCTTGTACCTCTAATACTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTTTACCACCCTCTTTAACTCTTTTACTTTCAAGAACAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR285347, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2186 Cricotopus sp. water mite diet isolate 2186-BHL072216-GBD25605_13250-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGTAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTATGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGAAATTGAATATTACCACCTTCTTTAACATTATAATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2188 Dicrotendipes sp. water mite diet isolate 2188-BHL072216-GBD14548_25102-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTAGAGCTCGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGATCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATACAAGTTTCTGACTATTACCTCCTTCTCTAACCCCTTCTTCTTTCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2189 Megaselia sp. water mite diet isolate 2189-BHL072216-GBD21213_14188-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATGTTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATCTTAATTGGGGGATTTGGAAATTGACTTTTACCATTAATGCTTGGAGCACCAGATATAGCTTTCCCCCGAATGAATAATATAAGTTTTTGACTTCTTCCCCCATCTTTAACCCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KX774883, identified in GenBank as Megaselia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2196 Diaphanosoma sp. water mite diet isolate 2196-BHL072216-GBD24260_11678-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTCGATCGGGGATAGTAGGTACTTCTCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2219 Chironomidae sp. water mite diet isolate 2219-BHL072216-GBD9574_11430-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCCTGATCCGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACTAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTTATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTTTACCACCCTCTTTAACTCTTTTACTTTCAAGATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KP037822, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2220 Diaphanosoma sp. water mite diet isolate 2220-BHL072216-GBD7382_16302-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCCCTAAGTATCCTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATTCTTTTGTTATAATTTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTGTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2221 Sididae sp. water mite diet isolate 2221-BHL072216-GBD18770_8964-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAAATAGGGCATCCTGGAACTTTAATTGGTGACGACAAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTAGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTCTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTCTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2227 Chironominae sp. water mite diet isolate 2227-BHL072216-GBD11397_6491-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTACTTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTCTTGTAACAGCTCATTCTTTTATTATAATTTTTTTCCATAGTTATACCCATTTTAATTTGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAGATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2233 Chironomidae sp. water mite diet isolate 2233-BHL072216-GBD5342_19975-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCATGATCCGGAATAGTAGGAACTTCTTTAAGTGTTTTAATTCGAGCTGAATTAGGGCATCCTGGAGCTTTAATTGGTGACGACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTATTATAATTTTTTTTAATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2256 Diaphanosoma sp. water mite diet isolate 2256-BHL072216-GBD21461_15687-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGGCAGTGTGGCAGATTTATTGGTGATGACCAATTTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGAGGCTTTGGAAATTGGTTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCGCGTTTAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2266 Tanytarsus sp. water mite diet isolate 2266-BHL072216-GBD16630_15070-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGCTTTGGAAATTGATTATTGCCTCTTATACTCGGGGCTCCCGACATAGCCTTTCCTCGAATAAATAACATGAGATTCTGATTGCTTCCCCCATCTATTTCTTTACTTCTTTCTAAATCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR966081, identified in GenBank as Tanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2268 Paratanytarsus sp. water mite diet isolate 2268-BHL072216-GBD8653_18062-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTATAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGCAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATTTAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTACCACCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2269 Chironomidae sp. water mite diet isolate 2269-BHL072216-GBD7328_20566-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGATTCTTGCCATTAATACTAGAAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCAATAACATTATTTTTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2275 Diaphanosoma sp. water mite diet isolate 2275-BHL072216-GBD20605_8017-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGGTCCGGAATAGTTGGAACATCCCTAAGTATACTTATTCGAGCTGAATTAGGGCACTGTGGCAGATTTATTGGTGATGACCAAATTTATAATGTTATTGTAGCCGCTCATGCTTTTGTTATAATTTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGACTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACCCTTCTTCTGGCTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2303 Chironomidae sp. water mite diet isolate 2303-BHL072216-GBD13953_14621-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTAATTGGTGACGACCAAATTTATAATGTAGTCGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAGTTGGGGGATTTGGTAATTGATTAGTACCATTAATATTAGGGGCTCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCATTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR285631, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2322 Diaphanosoma sp. water mite diet isolate 2322-BHL072216-GBD8605_22830-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTATATTGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCTTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTAGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2338 Megaselia sp. water mite diet isolate 2338-BHL072216-GBD14993_28869-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATTTTCGGAGCTTGATCTGGAATAGTCGGAACTTCTTTAAGTATATTAATCCGTGCAGAATTAGGACACCCGGGTACTTTAATCGGAGATGATCAAATTTATAATGTTATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATCTTAATTGGGGGATTTGGAAATTGACTTTTACCATTAATGCTTGGAGCACCAGATATAGCTTTCCCCCGAATGAATAATATAAGTTTTTGACTTCTTCCCCCATCTCTAACCCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KX774883, identified in GenBank as Megaselia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2340 Chironomidae sp. water mite diet isolate 2340-BHL072216-GBD27732_18284-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGCCAGA--CTT--ATTGGTGATGACTAAATTTATAATGTTATTGTAACCGCTCACGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGTGGATTTGGTAATTGACTAGTACCCCTTATACTAGGAGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTACTACCCCCTGCTTTAACCTTACTATTATCTAGCTCTATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.2% identical to accession ID KP954637, identified in GenBank as Ablabesmyia annulata. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2345 Chironomidae sp. water mite diet isolate 2345-BHL072216-GBD13651_22294-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGGGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTCTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCACCTTCTTTAACTCGCTGACGTTCTAGATAAATTGTCGAAAAGGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.6% identical to accession ID JF412118, identified in GenBank as Glyptotendipes tokunagai. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2356 Diptera sp. water mite diet isolate 2356-BHL072216-GBD18513_11483-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGAGGCTTTGGGAATTGATTAGTTCCCCTTATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAATAATATAAGCTTCTGACTTCTTCCCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.2% identical to accession ID KX356038, identified in GenBank as Pressatia choti. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2357 Diaphanosoma sp. water mite diet isolate 2357-BHL072216-GBD9391_18387-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTTGTTCCTTTAAAACTAGGTGCCCCTGAAATTGCTTTTCCCCCGTTAAACAATTTTAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID LC060042, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2404 Diaphanosoma sp. water mite diet isolate 2404-BHL072216-GBD18658_12643-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGGTCCGGGATAGTTGGAACTTCCCTAAGTATACTTATTCGAGCTGAATTAGGGGATTGTGGCAGTTTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTTTAATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATATTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATATAAGGTTTTGAGTATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2421 Chironomidae sp. water mite diet isolate 2421-BHL072216-GBD18863_12926-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTATTTTCGGAGCTTGATCAGGGATAGTTGGAACTTCTTTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCAGGCTCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACTATCAAGTTCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2437 Chironomidae sp. water mite diet isolate 2437-BHL072216-GBD17546_21647-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATAAAGATATTGGAACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTTTTCATAGTTATGCCTATTTTAATTGGGGGGTTTGGGAATTGATTAGTTCCCCTTATATTAGGATCACCAGATATGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCCTCTTTAACCCCCTTACCTTCCAGATCAATTGTCGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.0% identical to accession ID DQ648215, identified in GenBank as Kiefferulus brevibucca. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2439 Chironominae sp. water mite diet isolate 2439-BHL072216-GBD27316_21523-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTCAAGAATTCTAATTCGAGCAGAATTAATACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTGCTTTATCTCTTCTTCTTTCTAGTTCTATTGTATAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2440 Diptera sp. water mite diet isolate 2440-BHL072216-GBD7754_11100-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTATATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAACTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACACTATTATTAGTAAGAAGTATAGTAGAGAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID MG566056, identified in GenBank as Bactrocera limbifera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2443 Annelida sp. water mite diet isolate 2443-BHL072216-GBD15191_12612-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACGCTTTATCTTATTTTCGGTGTTTGAGCTGGATTAACAGGAACTATAATAAGAATTCTTATTCGTTTAGAGCTCTCACAACCAGGAAGTTTTATAGGAAGAGATCAACTTTACAATGTTTTAGTTACTGCTCACGCCTTTTTAATAATTTTTTTTTTTAGTTATACCTGTTTTTATTGGAGGGTTTGGAAACTGACTTTTACCTTTAATAATTGGAGCCCCAGATATAGCTTTTCCTCGCCTTAATAATTTAAGATTCTGATTTCTTCCCCCTTCTTTAATGTTACTTTTATTTTCTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.8% identical to accession ID HQ691224, identified in GenBank as Aeolosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2451 Diaphanosoma sp. water mite diet isolate 2451-BHL072216-GBD26136_6745-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTAAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAACTTAAGGTTGAGAATATGACCCCCTACGTTAACACATCATTAGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2465 Chironomidae sp. water mite diet isolate 2465-BHL072216-GBD11417_3201-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTCGGAGTATGGTCTGGTATAGTAGGGACCGCTCTTAGTATATTAATTCGAGCAGAGTTAGGCCAATGTGGTAGCCTTATTGGGGACGATCAAATCTACAATGTTATTGTAACTGCTCATGCTTTTGTTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2477 Orthocladiinae sp. water mite diet isolate 2477-BHL072216-GBD26049_11051-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCTAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTATAGTTATACCAATCTTAATTGGAGGGTTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATGATCAAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2478 Diaphanosoma sp. water mite diet isolate 2478-BHL072216-GBD23747_17223-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGTAACATCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCATATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTGTGGTAATTGGCTGGTGCCTTTAATACTATGTGCCCCTGATATGGCTTTTCCTCGTATAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTACTTTTAGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2501 Chironomidae sp. water mite diet isolate 2501-BHL072216-GBD18919_19557-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGCACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTCGGAACTTCTTTAAGCATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCACGCTTTTATCATAATTTTCTTCATAGTTATGCCTATTTTAATTGGGGTCTTTGGGAATTGATTAGTTCCCCTAATATTAGGAGCACCAGATACGGCTTTCCCGCGAATAAACAATATAAGCTTCTGACTTCTTCCCCCTTCTGTAACTCACTTACTTTCTAGATAAATTGTCGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 88.2% identical to accession ID JF412118, identified in GenBank as Glyptotendipes tokunagai. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2505 Tanypodinae sp. water mite diet isolate 2505-BHL072216-GBD13194_28315-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAATTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGTGGATTTGGTAATTGACTAGTACCCCTTATACTAGGAGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTACTACCCCCTTCTTTAACCTTACTATTATCTAGCTCTATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID KR775767, identified in GenBank as Tanypodinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2511 Chironominae sp. water mite diet isolate 2511-BHL072216-GBD8468_22129-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATCTTTTATTTTTGGAGCTTGATCAGGTATATTAGGAACTTCTTTATGAATATTAATCCGAACGTAATGAGGTCATCCTGGAACATTTATTGGTGATGACTAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATCTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGCGC	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2520 Paleoptera sp. water mite diet isolate 2520-BHL072216-GBD22890_12496-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTATACCTAATGTTTGGTGCATGAGCAGGTATAGTAGGTACTGCACTAAGTATATTAATTCGAGTTGAGTTAGGCCAACCTGGATCATTAATTGGGGATGATCAAATTTACAGCGTAGTAGTAACTGCACATGCGTTTGTAATAATTTTTTTTATAGTTATGCCAATTATAATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTAAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.1% identical to accession ID KR148702, identified in GenBank as Coenagrionidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2549 Diaphanosoma sp. water mite diet isolate 2549-BHL072216-GBD12299_12948-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACCGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTCGTTATAATTTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATATAAGGTTTTGAATATGACCCCCTTCTTCAACACTTCATTAAGATGGAAGGGCAGTTGAAAATGGAGCTGG	Using NCBI BLASTN in June 2018, this sequence was 94.7% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2579 Diaphanosoma sp. water mite diet isolate 2579-BHL072216-GBD25575_10523-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCAGGGATAGTTGGAACAGCTCTAAGTATATTTATTCGAGCTGAATTAGGGCAGTGTGGCAGATTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTTATAGTTATGCCTATTCTAATTGGAGGTTTTGGAAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCTTCTTTAACTCTACTTTTGGCTGGAAGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2591 Diaphanosoma sp. water mite diet isolate 2591-BHL072216-GBD12879_23475-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATATTTATTCGAGTTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGAACAAATTTATAATGTTATTGTAACCGCTCATGCTTTTTTTATAATTTTTTTTTATAGTAATGCCTATTCTCATTGGTGGCTTTGGTAATTGGTTGGTGCCTTTAATACTGGGTGCCCCTGATATGGCATTTCCTCGTTTAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTACTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2611 Diaphanosoma sp. water mite diet isolate 2611-BHL072216-GBD23303_24607-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATATTAGGTGCCCCTGATATGGCTTTTCCTCGTCTAAACAATATAAGATTTTGAATATTACCCCCTTCTTAAACTCTACTTTTAGCTGGAAGGACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2624 Chironominae sp. water mite diet isolate 2624-BHL072216-GBD7786_15990-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACTTCATTTAGTATATTAATTCGAGCAGAATTAGGTCACCCTGGGACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATCCTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTACCCCCTTCTTTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2644 Diaphanosoma sp. water mite diet isolate 2644-BHL072216-GBD29197_13847-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGGGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGTTAAAACAATTTAAGGGTTTGAATATTACCCCCAACTTCAACTTATCTATTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2658 Diaphanosoma sp. water mite diet isolate 2658-BHL072216-GBD16830_26280-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGCTTGGTCCGGGATAGTTGGAACATCCCTAAGTATACTTATTCGAGCTGAATTAGGGCATCGTAGGAGAATTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCTCGATTAAACAATATAAGGTTTTGAATATTACCCCCTTCTTTAACTCTACTTTTGGTTGGAAGGGCAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2663 Chironomidae sp. water mite diet isolate 2663-BHL072216-GBD27852_8571-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGGATAGTAGGTACTTCTCTAAGAATCTTAATTCGAGCTTAATTCGGTCATGCTGGTTCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCACCTTCTCTAACCTTATTACTATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2688 Chironomidae sp. water mite diet isolate 2688-BHL072216-GBD20395_2453-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACCTCTTTAAGAATATTAATCCGAACTGAATTAGGTCATGCTGGATAATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTAATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGTGTTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2690 Chironominae sp. water mite diet isolate 2690-BHL072216-GBD27701_20147-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATATTAATCCGAGCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTAAACACTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2692 Chironomidae sp. water mite diet isolate 2692-BHL072216-GBD23277_23323-Lq68 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATAGTTTATTTTTGGAGTTTGGTCCGGTGATAGTAGTTACTTCTCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGTGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAAGGTTTGGAAACTGATTAGTTCCTTAAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCCTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM992869, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2696 Chironominae sp. water mite diet isolate 2696-BHL032417-GBD8893_26871-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAATTTTATAATGTAATTGTTACTGCTCATGCTTTTATTATATTTTTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTGCTTTCAAGAAGGATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2697 Chironomus riparius water mite diet isolate 2697-BHL032417-GBD17851_25217-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATATATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGACTAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTACTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2699 Chironominae sp. water mite diet isolate 2699-BHL032417-GBD10219_9288-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATCCGAACGGAATTAGGTCTTCCTGGAACATTTATTGGTGATAACCAAATTTATAATGTAATTGTTACTACTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGAATTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTATTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACGTACAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2700 Chironomus riparius water mite diet isolate 2700-BHL032417-GBD7908_8567-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAAAAGTGGAAACTTCATTAAGAATGCTTATTCGTGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2701 Paratanytarsus sp. water mite diet isolate 2701-BHL032417-GBD18841_12655-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGAAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2704 Chironominae sp. water mite diet isolate 2704-BHL032417-GBD11028_2888-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTTTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCCGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGTTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2705 Chironominae sp. water mite diet isolate 2705-BHL032417-GBD3242_20451-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTTTTTTATTGGAGTTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCCTCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAGTTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2706 Chironominae sp. water mite diet isolate 2706-BHL032417-GBD6755_13212-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTAGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGATTATTATTCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCCGATAGGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2710 Mucor sp. water mite diet isolate 2710-BHL032417-GBD7588_5868-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACTTTATATATCATCTTCTCTATTTTTGCGGGTATGATTGGTACTGCTTTTTCTATGTTAATTAGACTATAATTAGCTGGTCCTGGAATTCAATATCTTCATGGTGATCATCAATTATATAATGTAATTGTAACTGCTCACGCATTTGTAATGATTTTCTTCTTAGTAATGCCTGCAATGATTGGAGGTTTTGGTAACTGGTTTGTTCCTTTAATGATTTGGAGCTCCTGATATGGCCTTCCCTCGATTAAATAATATTTCATTCTGGTTATTACCACCTTCTTTAATTCTTTTAGTAGCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR809877, identified in GenBank as Mucor circinelloides f. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2712 Chironomus sp. water mite diet isolate 2712-BHL032417-GBD12790_11366-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGACTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAACTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2713 Chironominae sp. water mite diet isolate 2713-BHL032417-GBD29304_13393-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTATTTGGTGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATGTTAATCCGAACGGAATTAGGTCATCCTGTAACATTTATTGGTGATTACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTATAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2715 Chironominae sp. water mite diet isolate 2715-BHL032417-GBD26944_9847-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGAAGGCACTTCTTTAAAAATATTAATCCGAACGTAATTAGGTCATCCTGTAACATTTATTGGTTATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATCCCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAACCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACGTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2716 Chironominae sp. water mite diet isolate 2716-BHL032417-GBD15188_8635-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGTAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGCATATTAATCCGAACGGAATTAAGTCATCCTGTAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTATCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2717 Chironominae sp. water mite diet isolate 2717-BHL032417-GBD15058_22745-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTTGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATGATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTACTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2718 Psectrocladius sp. water mite diet isolate 2718-BHL032417-GBD22809_13132-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGGTGATCAAATTTTTAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTATTACCAACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2719 Chironominae sp. water mite diet isolate 2719-BHL032417-GBD25739_21939-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGATCTTGATCAGTTATAGTAGGAACTTCTTTAAGAATATTAATCCGACCGGAATTAGGTCATCCTGGAACTTTTATTGGAGATGACCAATTTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAGGAAGAATAGTAGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2720 Chironominae sp. water mite diet isolate 2720-BHL032417-GBD21502_27260-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGTGCTTGATCAGGTATAGTCGGAACTTCTTTAAGTATATTACTCCGAACGGCCTTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTGTAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCTTGATATGGCTTTTCCACGAATAAAAAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2721 Chironomidae sp. water mite diet isolate 2721-BHL032417-GBD3327_19124-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AATCATAAAGATATTGGTTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCTCTAATGCTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCTCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.2% identical to accession ID KP697593, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2722 Chironominae sp. water mite diet isolate 2722-BHL032417-GBD24442_11200-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTCTTGGAGCTTGATCGGGTATAGTGGGAACTTCTTTAAGAATATTATTCAGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACAAAATTTATAATGTAATTGTTACTGCTTATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2723 Psectrocladius sp. water mite diet isolate 2723-BHL032417-GBD11031_20896-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAAAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCAGTAACATTACTATTATCTAGCTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2724 Chironomus sp. water mite diet isolate 2724-BHL032417-GBD20289_5609-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTTTTTTGGAGCTTGATCAGGTATAATAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR756187, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2725 Chironominae sp. water mite diet isolate 2725-BHL032417-GBD19802_8132-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTGAGCTTGATCCGGTATAGGAGGAACTTCTTTAAGAATTTTAATCCGAACGGGATTAGGTCATCCTTGAACATTTATTGATGATGACCGAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2726 Drosophila sp. water mite diet isolate 2726-BHL032417-GBD15783_3392-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCT-GAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACCGCACATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAAAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.9% identical to accession ID AY750090, identified in GenBank as Drosophila lacertosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2727 Chironominae sp. water mite diet isolate 2727-BHL032417-GBD10914_12488-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTATTATATTTTTTTTTTTTGGTACTTGATCAGGTCTAGTAGGAACTTCTTTAAGAATATTAATCCGAATGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATATTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2728 Paratanytarsus sp. water mite diet isolate 2728-BHL032417-GBD20748_9296-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTTTTTTTGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2729 Paratanytarsus sp. water mite diet isolate 2729-BHL032417-GBD16278_26655-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAAATTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCTCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTGACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2730 Chironominae sp. water mite diet isolate 2730-BHL032417-GBD17162_8606-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTTTGGAGCTTGATCAGGTATATTAGGAACTTCTTTAAGAATATTAATTAGAACGGAATTAGGTCATCCTTGAACATTTATTGGTGATTACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2731 Chironominae sp. water mite diet isolate 2731-BHL032417-GBD19515_22704-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTTATCCGAACGGAATTAGGTCATCCTGGAACATTTTTTGGTTATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2732 Chironominae sp. water mite diet isolate 2732-BHL032417-GBD7539_5448-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTTATTCGAACGGAATTAGGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCCATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATAAGGCTTTTCCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATCACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2733 Chironominae sp. water mite diet isolate 2733-BHL032417-GBD22826_8472-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTT-TTTTTGGAGCTTGATTAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTTATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGATATGGCTTCTCCACGAATAAATAATATAATATTTTGATTATAACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2734 Chironominae sp. water mite diet isolate 2734-BHL032417-GBD14651_2535-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTTTTGGAGATTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAAGCCGAACGGAATTAGGTCATCCTGTAACATTTATTGGTGATGACCATATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATTATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2735 Chironomus riparius water mite diet isolate 2735-BHL032417-GBD20866_27144-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAAGCTTCATTGGAGATGGCCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTGGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2736 Chironominae sp. water mite diet isolate 2736-BHL032417-GBD20656_4300-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGTTTGCTCAGGTATAGTAGGAACTTTTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAATATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAACACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCTACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACGTTCAAGAAGAAAAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2737 Chironominae sp. water mite diet isolate 2737-BHL032417-GBD24575_22019-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATACTGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAACCCCTGATATGGCTTTTTCCACCGAAAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAAGGGAGCTGGAA	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2738 Chironominae sp. water mite diet isolate 2738-BHL032417-GBD12170_24139-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATATTAATCCGAACGGAATTATGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGATTTTATAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTACTACCACTAATATTAGGAGCCCATGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAAAAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2739 Chironomus sp. water mite diet isolate 2739-BHL032417-GBD25788_20215-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCAATAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTATTACTTGGAGCACCTGACATAGCTTTTCCTCGATTAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2740 Chironominae sp. water mite diet isolate 2740-BHL032417-GBD25716_21685-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGGATTTCTTTAAGTATATTAATCCGAACGGAATTAGGGCATCCTGGAACATTTATTGGTGATGAATAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2741 Chironominae sp. water mite diet isolate 2741-BHL032417-GBD24312_5895-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGGATAGTAGGAGCTTCTTTAAGAATATTAATGCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACAAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGTAGGATTTGGAAATTGGTAATTACCACTAATATTAGGAGCCCCTGGTATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2742 Chironominae sp. water mite diet isolate 2742-BHL032417-GBD14660_17483-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATTGTAGGGACTTCTTTTAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTATTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTACTACCACTAATAGTAGGAGGCCCTGATATGGATTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATCACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2743 Chironominae sp. water mite diet isolate 2743-BHL032417-GBD14888_3947-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGGAGCTTGAGCAGGAATAGAAGGAACTTCTTTAAGAATATTAATCCGAAGGGAATAAGGTCATCCTGGAACATTTATTGGTGATGACCAATTTAATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGTAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2744 Chironominae sp. water mite diet isolate 2744-BHL032417-GBD24156_18581-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCATGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAATGGAATTAGGTCATCCTGGAACATTTATTGGTAATGACCAAATTTATAACGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTAGTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCATGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2745 Chironominae sp. water mite diet isolate 2745-BHL032417-GBD9820_23939-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATATTATTTTTGGGACTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAACTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCGTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2747 Chironominae sp. water mite diet isolate 2747-BHL032417-GBD6681_19387-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGAACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTAACAACATCTCTTACTTGATTACGTACAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2748 Chironominae sp. water mite diet isolate 2748-BHL032417-GBD15504_21674-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTTGTGATGACCAAATATATAATGTAATTGTTACTGCTAATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAAGATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCCCTTACTTTATTACTTTCAAGAAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2749 Chironominae sp. water mite diet isolate 2749-BHL032417-GBD15227_11846-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGCTCGGGTATAATAGGAATTTCTTTAAAAATATTATTCCGCACGGAATTAGGTCACCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGTTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2750 Paratanytarsus sp. water mite diet isolate 2750-BHL032417-GBD20102_3580-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAATAGAATAGCGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2751 Chironomus sp. water mite diet isolate 2751-BHL032417-GBD7252_5887-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTTTTAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCCCAAGCATTTATTATAATTTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2752 Chironominae sp. water mite diet isolate 2752-BHL032417-GBD19583_25786-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTTGAGCTTGATCAGGTATAGTAGGAACTTCTTTAATAATATTAATCCGAACGGAATTATGTCATCCTGTAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGATCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTAGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGATTTTCCACGAATAAAAAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2753 Drosophila sp. water mite diet isolate 2753-BHL032417-GBD9954_3008-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATACAGATATTGGAACTTTATATATTATTTTTGGGACTTGATCCGGAATAGTGGGAACTTCATTCAGAATGCTTATTCGAGCAGAACTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAACTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTAACACCATTCTCTTACTTTATTACGTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.2% identical to accession ID AY750090, identified in GenBank as Drosophila lacertosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2754 Chironominae sp. water mite diet isolate 2754-BHL032417-GBD8003_19861-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGGGCTTGATCAGGTATAGTAGGAACTTCTTTATGAATATTAATCCGCACGGGATTAGGTCATCCTGTAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATATTATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2755 Chironominae sp. water mite diet isolate 2755-BHL032417-GBD11408_27615-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGCTCAGATATATTAAGAACTTCTTTAAAAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTGTAGTAATACCTATTTTAACTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2756 Chironominae sp. water mite diet isolate 2756-BHL032417-GBD15834_12822-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGTGTTTGATCAGGTATATTCGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGATCATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACAATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2757 Chironominae sp. water mite diet isolate 2757-BHL032417-GBD24039_16447-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAAAATAAGATTTTGATTATAACCACCATCTCTTACTTTATTACTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2758 Chironominae sp. water mite diet isolate 2758-BHL032417-GBD23230_12627-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACAGAATGAGGTCATCCTGTAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTATGAGACCCTGATATGACTTGTCCACGAATAAATAATATAAGATTTTGATTATGACCACCATCTCTTACTTTATTACTTTCAAGAAAAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2759 Chironominae sp. water mite diet isolate 2759-BHL032417-GBD26873_18518-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCATTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTTATTACAATCTAGACGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2760 Chironominae sp. water mite diet isolate 2760-BHL032417-GBD5654_7316-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTCTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTTCACGAATAAATAATATAAGATTTTGATTATTACTACCATCTCTTACTTTATTACTTTCAAGAAGATTAGTATAAAATGGCGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2761 Chironominae sp. water mite diet isolate 2761-BHL032417-GBD12077_23079-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGCGACTGATAATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCTCCTGATATGGCTTTTCCACGAATAAATAATAAAAGATTTTGATTAATACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2763 Chironominae sp. water mite diet isolate 2763-BHL032417-GBD9311_3390-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGCGCTTGATCCGGTATTGTATGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAACGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTCTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2764 Chironominae sp. water mite diet isolate 2764-BHL032417-GBD10408_19522-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCAGGTATTATAGGAACTTCTTTAATAATATTATTCCGTACGGTATTAGGTCATCCTGTAACATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2765 Chironominae sp. water mite diet isolate 2765-BHL032417-GBD11274_15411-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCTTTTTTTTGGAGCTTGCTCAGGTATAGTAGGAGCTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGTCCCTGATATGGCTTTTCCACGAATAAGTAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGACGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2766 Psectrocladius sp. water mite diet isolate 2766-BHL032417-GBD10858_27189-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGCCGATTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGTGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTATTTTGATTACTTCCCCCATCATTAACTTTACTATTATCTAGCTCTCTAATTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2767 Chironominae sp. water mite diet isolate 2767-BHL032417-GBD21013_3308-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATATTAGGTACTTCTTTACGAATATTACTCCGAACGTAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTGCCACGAATAAATAATATAAGATTGTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAGAAGAGTAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2769 Chironominae sp. water mite diet isolate 2769-BHL032417-GBD22602_22141-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTCTTTTTTTGGCGCTTGATCAGGTATAGTAGGAACTTTTTTAAGTATTTTTTTCCGCACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGTTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2771 Chironominae sp. water mite diet isolate 2771-BHL032417-GBD14830_4565-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTTGAACATTTATTGGGTATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTAATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTATTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2772 Chironominae sp. water mite diet isolate 2772-BHL032417-GBD17742_16947-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTAATCAGGTATAGTAGGAACTTCTTTAAGATTTTTATTCCGAACGGAATTAGTCCTTCCTGGAACATTTATTGGTGAAGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGTCCCTGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAAAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2773 Chironominae sp. water mite diet isolate 2773-BHL032417-GBD11346_21416-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTGTTTTTGGAGATTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTAGTTATTACCACTAATATTAGTATCCCCTGATATGACCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2774 Chironominae sp. water mite diet isolate 2774-BHL032417-GBD4870_14918-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTGGAGTTTGATCAGGTTTAGTAGGAATTTTTTTAAGAATTTTATTCCGAACGGAATTAGGTCATCCTGGAACTTTTATTGGTGATGACCAAATTTTTAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAATTTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2775 Chironominae sp. water mite diet isolate 2775-BHL032417-GBD4689_15904-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAACGGAATTAGGTCATCCTGTTTCTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2776 Chironomidae sp. water mite diet isolate 2776-BHL032417-GBD16378_25294-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGTGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCATTCATTAACCTTACTTTAATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2777 Chironominae sp. water mite diet isolate 2777-BHL032417-GBD15142_4248-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGGGAGCTAGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAACCCGAACGGAATTAGGTCATCCTGCAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTAGTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGAATTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2778 Chironominae sp. water mite diet isolate 2778-BHL032417-GBD25065_15612-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTATGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGAAAAGACCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2779 Psectrocladius sp. water mite diet isolate 2779-BHL032417-GBD14053_2374-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGGCACGCCGGTTCCTTAATTGGAGATTATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGATGCTTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2780 Chironominae sp. water mite diet isolate 2780-BHL032417-GBD7253_11995-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCAGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTACCACCATCACTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2781 Chironominae sp. water mite diet isolate 2781-BHL032417-GBD25123_25400-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCCTGCTCTGGTATAGTTGGAACTTCTTTAATATTATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAAAAAATAATATAAGAGTTTGATTAATACCACCATCTCTTACTTAATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2782 Chironominae sp. water mite diet isolate 2782-BHL032417-GBD16146_18106-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTGGAGCTTGTTCCGGTATAGTAGGAACTTCTTTTAGAATATTAATTCGAACGGAATTTGGTCATCCTGGAACATTTATTTGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGTCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCATCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2783 Chironominae sp. water mite diet isolate 2783-BHL032417-GBD10235_9265-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTTTTGAGCTTGATCAGGTATAGTATGACCTTCTTTTAGAATATTAATCCGAACGGAATTAGGTCATCCTTGAACATTTATTGGTTATGACCAAATTTATAATGTAATTGTTACTGGTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGATATGGCTATTCCACGAATAAATAATATAAGATTTTGATTATAACCAACATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2784 Chironominae sp. water mite diet isolate 2784-BHL032417-GBD17101_27464-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTTGGAGCTTGGTAAGGGATAGTAGGGAATTCTTTTAGGATATTAATCCGGACGGGATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2786 Chironominae sp. water mite diet isolate 2786-BHL032417-GBD23561_6471-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACTTTTATTAGTGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGGTTTTTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGAATATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2787 Chironominae sp. water mite diet isolate 2787-BHL032417-GBD6985_21606-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAAACCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAAAAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCATTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2788 Chironominae sp. water mite diet isolate 2788-BHL032417-GBD25623_23198-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGTTATACTTGTAACTTCTTTAAGAATTTTAATCCGAACGGAATTAGGTCATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTAACACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGTGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2789 Cricotopus sp. water mite diet isolate 2789-BHL032417-GBD24387_7079-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAAAATTAGGTCATTGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGAACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2790 Chironominae sp. water mite diet isolate 2790-BHL032417-GBD4845_19663-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATAATTTTTTTTTTGGAGCTTGATCAGGTTTAGTAGGAACTTCTTTAAGATACTTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGCCCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATATTTTTTTTATAGTAATACCTATTTTAATTGGCGGATTTGGAAATTGGTTATTACTACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATATATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGATGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2791 Chironominae sp. water mite diet isolate 2791-BHL032417-GBD16387_27705-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTTTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGTTTATTACCTCTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTCCCTCCATCTCTAACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2792 Chironominae sp. water mite diet isolate 2792-BHL032417-GBD4530_18581-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTGTTGGAGCTTGATCAGGTTTAGTAGGAACTTCTTTAAGAATTTTAATCGGAATGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTATTTTTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2793 Chironominae sp. water mite diet isolate 2793-BHL032417-GBD21425_5958-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATATTATTCCGACCGGAATTAGGTCATTCTTGAACATTTATTGGTGATGACCAAATTTATAATGTCATTGTTACTGCTAATGATTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGAATATTACCACCATCTCTTACTGTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2794 Chironominae sp. water mite diet isolate 2794-BHL032417-GBD11693_25322-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATCGGTTATTACCACTAATATTAGGAGCCCCTGAGATGGCTTTTCCACGAATAAATAATATAAGATATTGATTATTACCACCATCTCTTACATGATTACTGTCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2795 Chironominae sp. water mite diet isolate 2795-BHL032417-GBD22721_15678-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTTTTTGGGCTTTATCCGGTTTTGTAGGAACTTTTTTTAGAATATTAATCCGAACGGA-TTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCGTGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2796 Chironominae sp. water mite diet isolate 2796-BHL032417-GBD26277_23679-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGATTGATCAGGTATAGTTGGAATTTCTTTAAGATTTTTAATCCGAACGGAATTAGGTTATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTTCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2797 Chironominae sp. water mite diet isolate 2797-BHL032417-GBD14046_7409-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2798 Chironomus riparius water mite diet isolate 2798-BHL032417-GBD8626_5410-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGGCCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTTTCCCCCTAATATTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTTCTTCTTTCAAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2799 Chironominae sp. water mite diet isolate 2799-BHL032417-GBD27059_14185-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCAGATATAGTAGGTACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGGTTAAATAATATAAGATTTTGATTATTACCACCAACTCTAACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2800 Chironominae sp. water mite diet isolate 2800-BHL032417-GBD8873_13614-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATGGTAGGAACTTCTTTAAGAATTTTAATTCGAACGGAACTAGGTCACCCTGGATCATTTATTGGTGACGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGCAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2801 Chironominae sp. water mite diet isolate 2801-BHL032417-GBD15023_2646-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGATTGATCAGATATAGTAGGAACTTCTTGAAGAATATTAATCCGAGCGGAATTAGGGCATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2802 Chironominae sp. water mite diet isolate 2802-BHL032417-GBD16720_15071-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACTGAATTAGGTCATCCTGGAACATTTATTGGTAATGACCAAATTTATAATGTAATTGTTACTGCTCATGCCTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCATTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACTATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2803 Chironominae sp. water mite diet isolate 2803-BHL032417-GBD17124_25529-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATAATAATCCGAACGGAATTAGGTCATCCTGGTACATTTATTGGTGATGTCCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTAGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAGTAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2804 Chironominae sp. water mite diet isolate 2804-BHL032417-GBD14405_11417-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGATGGAACTTCTTTTAGAATATTAATCCGGACGGAATTATGTCATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGTAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2806 Chironominae sp. water mite diet isolate 2806-BHL032417-GBD9417_20090-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGAGCTTTATCAGGGATAGGAGGAACTTCTTTTAGGATATTTATCCGAACGGGATTTGGTCATTCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2807 Chironominae sp. water mite diet isolate 2807-BHL032417-GBD17522_25776-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTCTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACTTCTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTGAATACGTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2808 Chironominae sp. water mite diet isolate 2808-BHL032417-GBD28836_18450-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCCTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTTCTGCTCATGCTTTTATTATAATTTTTTTTTAGAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCATTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACGTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2809 Chironominae sp. water mite diet isolate 2809-BHL032417-GBD26732_13690-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGTACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCGCTAATATTAGGAGCTCCTGATATGGCATTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2810 Chironominae sp. water mite diet isolate 2810-BHL032417-GBD16731_2090-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGACCAGGTATAGTAGGAATTTCTTCAAGAATATTATTCCGAACGGAATTAGGTCACCCTGTAACATTTAATGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2812 Chironominae sp. water mite diet isolate 2812-BHL032417-GBD17493_8926-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTTTTTGGTGATGACCAAATTTATAATGTAATTGTTACTACTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCAGCTCTTACTTTATTACTAGCAAGAAGAATAGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2813 Chironominae sp. water mite diet isolate 2813-BHL032417-GBD2225_15098-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTTTTTGGACCTTGATCAGGTTTAGTAGGAACTTCTTTAAGAATTTTAATCCGACCGGAATTGGGTCATCCCGGAACATTTATTGGTGATGACCATATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTT-ATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2816 Psectrocladius sp. water mite diet isolate 2816-BHL032417-GBD19891_23792-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTACCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCAGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCCAACACAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2817 Chironomus sp. water mite diet isolate 2817-BHL032417-GBD8608_12870-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTTTTTTGGAGCTTGATCCGGAATAGTGTGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACCTTCATTGGAGATGGCCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATATTTTTTTTCATAGTTATACCAATTCTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATACAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KR756187, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2818 Paratanytarsus sp. water mite diet isolate 2818-BHL032417-GBD26469_17616-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTTTTTTTTGGAGCTTGCTCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGTTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2819 Chironominae sp. water mite diet isolate 2819-BHL032417-GBD23356_10651-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATAACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATATTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCATTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTAATTACTTGCAAAAAGAATAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2821 Chironominae sp. water mite diet isolate 2821-BHL032417-GBD17101_14500-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTCTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCGGAATTAGGTCATCCCGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTAGTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2822 Chironomus sp. water mite diet isolate 2822-BHL032417-GBD16766_9988-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2824 Chironominae sp. water mite diet isolate 2824-BHL032417-GBD4054_14485-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATATTTTTTTTTTTTGGAGCTTGATCAGGTATAGTTGGAACTTCTTTAAGTATATGAATCCGAACGGAATAAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTTTAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCAGCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2826 Chironominae sp. water mite diet isolate 2826-BHL032417-GBD22303_22050-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTAATGTTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTTGTTATTACCACTAATATTAGGAGGCCCTGATATGGCTTTTCCATGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2827 Chironomus riparius water mite diet isolate 2827-BHL032417-GBD12337_10613-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGATCTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGGCCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGAGATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTTACCCCCCTTTCTTACTCTTCTTCTTTTTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2829 Chironominae sp. water mite diet isolate 2829-BHL032417-GBD10266_21362-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATTCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTAGAGGATTTGGAATTTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2830 Chironominae sp. water mite diet isolate 2830-BHL032417-GBD24875_17799-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCATTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTTATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATGAGATTTTGATTATTACCACCAGCTCTTACATTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2831 Chironominae sp. water mite diet isolate 2831-BHL032417-GBD17821_20542-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGTAACATTTATTGGTGATGACCAAATTTATAATGGAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATTCCTATTTTAATTGGAGGATTTGGAAACTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGGTTATCACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2832 Chironominae sp. water mite diet isolate 2832-BHL032417-GBD10921_18148-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTGCTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGTTTATTACCACTAATATTAGGAGCCCATGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATAACCACCATCTCTTAATTTATTACGGTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2833 Chironominae sp. water mite diet isolate 2833-BHL032417-GBD22479_4265-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTGGAGCTTGATCAGTTATAGTAGGAAGTTCTTTAATAATATTAATCCGAACGGTATTATGTCATCCTTGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCAGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2834 Chironominae sp. water mite diet isolate 2834-BHL032417-GBD11612_7874-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTGAGATCATGACCACCATCGCCTACATTATTACATGCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2835 Amphichaeta raptisae water mite diet isolate 2835-BHL032417-GBD3144_15194-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACATTAGTTACTGCACATGCATTTTTAATAATTTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCACCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL2836 Chironominae sp. water mite diet isolate 2836-BHL032417-GBD2677_12365-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGTAACTTCTTTAAGACTTTTAATCCGAACTGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTACTTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATAAAAGATTTTGATTATTACCACCATCTCTTACATGATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2837 Chironominae sp. water mite diet isolate 2837-BHL032417-GBD13906_24694-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGGACTTCTTTAAGAATATTTATTCGAACGGAATTTAGGCCATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGTGCCCCAGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2838 Psectrocladius sp. water mite diet isolate 2838-BHL032417-GBD11188_14573-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATAATCAAATTTATAATGTATTTGTTACCGCTCACGCTTTTGTAATATTTTTTTTATAGTAATACCTTTTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTCGATTACTTCCCCCGTCATTAACTTTACTATTATCGAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2842 Chironominae sp. water mite diet isolate 2842-BHL032417-GBD4751_23729-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTGTTGAGGCTTGATCAGGTATAGTAGGAACTTCTTTAGGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGTTGATGAACAAATTTATAATGTAATTGTTACTGGTCATGCTTTTATTATATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATAGGGCTCTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2843 Chironominae sp. water mite diet isolate 2843-BHL032417-GBD21106_26274-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGGGTTTGTTTAGGTATAGTGGGAACTTTTTTAAGAATTTTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACAACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2844 Chironomus riparius water mite diet isolate 2844-BHL032417-GBD11880_4768-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTAATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCCTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGGCCCCTTATTACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTCCCCCCCCTCTCGTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2845 Chironominae sp. water mite diet isolate 2845-BHL032417-GBD16430_17290-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAGCAGAATTCGGTCATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCTCTAATATTAGGAGCCCATGATATGGCATTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2846 Chironomidae sp. water mite diet isolate 2846-BHL032417-GBD25115_6743-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTGTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACCAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAACAATATAAGTTTTTGATTGTTGCCCGCATCATTAACTTTATTATTATCTAGAACAATTGTGGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2847 Chironominae sp. water mite diet isolate 2847-BHL032417-GBD11881_17717-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTTATCAGGTATAGTAGGAACTTCTTTATGAATATTAATCCGAACAGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTAAAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATTTCTTACTTTATTACCTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2848 Chironominae sp. water mite diet isolate 2848-BHL032417-GBD6565_24557-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGCATAGTCGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTAGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAAAATAAGATTTTGATTATTACCAGCATCGCTTACTTAAGTACTTTCAAGAAGAAGAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2851 Chironominae sp. water mite diet isolate 2851-BHL032417-GBD10266_15384-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGTTCGGGATTGGTAGGACCTTCTTTAAGATTATTAATCCGAACGGAATTAGATCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCATGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2853 Chironominae sp. water mite diet isolate 2853-BHL032417-GBD4195_9410-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGATTTTATTATAATTCTTTTTATAGTAATACCTATTTTAATTGGAGGATTCGGAAATTGGTTATTACCGCTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAGATAATATAAGATTTTGATTATTACTACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2855 Chironominae sp. water mite diet isolate 2855-BHL032417-GBD3777_16482-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGGATAGTAGGAAGTTCTTTAAGAATTTTAATCCGAACGGGATTAGGTCATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGGTACTGCTCATTCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCATGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTCTCAAGAAGAATAGTAGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2856 Chironominae sp. water mite diet isolate 2856-BHL032417-GBD3604_19819-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTGGAGCTTGATCAAGTATAGTAGGTACTTCTTTAAGAATATTTATCCGAGCGTAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGAGTTGGAAATTGGTTATTACCACTAATATTAGGAGACCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2857 Chironomus riparius water mite diet isolate 2857-BHL032417-GBD16005_3540-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGAGCCGGAATAGTGGGAACTTCATTAAGAATGCTTATGCGAGCAGAATTAGGACGACCCGGAACCTTCATTGGAGATGTCCAAATTTATAATGTGGTAGTTACTGCACATGCTTTTATGATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTAGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2859 Chironominae sp. water mite diet isolate 2859-BHL032417-GBD13634_4300-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTTGGGAGCTGGACCAGGTAAAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGTTTATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGCGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2860 Chironominae sp. water mite diet isolate 2860-BHL032417-GBD29319_12509-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTT-TTTTTGGAGCTTGATCAGGTATTGTAGGCACTTCTTTTAGAATTTTAATCCGAACGGTATTTGGGCCTCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTTATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTCATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2861 Chironominae sp. water mite diet isolate 2861-BHL032417-GBD25943_20161-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTTTATTTCTTTTTTGGAGCTTGATCAGGTATAGTACGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAAATTTATAATGTAATTGTTACTGCTCATGCTTTTTTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTAGCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2862 Orthocladius sp. water mite diet isolate 2862-BHL032417-GBD23825_9483-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTATGTTATAATTTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2863 Chironominae sp. water mite diet isolate 2863-BHL032417-GBD22758_10863-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAATAATATTAATCCGAACTGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTATATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATGAATAATATAAGAGTTTGATTATTACCACCATCTCTTACTTTATCACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2864 Chironominae sp. water mite diet isolate 2864-BHL032417-GBD14143_2614-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTTTGGAGCTTGAACAGGTAGAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTAGAAAGTAATTGTTACTGCTCATGCTTTTATTAGAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2865 Chironominae sp. water mite diet isolate 2865-BHL032417-GBD25973_8518-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCGTGATCAGGTATTGGAGGAACTTCTTTAAGTATTTTATTCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCAGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2866 Chironominae sp. water mite diet isolate 2866-BHL032417-GBD9032_9816-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGTTCAGGTATAGTAGGAACTTCTTTAATAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGTGCCCCTGATATGGCTTTCCCACGAATAAATAATATAAGATTATGATTATTACCACCATCTCTTACTTTATTACTTCCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2867 Chironominae sp. water mite diet isolate 2867-BHL032417-GBD4657_12457-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCCGGTATAGTAGGAACTTCTTTTTGTATTTTAATCCGAACGGAATTAGGTCATCCTTGAACATTTATTGGTGATGACCAATTTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTCTAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2869 Chironominae sp. water mite diet isolate 2869-BHL032417-GBD3554_14539-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCAGGTATAGGAGGAACTTCTTTAAGAATATTAATCCGTACGGAATTAGGTCATCCTGGAATATTTATTGGTGATGACCAAATTTATAATATAATTGTTACTGTTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2870 Chironominae sp. water mite diet isolate 2870-BHL032417-GBD18031_14938-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGTGGTTGACCAGGTATAGTAGGAACTTTTTTAAGAATATTATTCCGACCGGAATTAGGTCATCCTGAAACATTTATTGGTGATGACCAATTTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTCAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2871 Chironominae sp. water mite diet isolate 2871-BHL032417-GBD22388_6425-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGATCTTGATCAGGTATATGAGAAACTTCTTTAATAATATTAATCCGAACGGAATTAGTTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTCTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2872 Chironominae sp. water mite diet isolate 2872-BHL032417-GBD14469_6722-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCAGGATTAGTAGGAACTTCTTTAGGAATATTATTCCGAACAGAATTAGGCCATCCTGGAACATTTATGGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCCTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2877 Chironominae sp. water mite diet isolate 2877-BHL032417-GBD9257_8592-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGTTCAGGTTTGGTAGGAACTTTTTTAAGAATATTATTCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATATTGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAACTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2879 Chironominae sp. water mite diet isolate 2879-BHL032417-GBD3700_8287-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATTTAATTGTTACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGGCTATTACCACTAATTTTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAGGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2880 Chironominae sp. water mite diet isolate 2880-BHL032417-GBD11338_22227-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAAAACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTTCACGAATAAATAATAAAAGATTTTGAATAATACCACCATCTCCTACCTTATTTCCTTCAAGAAGAATAGGAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2881 Chironominae sp. water mite diet isolate 2881-BHL032417-GBD22520_21474-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCTAAGGGAATTAGGTAATCCTGGAACATTTATTGGTGATGACAATATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATAAGGCCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2882 Chironominae sp. water mite diet isolate 2882-BHL032417-GBD25642_20428-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGTTTTAGTAGGAACTTCTTTAAGAATCTTAATCCGACCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTTTATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTATATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2883 Chironominae sp. water mite diet isolate 2883-BHL032417-GBD25369_12661-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGGGCTTGATCCGGTATAGTAGGAACTTCTTTAAGAATATTTATTCGAACGGAATTAGTTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTAAGTAATACCTATTTTAATTGGAGGATATGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCGTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2884 Mucor sp. water mite diet isolate 2884-BHL032417-GBD8220_22742-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACTTTATATATCATCTTCTCTATTTTTGCGGGTATGATTGGTACTGCTTTTTCTATGTTAATTAGACTAGAATTAGCTGGTCCTGGAATCCAATATCTTCATGGTGATCATCAATTATATAATGTAATTGTAACTGCTCACGCATTTGTAATGATTTTCTTCTTAGTAATGCCTGCAATGATTGGAGGTTTTGGTAACTGGTTTGTTCCTTTAATGATTGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KR809877, identified in GenBank as Mucor circinelloides f. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2886 Chironominae sp. water mite diet isolate 2886-BHL032417-GBD3620_9918-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAATACTATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTTCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGACCCTGATATGGCTTTTCCACGAATAAATGATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2887 Chironominae sp. water mite diet isolate 2887-BHL032417-GBD7779_16109-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGGTTAGTAGGAACTTCTTTTAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATAGGTGATGACCAAATTTATAATGTAATTGTTACTGCTAATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCCTACTTTATTACATTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2889 Chironominae sp. water mite diet isolate 2889-BHL032417-GBD18893_4376-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTTTTTTTTTGGAGCTTGAGCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACAGAATTAGGTCATCCTGGAACATTTATTGGGGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATCACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCATGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATATTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2890 Chironominae sp. water mite diet isolate 2890-BHL032417-GBD8623_12983-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCGAATTTATAACGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAAGACCTATTTTATTTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTGCCACCATCTCTTACCTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2891 Chironominae sp. water mite diet isolate 2891-BHL032417-GBD15628_7163-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGGGCTTGATTAGGTATTGTAGGAACTTCTTTTAGAATATTTGGCCGAACGGGATCAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2895 Lebertia sp. water mite diet isolate 2895-BHL032417-GBD7315_15275-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAAATCAGAGCCCCTAATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTTCTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2896 Chironominae sp. water mite diet isolate 2896-BHL032417-GBD12352_7791-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGATTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTTGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAACTTGTTATTACCACTAATGTTAGGAGACCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTGTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2899 Chironominae sp. water mite diet isolate 2899-BHL032417-GBD18530_15557-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGCGCTTGCTCAGGTATAGTAGGAATTTTTTTAAGAATTTTATTCCGAACGGAATTAGGTCGTAATGTAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2900 Chironominae sp. water mite diet isolate 2900-BHL032417-GBD11888_23457-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATATTGGGAATTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2901 Chironominae sp. water mite diet isolate 2901-BHL032417-GBD17669_19617-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGGTCATGCTTTTATTATAATTTTTTTTTACAGTAATACCTATTTTAATTGGAGGAATTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCCGAGATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2903 Chironominae sp. water mite diet isolate 2903-BHL032417-GBD9702_10685-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGATCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGTATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTACGAGCCCCTGATATGGCATTTCCACGAATAAATAAAAAAAGATATTGATTATTACCACCATCTCTTACTTTATTACTGTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2905 Chironominae sp. water mite diet isolate 2905-BHL032417-GBD12148_15655-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTGGGCTTGGTCCGGTATTGTAGGGACTTTTTTTAAAATTTTTATTCGAACGGAATTAGGTCATTCTTGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2906 Chironominae sp. water mite diet isolate 2906-BHL032417-GBD24102_19802-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATGTATTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAGTTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTCGGAAGTTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATATTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2907 Chironominae sp. water mite diet isolate 2907-BHL032417-GBD13387_22069-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTTTTGGCGCTTGATCAGGTATAGTAGGAACTTTTTTAAGAATATTAATTCGAACGGAATTATGTCATCCTGGAACATTTATTGGTGATGACCAATTTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTGTTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2912 Psectrocladius sp. water mite diet isolate 2912-BHL032417-GBD10237_22219-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTACGAATTTTAATTCGAGCAGAACTCGATCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCTCGTTAATATTAGGATCCCCCGACATAACATTCCCCCGAAAAAATAATATAAGTTTTTTGATTACTTCCCCCGTCATTAACATTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2915 Chironominae sp. water mite diet isolate 2915-BHL032417-GBD15969_4911-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGAGCAGGTAGAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGTAACATTTATTGGTTATGACCAAATTTATAATGAAATAGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATAACTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTAACACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAACTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2916 Chironominae sp. water mite diet isolate 2916-BHL032417-GBD5371_8579-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTTTAGTAGGAACTTCTTTATGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTACTGGTGATGTCCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTTACTTTATTACTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2918 Chironominae sp. water mite diet isolate 2918-BHL032417-GBD27756_15792-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTGTATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATATTAATCCGAACGGATTTAGGACATCCTGAAACATTTATTGGTAATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2919 Chironominae sp. water mite diet isolate 2919-BHL032417-GBD19202_23908-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTGTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAGTATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCATGAATAAAGAATATAAGATTTTGATTATGACAACCATCTCTTACTTTATTACTGTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2920 Chironominae sp. water mite diet isolate 2920-BHL032417-GBD11093_27913-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTCTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAATAATATTTATCCGAACGGAATTAGGTCATCTTGGAACATTTATTGGTGATGACCAAATTTATAATTTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTTCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2921 Chironominae sp. water mite diet isolate 2921-BHL032417-GBD7504_6646-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATCATATTTTATTTTTGGAGCTTGATCTGGTGTAGTAGGTACTTCTTAAAGTATGCTAATTCGAGCAGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGTCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTGTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2922 Chironominae sp. water mite diet isolate 2922-BHL032417-GBD6941_5924-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAACTTGCTCGGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTGATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAGAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2926 Chironominae sp. water mite diet isolate 2926-BHL032417-GBD26022_15123-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTTTTCTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTCAGAATATTAATCCGAACGGTATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAGTGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTAGATTATTACCACCATCTCTTACATTATAACAATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2927 Chironominae sp. water mite diet isolate 2927-BHL032417-GBD17973_4107-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGAAAAGGGATAGTAGGAACTGCTTTAAGAATATTAATCCGAACGGAAATAGGTCATCCTGGAACATTTATTGGGGATGACCAAATTTAAAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2928 Chironomus sp. water mite diet isolate 2928-BHL032417-GBD17107_24728-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACCTTCATTGGAGATGGTCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTAAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTGTTACCCCCTTCTCTAACTCTACTTCTATCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2929 Chironominae sp. water mite diet isolate 2929-BHL032417-GBD12809_16384-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTAAAAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGTTTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAACATAAGATTTTGATTATTACCACCATCTCTTACATTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2930 Chironominae sp. water mite diet isolate 2930-BHL032417-GBD15681_24169-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTTAGAATATTAATCCGAACGGAATTTGGGCATCCTGGAACATTTATTGATGATGACCATATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTT-ATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGGAGAATAGTAGAAAATGGAGCTGGAA	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2932 Chironominae sp. water mite diet isolate 2932-BHL032417-GBD10568_12171-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACAACTAATATTAGGAGCCCCTGATATGGCTGTTCCACGAATAAACAATATAAGATTTTGATTATTACCACCATCTCCTACTTTATCACTTTCAAGAAGAAGAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2933 Chironominae sp. water mite diet isolate 2933-BHL032417-GBD10948_28054-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGATCTTGATCAGGTATAGTAGGAACTTCTTTAAAAATATTAATCCGAACGGAATTAGTTCAGCCTGTAACATTTATTGGTGAAGACCAACTTTATAATGTAATTGTTACTGCTCATGCTTTTTTTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATATGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2934 Chironominae sp. water mite diet isolate 2934-BHL032417-GBD21005_23835-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTATTGGAGCTCGATCAGGTATAGTAGGACCTTCTTTAAGAATATTAATCCGACCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAACACCTATTTTAATTGGAGGATTTGGAAAATGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAGTAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2935 Chironominae sp. water mite diet isolate 2935-BHL032417-GBD21272_10905-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATAAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAGCGGGATTAGGTCATCCTGGAACATTTATTGGCGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATGCCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATCAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2936 Chironominae sp. water mite diet isolate 2936-BHL032417-GBD27917_13273-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTTTATTTTTTTTTTGGAGCTTGATCCGGTATAGTAGGAACTTCTTTAAGAATATTACTCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCTCTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGGTTATTACCACCAACTCTTACTTTATTACAATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2938 Chironominae sp. water mite diet isolate 2938-BHL032417-GBD8591_5542-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCAGAACGGAATTAGTTCATCCTGGAAAATTTATTGGTTATGACCATATTTATAATTTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATGTGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2939 Chironomus sp. water mite diet isolate 2939-BHL032417-GBD25181_20679-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGGCCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCTGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATCAAAAATATAAGTGTCTGACATTTACCCCCCCCTCTCTAACTCTTCTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2940 Chironominae sp. water mite diet isolate 2940-BHL032417-GBD10349_2736-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGGACGGAATTAGGTCATCCTTGAACATTTATTGGTGATGGCCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAGGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2941 Chironominae sp. water mite diet isolate 2941-BHL032417-GBD26401_19979-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTCTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTTTGTCATCCTGGAATATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGTTTTTATTATAATTTTTAT-ATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTAGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAAAAAATAATATAAGATTTTGATTATTACCACCAACTCTTACTTAAGTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2942 Chironominae sp. water mite diet isolate 2942-BHL032417-GBD3819_20775-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTTGGTCATCCTGGAACATTTATTGGTGCTGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATATTAATTGGAGGATTTGGAAAATGGTTATTACTACTAATATCAGGAGCCCCTGATATGGCTGTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2943 Chironominae sp. water mite diet isolate 2943-BHL032417-GBD16647_16981-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATCCGAACGGGATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTAACAGAATTTTTTTTATAGTAATACCTATTTTAATTGGATGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATAACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2944 Chironominae sp. water mite diet isolate 2944-BHL032417-GBD17763_8270-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTCTTTTTTATGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAATAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGATGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAAGACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTATGAGGCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2947 Chironominae sp. water mite diet isolate 2947-BHL032417-GBD8902_18519-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGGTTGGTCAGGGATAGTAGGAACTTCTTTTATAATATTTATCCGAACGGAATTAGGTCATCCTGGAACATTTATTTGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATATTATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2948 Chironominae sp. water mite diet isolate 2948-BHL032417-GBD16613_28701-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGGACTTCTTTAAGAATTTTAATTCGAGTAAAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATATATAATGTAATTGCTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAAATAGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2949 Psectrocladius sp. water mite diet isolate 2949-BHL032417-GBD28165_18366-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGACACCCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGATCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTATTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2950 Chironominae sp. water mite diet isolate 2950-BHL032417-GBD22763_25341-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTCGCTCAGGTATAGTAGGAACTTCTTTAAGATTATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTGTAACGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCATACTCTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2952 Chironominae sp. water mite diet isolate 2952-BHL032417-GBD27789_10045-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTATGAACTTCTTTAAGAATATTAATCCGAACGAAATTAGGTCATCCTGAAACATTTATTTGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGGGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACCTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2953 Chironominae sp. water mite diet isolate 2953-BHL032417-GBD26390_11678-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGTTATAGTAGTAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTTATTACCAAATTTATAATGTAATTGTTAATGCTCATGACTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2954 Chironominae sp. water mite diet isolate 2954-BHL032417-GBD19273_3120-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGAACAGGTATAGTAGGGACTTATTTGAGAATATTAATCCGAACAGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGAATTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2955 Chironominae sp. water mite diet isolate 2955-BHL032417-GBD15043_26005-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTACTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTAATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2956 Chironomus sp. water mite diet isolate 2956-BHL032417-GBD22015_4676-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTTTACATTATTTTCGGTGCTTGATCAGGAATGGTAGGGACTTCTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCATTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2958 Chironominae sp. water mite diet isolate 2958-BHL032417-GBD21260_10519-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTCGGAGCTTGATCAGGTATAGTAGGAACTTCTTTATGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAACTGGTTATTACCACTAATAATAGGAGCGCCTGATATGGCTTTTCCATGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTGATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2959 Chironominae sp. water mite diet isolate 2959-BHL032417-GBD28397_19617-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTAATTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTACCCCCATCTCTTACTTTATTACTTTCAAGAAGAATAATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2961 Chironominae sp. water mite diet isolate 2961-BHL032417-GBD5885_25164-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTCTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTAATCCTGGAACATTTATTGGTGATGACCTAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGTATTGGAAATTGGTTATTACCACTAATATTAAGTGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2962 Chironominae sp. water mite diet isolate 2962-BHL032417-GBD17567_7698-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGTGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTATGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGAGTTTGATTATTACCACCATCGCTTACTTTATTATTTGCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2963 Chironominae sp. water mite diet isolate 2963-BHL032417-GBD23824_8010-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGTTCAGTTTTAGTAGGAACTTCTTTAAGATTTTTATTCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGAGATGACCAATTTTTTAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2965 Chironominae sp. water mite diet isolate 2965-BHL032417-GBD21713_27865-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTTATCAGGTATAGTAGGAACTTCCTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATCGGAGATGACCAAATTTATAATGTAATTGTTACTTCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCATTTCCACGAATAAATAATATAAGATTTTGATTATTAGCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2967 Drosophila sp. water mite diet isolate 2967-BHL032417-GBD18734_27764-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATATTATTTTTGGGACTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAACTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATCGGAGGATTTGGAAATGGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTGTATTACTTTCAAGAAGAATAGTAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.7% identical to accession ID AY750090, identified in GenBank as Drosophila lacertosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2968 Chironominae sp. water mite diet isolate 2968-BHL032417-GBD24959_17881-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTTTATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATATTTATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTAAAGTAAAACCTTTTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2969 Chironominae sp. water mite diet isolate 2969-BHL032417-GBD4289_16164-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCGGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTATTTGGAGGATTTGGAAATTGATTATTCCCACTAATATTAGGAGCCCCTGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2970 Chironominae sp. water mite diet isolate 2970-BHL032417-GBD5849_8390-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATTAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTATGTCATCCTGGAACATTTATTGGTTATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTATTTGGAAGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2971 Chironominae sp. water mite diet isolate 2971-BHL032417-GBD11993_20053-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTGTGATCATTATCACCATCGCTTACATTATATCTATCAAAAAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2972 Chironominae sp. water mite diet isolate 2972-BHL032417-GBD9862_14166-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCAGGTATTGTAGGAACCCCTTTAAGATTATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAATTTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTAACACCATCTCCTACTTTAATAATTTCAAAAAGAATAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2975 Chironominae sp. water mite diet isolate 2975-BHL032417-GBD26013_11117-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCCGGTATAGTAGGTGCTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTCATCATGCTTTTATTATAATTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2976 Chironominae sp. water mite diet isolate 2976-BHL032417-GBD9084_21541-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGGGCTTGATCAGGTTTAGTTGGAACTTCTTTTAGAATATTTATCCGAACGGGATTAAGTCATACTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTTGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2977 Chironominae sp. water mite diet isolate 2977-BHL032417-GBD8263_13427-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTTATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAGTTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCATGAATAAAAAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACCTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2979 Chironominae sp. water mite diet isolate 2979-BHL032417-GBD26447_12534-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGACCGGAATTAGGTCATCCTGGAACATTTATAGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCGTTTCCACGAATAAATAATATAAGATTTTGATTATGACCACCAACTCTTACATAATTACAATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2984 Chironominae sp. water mite diet isolate 2984-BHL032417-GBD28074_14220-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTTAGAATATTAATTCGAATAGAATTAGGTCAACCTGGAACATTTATTGGAGATGCTCAAATTTATAACGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL2985 Chironominae sp. water mite diet isolate 2985-BHL032417-GBD22995_22797-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATATTAGGAACTTCTTTATGAATATTAATCCGAACGGAATTATGTCATCCTGGAACATATATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATGCCTATTTTAATTGGAGGATTTGGAAATTTGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGAGTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2987 Chironominae sp. water mite diet isolate 2987-BHL032417-GBD25875_13882-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTCCCACTAATATTAGGAGCACCTGACATGGCTTTTCCACGAATAAATAACATAAGATTCTGAATATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2988 Chironominae sp. water mite diet isolate 2988-BHL032417-GBD28360_21065-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGCTCATGGATAGTAGGAACTTCTCTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGTAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACTATCTCTTACTTTATTATTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2989 Chironominae sp. water mite diet isolate 2989-BHL032417-GBD8692_20274-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAATAATATTAATCCGAACGGAATTTGGACATCCTTGAACATTTATTGGTGATGACCAAATTTATAATGTAATTTTTACTGCTCATGCTTTTATTATAATTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTTGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2990 Chironomidae sp. water mite diet isolate 2990-BHL032417-GBD7350_13698-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGTATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCATTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2992 Chironominae sp. water mite diet isolate 2992-BHL032417-GBD19890_15251-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGACTTTGTCCGGGTATAGTGGGAACTTTTTTAAGATTTTTATTCCGAAGGGAATTAGGCCATCCTGGAAAATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2994 Chironominae sp. water mite diet isolate 2994-BHL032417-GBD21094_15719-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGACCTTTTTCAGGTATAGTAGAAACTTCTTTAAGATTATTAATCCGACCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGTTTATTACCACTAATATTAGGAGCCCCTGATTTGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2996 Chironominae sp. water mite diet isolate 2996-BHL032417-GBD27043_13853-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGATCTTGATCAGGTATTGTAGGGACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTAATCCTGGAACATTTATTGGTGATGACCAAATGTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGATGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL2998 Chironominae sp. water mite diet isolate 2998-BHL032417-GBD6226_8079-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAATTTCTTTAAGAATATAAATCCGCACGGAATTAGGTCATCCTGGAACATTTTTTGAAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3000 Chironominae sp. water mite diet isolate 3000-BHL032417-GBD16665_14449-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGAGCTTGATCAGGGATAGTAGGGACTTCTTTAAGGATATTAATTCGAACGGGAATAAGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTAATGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3002 Chironominae sp. water mite diet isolate 3002-BHL032417-GBD25360_24460-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGTTTGATCAGGTATAGTTGGAACTTTTTTAAGTATATTAATCCGTACGGTATTAGGTTATCCTGGAACATTTATTGGTTATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3003 Mucor sp. water mite diet isolate 3003-BHL032417-GBD14587_19717-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACTTTATATATCATCTTCTCTATTTTTGCGGGTATGATTGGTACTGCTTTTTCTATGTTAATTAGACTAGAATTAGCTGGTCCTGGAATTCAATATCTTCATGGTGATCATCAATTATATAATGTAATTGTAACTGCTCACGCATTTGTAATGATTTTCTTCTTAGTAATGCCTGCAATGATTGGAGGTTTTGGTAACTGGTTTGTTCCTTTAATGATTGGAGCTCCCGATATGGCCTTCCCTCGATTAAATAATATTTCATTCTGGTTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR809877, identified in GenBank as Mucor circinelloides f. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3004 Chironominae sp. water mite diet isolate 3004-BHL032417-GBD18817_18091-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGATTATTAATCCGACCGGAATTAGGTCATCCTGTAACATTTATTGTTGATGACCAAATTTATAATGTAATTTTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATCACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3006 Chironominae sp. water mite diet isolate 3006-BHL032417-GBD14574_9077-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAAT-TTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATATTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGTCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3007 Chironominae sp. water mite diet isolate 3007-BHL032417-GBD20976_22908-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGTTCGGGTTTAGTAGGAACTTCTTTAAGATTTTTATTCCGACCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAAAGTAATTGTTACTGCTCACGCTTTTATTATATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACATTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3008 Chironominae sp. water mite diet isolate 3008-BHL032417-GBD16334_20324-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTTTTGGAGCTTTATCAGGTATAGTAGGAATTTCTTTATGAATTTTAATCCGAACGGTATTAGGGCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGATCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTAGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3011 Chironomus riparius water mite diet isolate 3011-BHL032417-GBD24518_18014-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGACTTGATCCGGAATAGCGTGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACCTTCATTGGAGATGGCCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAAATTTTCTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCCGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCTCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3013 Chironominae sp. water mite diet isolate 3013-BHL032417-GBD19184_27465-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTTGGAGCTTGATCAGGGATTGTAGGTACTTTTTTTAGATTTTTTATCCGATAGGGATTATGGCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3014 Psectrocladius sp. water mite diet isolate 3014-BHL032417-GBD14050_11726-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTATTACCTATTTTAATTGGATGATTTGGAAATTGATTAGTCACGTTAATATTAGGTACCCCCGACATAGCATTCCCCCGAATAAATAATATAAGGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3015 Chironomidae sp. water mite diet isolate 3015-BHL032417-GBD26870_10471-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCGGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCGTTAATATTAGGAACCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3016 Chironominae sp. water mite diet isolate 3016-BHL032417-GBD23767_15290-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTT-TTTTTGGAGCTTGATCAGGTATTGTTGGAACTTCTTTATGAATATTTATTCGAACGGGATTTGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTAATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCAGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTATCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3019 Chironominae sp. water mite diet isolate 3019-BHL032417-GBD5448_18619-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTT-TTTTTGGAGCTTGGTCCGGTATTGTTGGAACTTCTTTTAGAATTTTAATTTGAACGGGATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGTTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACCTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3022 Chironominae sp. water mite diet isolate 3022-BHL032417-GBD23658_25803-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTG-AGCTTGATCCGGTATAGTAGGAACTTCTTTTAGAATATTAATCCGGACGGGATTAGGTAATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAAGTGTTACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3023 Chironominae sp. water mite diet isolate 3023-BHL032417-GBD3627_17116-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCCGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGTATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTGTTTTAATTGGAGGATTGGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACCTTCAAGGAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3024 Chironominae sp. water mite diet isolate 3024-BHL032417-GBD5642_9725-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACACCCATCTCTTACCTTATTTCTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3025 Chironominae sp. water mite diet isolate 3025-BHL032417-GBD10693_25072-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTAATCAGGTATAGTAGGAACTTCTTTTAGAATATTAATCCGAACGGGATTAGGTCATCCTGGAAAATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCGCATGCTTTTATTATAATTTTTTTTATATTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATGTAAGATTTTGATTATTACCACCGTCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3026 Psectrocladius sp. water mite diet isolate 3026-BHL032417-GBD9579_11799-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGTGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTTCTTCCCCCGTCATAGACTTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3027 Chironominae sp. water mite diet isolate 3027-BHL032417-GBD25330_14321-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTATGAATATTAATCAGAACGGAATTAGGTTATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGTTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAGATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTAATTACTTTCAATAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3028 Chironominae sp. water mite diet isolate 3028-BHL032417-GBD14151_15125-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCACTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCACCCTGGATCATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATAGGTTATTACCATTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGTGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3029 Chironominae sp. water mite diet isolate 3029-BHL032417-GBD16526_12085-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGGGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTATATAGTAATACCTATTTAAATTGGATGATTTGGAAACTGGTTATTACCACTAATATTAGGATCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTGCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3030 Chironominae sp. water mite diet isolate 3030-BHL032417-GBD25817_21952-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCAATATATTTTTTTTTTG-AGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATCTTAATCCGAACGGGATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATTTAATTGTTACTTCTCATGCTTTTTTTATAATTTTTTTTATAGTAATACCTATTTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3032 Chironominae sp. water mite diet isolate 3032-BHL032417-GBD21730_6525-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTCAGAATATTAATCCAAACGGAATTAGGTCATCCTGGAACGTTTATTGGTGATGACCAAATTTATAATGTAATTGATACTGCTCATGCTTATATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGACCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3035 Chironominae sp. water mite diet isolate 3035-BHL032417-GBD17056_7290-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTATTCCGAACAGAATTAGGTCCTCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGATCATGCTTTTATTATAATTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCATTAATATTAGGAGCCCCTGATATGGCTTTACCACGAATAAATATTATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3039 Chironominae sp. water mite diet isolate 3039-BHL032417-GBD22336_10179-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGTAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAAGTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAGTATAAGGAGAACATGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTAAAACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3041 Chironominae sp. water mite diet isolate 3041-BHL032417-GBD8766_23384-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGCACTTCTTTTAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTAGTTATTACCACTAATATTAGTAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3045 Chironominae sp. water mite diet isolate 3045-BHL032417-GBD24635_22621-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCTGGTATAGTAGGAATTTCTTTAAGTATATTAATCTGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCCAATTTATAATGTAATTGTTACTGCTTATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAAAAAATAATATAAGAATTTGATTATTACCACCATCTCTTACTTTATTACTATAAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3046 Chironominae sp. water mite diet isolate 3046-BHL032417-GBD21323_22507-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATAAGTTATATTAGTAACTTCTTTAAGATTATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGTTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAAAAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3047 Chironominae sp. water mite diet isolate 3047-BHL032417-GBD27841_12705-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAATATTTTTAATCCGAACGGAATTAGTTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCGAATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGTCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCAGCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3048 Chironominae sp. water mite diet isolate 3048-BHL032417-GBD29144_13704-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGCGCTTGTTCAGGTATAGTTGGAACTTCTTTAAGATTATTATTCCGATCGGAATTAGGTCATCCTGGAACATTTACTGGTGATGACCAAATTTATAATGTAATTGTTACTGTTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTAATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAAAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3050 Chironominae sp. water mite diet isolate 3050-BHL032417-GBD18657_18127-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCATCCTGGAACATTTATTGGTGATGAACAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCATTTCCACGAATAAATAGTATAAGATTTTGACTATTACCACCATCTCTTACTTTACTACTGTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3051 Chironominae sp. water mite diet isolate 3051-BHL032417-GBD25605_10288-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGTTTGATCGGGTTTAGTAGGAACTTTTTAAGATTTTTATTCCGAACGGATTTAGGCCAGCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTATTGCTCATGCTTTTATTATATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3052 Chironominae sp. water mite diet isolate 3052-BHL032417-GBD29230_17485-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGCTCCGGTATAGTAGGAACTTCTTTAAGAATTTTAATCCGAACGGACTTAGGTCATCCTGGAACATTTCTTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCGCTGACGGGAGGACGGGCAAGAAGAAGAGGAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3054 Chironominae sp. water mite diet isolate 3054-BHL032417-GBD12735_17431-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGATCTTGCTGAGGTATAGTAGGAACTTCTTTAAGTATTTTAATCCGCACGTAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTAATATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3056 Chironominae sp. water mite diet isolate 3056-BHL032417-GBD18646_25123-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTT-TTTTTGGAGCTTTATCAGGTATTGTAGGAACTTCTTTCTGAATTTTTATCCGAACGGAATTAGTTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTATTTGTTACTGCTCATGCTTTCATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3057 Chironominae sp. water mite diet isolate 3057-BHL032417-GBD13391_6471-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTGGATCAGGGATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCAACCTGGAACATTTATGGGTGATGACCAAATGTATAATGGAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3059 Chironominae sp. water mite diet isolate 3059-BHL032417-GBD20572_2644-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGGTTGATAAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAAAGGAATTAGGGCATCTTGGAACATTTATTGGTGATGACCAAATTTATAATGTATTTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCAGGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3060 Psectrocladius sp. water mite diet isolate 3060-BHL032417-GBD22253_24877-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATCTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGTAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCAAGATTTTGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGTAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3061 Chironominae sp. water mite diet isolate 3061-BHL032417-GBD3211_19670-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTTATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGAAACATTTATTGATGATGACCAAATTTATAATGTAATTGTTACTGATTATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTTGAGGTTTTGGAAAATGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3063 Chironominae sp. water mite diet isolate 3063-BHL032417-GBD3837_11184-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGGGCTTGATCGGGTTTAGTGGGAATTTTTTTAAGATTTTTATTCCGACCGGAATTGGGTCATCCTGGAACATTTATTGGTGATGACCAATTTTATAATGTAATTGTTACTGCTCATGCTTTTATTATATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTGCCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3065 Chironominae sp. water mite diet isolate 3065-BHL032417-GBD17878_21590-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTCTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGATTATTATTCCGGACAGAATTAGTTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGATACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAAATGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGAATATTACCACCATCTCTTACATTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3066 Chironominae sp. water mite diet isolate 3066-BHL032417-GBD4793_14943-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGTTATAGTAGGAACTTCTTTATGAATATTAATCCGAACGAAATTAGGTCATCCAGGAACATTTTTTGGTGATGACCAAATTTATAATGTAATTGTTACTTCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGAATTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3072 Chironominae sp. water mite diet isolate 3072-BHL032417-GBD23963_25131-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATCCGACCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTATGTGCCCCCGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTAACTTTATTACTATAAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3073 Chironominae sp. water mite diet isolate 3073-BHL032417-GBD21920_24790-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGTGGAGGTTGATCGGGTATAGTAGGCACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTGATCCTGAAACATTTTTTGATGATGACCAAATTTTTAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAAATAGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3076 Chironominae sp. water mite diet isolate 3076-BHL032417-GBD21412_24938-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTTTGAATATTAATCCGAACGTAATTAGGTCATCCTGGAACATTTATTGGTGATGACTAAATTTATAATGTAATTGTTACTTCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGTGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTAATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3078 Chironominae sp. water mite diet isolate 3078-BHL032417-GBD2958_17871-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGTTCTAGTAGGAACTTCTTTAAGAATATTAATCCGAACGTAATTAGTTAATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3079 Chironominae sp. water mite diet isolate 3079-BHL032417-GBD10402_25304-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTCTGGAGCTTGATCAGGTATAGTATAAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATTACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGCTATTACCACGAATATTAGGACCCCCTGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3083 Chironominae sp. water mite diet isolate 3083-BHL032417-GBD6391_17218-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTTTATTTTTTTTTTGAAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATATTAATTCGAGCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTAAATTGGAGGATTTGGAAATTGG-TATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3084 Chironominae sp. water mite diet isolate 3084-BHL032417-GBD19054_4460-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTATGAACTTCTTTAAGAATATTAATCCGAACGGAATTATGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGCTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTTGAGGATTTGGAAATTTGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTAATACCACCATCTCTTACTTTATTACCTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3085 Chironominae sp. water mite diet isolate 3085-BHL032417-GBD27760_13244-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTTCTCAGGTATAGTAGGAACTTCTTTTATAATTTTAATCCGAGCGGAATTAGGTCATCCTGGAAAATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTAGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3086 Chironominae sp. water mite diet isolate 3086-BHL032417-GBD10631_10232-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGACCGGAATTGGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTAATGCTCATGGTTTTATTATAATTTTTTTTATAGTAATCACTACTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3090 Chironominae sp. water mite diet isolate 3090-BHL032417-GBD25115_16995-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGATTATTAGGACCTTCTTTAAGATTTTTATTCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCATTAATATTAGGAGCCCCTGATGTGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3091 Chironominae sp. water mite diet isolate 3091-BHL032417-GBD25312_10618-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGAAGCTTGATCTGGAATAGTAGGAACTTCTTTAAGTGTATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTTATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACAACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3095 Chironominae sp. water mite diet isolate 3095-BHL032417-GBD6034_15871-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCCTTAAATAATATTAATCGGAACGGAATTAGGTAATCCTGGAAGATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATGTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3096 Chironominae sp. water mite diet isolate 3096-BHL032417-GBD21686_26263-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTATGGAGCTTGCTCAGGTATAGTATGAACTTCTTTAAGAATATTAATCCGAACGGCATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGAACATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCATACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3097 Chironominae sp. water mite diet isolate 3097-BHL032417-GBD22667_11946-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGACCTTGTTCGGGATTAGTAGGAATTCCTTTAAGATTATTATTCCGACCGGAATTAGGCCATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3098 Chironominae sp. water mite diet isolate 3098-BHL032417-GBD24548_21019-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGGGCTTGATCAGGTATAGTAGGAATTTCTTTAAGAATATTCATCTGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTTAATTGGAGGATTTGGAAATTGGTTATTATCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3099 Chironominae sp. water mite diet isolate 3099-BHL032417-GBD28013_19745-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGCTCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGATCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGATATGGCTTATCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTGCAAGAAGAAGAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3101 Chironominae sp. water mite diet isolate 3101-BHL032417-GBD15832_2796-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGAGCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATGAGGTCATCCTTGAACATTTATTGGTTATGACCAAATTTAAAATGTAATTGTTACTGCTCATGCTTTTTTTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTAATATGGCCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3102 Chironominae sp. water mite diet isolate 3102-BHL032417-GBD19247_3049-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGTTGGATCAGGTATAGTAGGAATTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAATATTTATTGGTAAGGACCAAATTTATAATGTAATTGTTACTGCTCATGTTTCTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3103 Chironominae sp. water mite diet isolate 3103-BHL032417-GBD9464_26096-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGATTATTAATCCGAACGGAATTAGGTCATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGACCCTGATATGGCATTTACACGAATAAATAATATAAGATTGTGATTATTACCACCATCTCTAACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3105 Chironominae sp. water mite diet isolate 3105-BHL032417-GBD7598_12459-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTGCTTTAAGAATATTAATCCGAACGGCATTAGGTCATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTTCTCATGCTTTTATTATAATTTTTTTTATAGTAAGACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTGTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTGATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3106 Chironominae sp. water mite diet isolate 3106-BHL032417-GBD28026_16030-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCCTGATCAGATATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAAGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGATCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACCTTATTATTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3107 Chironominae sp. water mite diet isolate 3107-BHL032417-GBD19391_3227-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTT-TTTTTGGAGCTTGATCAGGTATAGTTGGAACTTTTTTTAGAATATTAAACTGAACGGGAGTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAACTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3108 Chironominae sp. water mite diet isolate 3108-BHL032417-GBD22814_16169-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAAAGGAATTAGGTCATCCTAGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTATTACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATAAGGAGCCCTTGATATGGCTTTTCCACGAATAAATAATATGAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3112 Chironominae sp. water mite diet isolate 3112-BHL032417-GBD16998_7988-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTCTGTCATCCTGGAGCATTTATTGGTGATGACCAAATTTATAATGTAATTGCTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAACTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACAAGCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3114 Chironominae sp. water mite diet isolate 3114-BHL032417-GBD25982_5855-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGAGATGACCAAATTTATACTGTAATTGGTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGTAGCCCCTGATTTGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATAACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3117 Chironominae sp. water mite diet isolate 3117-BHL032417-GBD12005_22239-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTGGTGCTTGTTCAGGTTTAGTAGGAACTTCTTTAAAATTATTAATCCGAACGGCCTTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTATTACTGCACATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3118 Chironominae sp. water mite diet isolate 3118-BHL032417-GBD22944_16697-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGCGTTTGCTCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTTATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGTTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCATTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3121 Chironominae sp. water mite diet isolate 3121-BHL032417-GBD10826_2740-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGTTTGATAGGGTATAGGAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTGGGTCTTCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGGTTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3122 Chironominae sp. water mite diet isolate 3122-BHL032417-GBD18983_27661-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGCTCAGGTATAGTAGTAACTTCTTTATGAATATTCATCCGAACGGAATTAGGTCATCCTGGAACTTTTATTGGTAATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGAGTTGGAAATTGTTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3124 Chironominae sp. water mite diet isolate 3124-BHL032417-GBD27578_9682-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGACATCCTGGAACATTTATTGGTTATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTAGATATTACCACTAATATTAGGAACCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3125 Chironominae sp. water mite diet isolate 3125-BHL032417-GBD19214_20017-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTGATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAATAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTAACACTAATATTAAGAGCCCCTGATATAGCCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3126 Chironominae sp. water mite diet isolate 3126-BHL032417-GBD15051_22866-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATTGTAGGAACTTCTTTAAGATTTTTAATCCGATCGGATTTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATGATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3128 Chironominae sp. water mite diet isolate 3128-BHL032417-GBD25661_24294-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTT-TTTTTGGAGCTTGATCAGGTATTGTAGGAACTTTTTTTAGGATTTTAATTCGAACGGGATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGTGCCCCTGATATGGCATTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACCTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3129 Chironominae sp. water mite diet isolate 3129-BHL032417-GBD2656_15084-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTGAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATAGTTACTTCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGGACCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3130 Chironominae sp. water mite diet isolate 3130-BHL032417-GBD11825_10823-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCAAACGGAATTAGGTCATCCTGGAACATTTATTGGTAATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCACCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTAACCTTATTACTTTCAAGAATAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3131 Chironominae sp. water mite diet isolate 3131-BHL032417-GBD22050_10494-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTCTTGGAGCTTGATCAGGTGTAGTAGGAACTTCTTTAAGAACATTAATCCGAACGGAATTAGGTCATCCTGGAACGTTTATTGGTGATGCCCAAATTTATAATGTAAGTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAGTTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3132 Chironominae sp. water mite diet isolate 3132-BHL032417-GBD24015_13528-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGATTTTATTATAATTTTTTTTACAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTATGAGACCCTGATATGGCTATTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTGATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3133 Chironominae sp. water mite diet isolate 3133-BHL032417-GBD13830_3802-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTTTGGAGGTTGATCAGGTATAGAAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGGCATCCTGTAAAATTTATTGGTTATGACCAATTTTAAAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3135 Chironominae sp. water mite diet isolate 3135-BHL032417-GBD9897_10521-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATTTTAATCCAAACGGAATTAGGTCCTCCTGTAACATTTATTGGTGATGACCAATTTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACTATCTCTTACTTTATTACTTTCAAGAATAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3138 Chironominae sp. water mite diet isolate 3138-BHL032417-GBD4003_12821-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTT-TTTTTGGAGCTTTATCCGGTATTGTAGGAACTTTTTTAAGAATTTTAATTTGGACGGGATTACGTCATCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATCATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3139 Chironominae sp. water mite diet isolate 3139-BHL032417-GBD18408_11139-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGTTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCAAACGGGATTAGGTCATCCTGGAATATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTATTTTGAGGATTTGGAAATTGGTTATTACCGCTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3140 Chironominae sp. water mite diet isolate 3140-BHL032417-GBD26119_21856-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGCGCTTGATCGGGTATAGTAGGAACTTCTTTAAGATTATTAATCCGACCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTATTTGGAGGATTTGGAAATTGGTTAATACCACTAAGATTAGGAGCCCCTGATTTGGCTTTTCCACGAATAAATAATATAAGATTTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3141 Chironominae sp. water mite diet isolate 3141-BHL032417-GBD2539_19698-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCATGTATAGTAGGAACTTCTTTAATAATATTAATCCGATCGAAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGGAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCCATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATACGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3145 Chironominae sp. water mite diet isolate 3145-BHL032417-GBD2434_16127-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGAGTTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTCTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATAATAGGAGCCCCTGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3147 Chironominae sp. water mite diet isolate 3147-BHL032417-GBD24504_21413-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAATATTTATTGGTGATGACCAAATTAATAATGTAATTGTTACTGCTCATTCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTTGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTCGATTATTACCATCATCTCTAACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3149 Chironominae sp. water mite diet isolate 3149-BHL032417-GBD12747_5732-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGGGCTTGAACAGGGATAGGAGGGACTTTTTTAAAATTTTAATCCGAAAGGGATTAAGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3152 Chironominae sp. water mite diet isolate 3152-BHL032417-GBD6881_19041-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTT-TTTTTGGAGCTTTATCCGGTATTGGAGGAACTTCTTTTAGGATTTTTATTTGGACGGGATTAGGGCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3157 Chironominae sp. water mite diet isolate 3157-BHL032417-GBD19090_15342-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTTATCCGGGATAGTAGGAACTTCTTTTAGAACATTAATCCGGACGGGATTAGGTCATCCTGGAACGTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTAATATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATGAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTCTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3158 Chironominae sp. water mite diet isolate 3158-BHL032417-GBD25278_21204-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGATCTTGATCAGGTATAGTATTAACTTCTTTAAGTATATTCATCCGCACGGAATTAGGTCCTCCTGGAACATTTATTGGTGATGACCAAATTTATAATTTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3160 Chironominae sp. water mite diet isolate 3160-BHL032417-GBD4630_17926-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATGGTAGGAATTTCTTTAGGATTTTTATTCCGACGGGAATTAGGTCATCTTGGAACATTTATTGGTGATGCCCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGTGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3162 Chironominae sp. water mite diet isolate 3162-BHL032417-GBD8760_3826-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTTTTTAAGATTATTATTCCGAACGGAATTTGGCCATCCTGGAACATTTATTGGTGATGACCAATTTTATAATGTAATTTTTACTGCTCATTCTTTTTTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCAGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3164 Chironominae sp. water mite diet isolate 3164-BHL032417-GBD15270_12145-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATATTGTAATTGTTATTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTACACGAATAAATAATATAAGATTTTGATTATAACCAACAGCTCTTACATTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3166 Psectrocladius sp. water mite diet isolate 3166-BHL032417-GBD7269_20036-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCATGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCAGGTTCCTTAATTGGAGAAGATCAAAATTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTATGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCGCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3169 Chironominae sp. water mite diet isolate 3169-BHL032417-GBD24974_6965-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTT-TTTTTGGAGCTAGATCAGGTATAGTAGGAACTTCTTTTAGAATATTAATCCGAACGGGATTAGGTCATCCTGGAACATTTAATGGTGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTCAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTAATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3170 Chironominae sp. water mite diet isolate 3170-BHL032417-GBD18684_9179-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAAACCTAACGGAATTAGGTCATCCTGTAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAGTTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTAATACTACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3172 Chironominae sp. water mite diet isolate 3172-BHL032417-GBD12724_28586-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGAACGGGTATATGAGGAACTTCTTTATGAATTTTATTCCGAACGGAATTAGGTCATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3173 Chironominae sp. water mite diet isolate 3173-BHL032417-GBD19040_24314-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAAAATTTTTTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTAAAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATGTAAGATTTTGATTATTACCACCATCTCTTACTGTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3174 Chironominae sp. water mite diet isolate 3174-BHL032417-GBD17518_26458-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATAAGGAATAATAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTAATCCTGGAAAATTTATTGGTTATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGATATTGGTTATTACCTCTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3175 Chironominae sp. water mite diet isolate 3175-BHL032417-GBD15388_13495-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGTTT-ATCCGGGATAAGAGGAACTTTTTTAAGAATATTTATCCGAACGGGATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGTCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3176 Chironominae sp. water mite diet isolate 3176-BHL032417-GBD2285_13203-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTCTTTTTGGATCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGCTGACCAAATTTATAATGTAATTGTTACTTCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGTAGCCCCTGATAGGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3177 Chironominae sp. water mite diet isolate 3177-BHL032417-GBD23494_9679-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGGGCTTGATCAGGTTTAGTAGGAACTTCTTTAAGATTATTAATCCGAACGGAATTAGGTCATCCTGGTACATTTATTGGTGATGACCAACTTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAACAATATAAGATTTTGATTATTACCAACATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3179 Chironominae sp. water mite diet isolate 3179-BHL032417-GBD29387_18207-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATCTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATTTAATTATTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAACTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCGGACGGGAGGACGGGCAAGAAGAAGAGGAGAAAAGGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3183 Chironominae sp. water mite diet isolate 3183-BHL032417-GBD8654_20555-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGTAGCTTGATTTGGTATAGTAGGAACTTTTTTATGAATATTAATCCGAACGGGATTATGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTATGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3184 Chironominae sp. water mite diet isolate 3184-BHL032417-GBD5887_15436-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGATTTTTAATCCGGACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATCTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTAGCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3185 Chironominae sp. water mite diet isolate 3185-BHL032417-GBD28211_18933-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTATCACTAATATTAGGAGCCCCAGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATAATTACCACCATCACTAACTTTATTACTTTCAAGAAGAACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3187 Chironominae sp. water mite diet isolate 3187-BHL032417-GBD18911_8526-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTTGGGGTTTGTTAGGGTATGGTAGGAATTTTTTTAGGAATTTTATTCGGAAGGGAATTAGGTCATCTTGGAACATTTATTGGTGATAACCAAATTTATAATGTAATTGTTACTGTTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3188 Chironominae sp. water mite diet isolate 3188-BHL032417-GBD13920_7369-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGGCCTTGTTCGGGTATAGTAGGAACTTCTTTAAGATTATTATTCCGCACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTCATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3189 Chironominae sp. water mite diet isolate 3189-BHL032417-GBD4901_14320-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGCACTTCTTTAAGAATATTAATCCGAACGGAATGTGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAAGATTTGGAAATTGGTTATTACCACTAATATTAGGTGCCCCTGATATGGCTTTTCCACGAATAAATGATATAAGATGTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3190 Chironominae sp. water mite diet isolate 3190-BHL032417-GBD24461_10119-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTTTAGTAGGAACTTCTTTAAGATTATTAATCCGAACGGATTTAGGTCATCCTGGAACATTTTTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTAATCCTACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3191 Chironominae sp. water mite diet isolate 3191-BHL032417-GBD26390_15396-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGACCGGTATTAGTTCATCCTGGAACATTTATTGGTGATGACTAAATTTAAAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTAGTACCACCATCTCTTACTTTATTACGTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3193 Chironominae sp. water mite diet isolate 3193-BHL032417-GBD23597_21719-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGCTCCGGTATAGTAGGAACTTCTTTAAGACTATTAATCCGATCGGAATTAGTTCTTCCTGGAACATTTTTTGGTGATGACCAAATTTATACTGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3194 Chironominae sp. water mite diet isolate 3194-BHL032417-GBD12331_21444-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTATTACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATAACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3200 Chironominae sp. water mite diet isolate 3200-BHL032417-GBD23430_17506-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGTTTGTCCAGGTAAAGTAGGAATTTCTTTAAGAATTTTATTCCGAACGGAATTAGGTCATCTTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAATTAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3201 Chironominae sp. water mite diet isolate 3201-BHL032417-GBD27000_19862-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGGGCATGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATTGAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATGGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATCAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATGATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3207 Chironominae sp. water mite diet isolate 3207-BHL032417-GBD8718_22157-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGTTATAGTAGGAACTTCTTTTAGAATTTTAATCCGAATGTAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTAATTTAATTGGAGGATTTGGAAATTAGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3208 Chironominae sp. water mite diet isolate 3208-BHL032417-GBD8725_3583-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTTAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTTTTGGTGATGACCAAATTTATAATGTACTTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGGAATACCAATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTATTATTAGGAGCCCCTGATACGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3209 Chironominae sp. water mite diet isolate 3209-BHL032417-GBD26054_16016-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATCTTTTTTTTTTGGAGCTTGCTCAGGTATAGTATGTACTTCTTTTTGAATTTTAATCCGAACGGAATTAGGTCATGCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGACTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAGTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3211 Chironominae sp. water mite diet isolate 3211-BHL032417-GBD20173_26342-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGCTGATGATCAAATTTATATTGTAATTGTTATTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATCTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTGCCACGAATAAATAATATAAGATTTTGATAATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3212 Chironominae sp. water mite diet isolate 3212-BHL032417-GBD23272_21447-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGTTGATTACCAAATTTATAATGTAATTGTTATTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGATCCCCTGATATGGCTTCTCCACGAATAAATAATATAAGATTTTGATTGTTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3215 Chironominae sp. water mite diet isolate 3215-BHL032417-GBD3803_13819-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGGGGCTTGATCAGGTTTAGTAGGAACTTCTTTAAGATTATTATTCCGAACGGAATTGGGTCATCCTGGAACTTTTATTGGTGATGACAAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCATTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3216 Chironominae sp. water mite diet isolate 3216-BHL032417-GBD20859_17459-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTT-TTTTTGGGGCTTGGTCAGGTATAGTTGGAACTTTTTTTAGAATTTTAATCCGGACGGGATTAGGTCCTCCTGGGACATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3217 Chironominae sp. water mite diet isolate 3217-BHL032417-GBD24949_12095-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGATCCCCTGATATGGCTTTTCCACGAAAAAAAAAAAAAGATTTTAATTATTTCCACCATCTCTTACTTTATAACTTGCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3220 Chironominae sp. water mite diet isolate 3220-BHL032417-GBD15093_7490-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTTATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATATAATTGTTACTGATCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGAAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATAACCAACATCTCTTACTTGATTACTGTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3221 Chironominae sp. water mite diet isolate 3221-BHL032417-GBD20414_26770-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGAAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAAAGTAATTGTTACTGCTCATGCCTTTATTATAATTTTTTTTTATGGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCGTCTCTTACTTTATTACTTTCAAGGATAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3225 Chironominae sp. water mite diet isolate 3225-BHL032417-GBD25980_11379-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCATTTTTATTTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGAAGCTCCAGATATGGCTTTCCCTCCAATAAATAATATAAGCTTTTGACTTCTTCCCCCCTTCATTAACTCTTTTACGATCAAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3226 Chironominae sp. water mite diet isolate 3226-BHL032417-GBD24878_12002-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTCTTTTTGGAGCTTGATCAGGTATATTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATACTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTCATTATTACCACCATCTCCTACTAAATTACTTTCAAGAAGAATAGTATAAAATGGCGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3227 Chironominae sp. water mite diet isolate 3227-BHL032417-GBD6212_19169-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTGTATTTT-TTTTTGGGGCTTGATCAGGGATAGTAAGAACTTCTTTTAGAATTTTAATCCGGACGGGATTAGGTCATCCTGGAACATTTATTGGTGATTAACAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3228 Chironominae sp. water mite diet isolate 3228-BHL032417-GBD11887_26227-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAATGGAATTAGGTCATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGTTTTGGAAATTGTTTATTACCACTAATATTAGGAGCCCCTGATATAGTTTTTCCACGAATAAATAATATAAGATTATGATTATTACCACCATCTCTTACCTTATTTCTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3229 Chironominae sp. water mite diet isolate 3229-BHL032417-GBD21762_18424-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGACCTTGTTCGGGTTTAGTGGGAACTTCTTTAAGATTATTATTCCGAACGGAATTAGGTCATCCTGAAACGTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAAAAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3230 Chironominae sp. water mite diet isolate 3230-BHL032417-GBD18463_8641-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCAGGTATTGTAGGAACTTCTTTAAGATTATTATTCCGAACGGTATTAGGTCATTCTGGAACATTTATTGGTTATGACCAAATTTATAATGTATTTGTTACTGCCCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTAAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCAGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTATCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3235 Cricotopus sp. water mite diet isolate 3235-BHL032417-GBD11144_15847-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAAAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTCCTGCTCATGCTTTTGTATTAATTTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTTCCCCCGTCTTTAACATTACTATTATCAAGCTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3237 Chironominae sp. water mite diet isolate 3237-BHL032417-GBD26793_21173-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCGGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTCTTCAACGAATAAATAATATAAAATTTTGATTATTACCACCATCTCTTACTCTATTACATTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3242 Chironominae sp. water mite diet isolate 3242-BHL032417-GBD28121_12959-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTT- TTTTTGGAGCTTGATCAGGTATTGTAGGAACTTCTTTTAGAATATTAATCCGAACGGGATTTGGTCATCCTGGAACATTTATTGGTGATTACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCACCATCACTTACCTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3245 Chironominae sp. water mite diet isolate 3245-BHL032417-GBD16919_6855-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGGACTTGATCAGTTTTGTTGGGACCTTTTTTAGAAATTTTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3246 Chironominae sp. water mite diet isolate 3246-BHL032417-GBD4458_8694-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCAGCTATAGTTGGAACTTCTTTAAGTATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTATTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTAGTTATTACCACTAATATTAGGAGCCTCTGATATGGCTGTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTGCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3247 Chironominae sp. water mite diet isolate 3247-BHL032417-GBD24937_8604-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGGGCTTTGTCAGGTTTAGTAGGAAATTCTTTTAGAATTTTAATCCGAACGGAATTAAGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCACATGCCTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3248 Chironominae sp. water mite diet isolate 3248-BHL032417-GBD2554_17187-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGGGCTTGATCGGGTTTAGTAGGAACTTCTTTAAGATTATTATTCCGACCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTCTAATGTAATGGTTACTGCTCATGTTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3250 Chironominae sp. water mite diet isolate 3250-BHL032417-GBD18448_24534-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGAACAGGTATAGTAGGAACTTCTTTTAGAATATTAATTCGAACGGAATTAGGTCAACCTGGAACATTTATTGGTGATTATCAAATTTATAATGTAATTGTTATTGCTCATGCTTTTATTATATTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTCCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3252 Chironominae sp. water mite diet isolate 3252-BHL032417-GBD17939_23934-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTT- TTTTTGGAGCTTTATCAGGTATAGTAGGTACTTCTTTTAGAATATTAATCCGTACGGAATTTGGTTATCCTGGAACATTTATTGGTAATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3254 Chironominae sp. water mite diet isolate 3254-BHL032417-GBD21908_16015-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCCGGTATAGTATGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTTATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTACTCATGCTTTTATTATAATTTTTTTCATAGTAATACCGATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATGTGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATCACCACCATCTCTTACTTTACTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3258 Chironominae sp. water mite diet isolate 3258-BHL032417-GBD18633_23771-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCATATTTATAATGTAATTGTTACTGCTAATGGTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3262 Chironominae sp. water mite diet isolate 3262-BHL032417-GBD21883_13272-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTTTGGGGCTTGTTCGGGTTTGTTAGGAACTTCTTTAAAATTATTATTCCGAACGGAATTGGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3264 Chironominae sp. water mite diet isolate 3264-BHL032417-GBD15772_27425-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGACCATGTATAGTAGTAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAACTTTTTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCTTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCTTCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3265 Chironominae sp. water mite diet isolate 3265-BHL032417-GBD18541_5361-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGACCTTGACCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCTGAACAGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCCAATTTATAATGTAATTGTTACTGCCCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGGAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3268 Chironominae sp. water mite diet isolate 3268-BHL032417-GBD24188_8756-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTT-TTTTTGGAGCTTTATCAGGTATAGTAGGAACTTCTTTCAGAATATTTATCCGGACGGGATTTGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCAGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3272 Chironominae sp. water mite diet isolate 3272-BHL032417-GBD27742_13980-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCGGGTCTAGTAGGAACTTCTTTAAGATTTTTAATCCGAACAGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATCTTGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3276 Chironominae sp. water mite diet isolate 3276-BHL032417-GBD3997_22023-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGTTCATCCTGTAACATTTATTGGTGATGACCAAATTTATAATTTAATTGTTACTGCTCATGTTTTTATTATAATTTTTTTGTATAGTAATACATAGTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3278 Chironominae sp. water mite diet isolate 3278-BHL032417-GBD25748_14188-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGTTTGCTCGGGTATAGTAGGAACTTCTTTAAAAATTTTAATCCGTTCGGAATTAGGTCCTCCTGTAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTAACACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3279 Chironominae sp. water mite diet isolate 3279-BHL032417-GBD29546_16648-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTACTCGGTTTTAGTAGGAACTTCTTTAAGATTATTAATCCGATCGGAATTAGGTCATCCTGGCACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCATTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3282 Chironominae sp. water mite diet isolate 3282-BHL032417-GBD17722_26834-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAATTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCTTGGAAAATTTATTGGAGATGACCAAATTTATAAAGTAATTGGTATTGTTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3284 Chironominae sp. water mite diet isolate 3284-BHL032417-GBD23023_15053-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTCTTTTTTTGGAGCTTGAACAGGTATAGTAGGAACTTCTTTAAGAATAGTAATCCGAACGGAATTATGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTTATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATGTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAATAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3286 Chironominae sp. water mite diet isolate 3286-BHL032417-GBD16939_11657-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTTGTCCGGTATAGTAGGGACTTCTTTTAGAATATTTATCCGAACGGGATTAGGTCATCCTGGAACATTTATTGGTGATTACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATAATTACCACCATCTCTTACTTTATTACTTTCATGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3288 Psectrocladius sp. water mite diet isolate 3288-BHL032417-GBD28583_13789-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCAGTTCCTTAATTGGAGATGATCAAATTTATAATGGAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCTCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCTGTCAGTAACTTTACTATTATCTAGCTCTCTAGTTTAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3290 Chironominae sp. water mite diet isolate 3290-BHL032417-GBD27797_20395-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTT-TTTTTGGAGCTTGATCCGGTATTGTTGGGACTTCTTTTAGAATTTTTATCCGGACGGGATTTCGTAATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTTTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTCTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3294 Chironominae sp. water mite diet isolate 3294-BHL032417-GBD12352_19143-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTAATCAGGTTTAGTAGGAATTTCTTTAAGATTATTATTCCGAACGGAATTGGGCCATCCTGGAACATTTATTGGTGATGACCAATTTTATAATGTAATTGCTACTGTTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3295 Chironominae sp. water mite diet isolate 3295-BHL032417-GBD14529_14875-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAAACCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTCCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGTCTTTTACACGAATAAATAATATAAGATTTTGATTATAGCCACCATCTCGTACATTATTACGGTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3298 Chironominae sp. water mite diet isolate 3298-BHL032417-GBD9917_6964-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTT-TTTTTGGAGCTTTATCAGGTATAGTAGGAACTTCTTTTAGAATTTTTATTCGAACGGAATTAGGGCCTCCTGGGACATTTATTGGTGATGACTAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3299 Chironominae sp. water mite diet isolate 3299-BHL032417-GBD10729_14949-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGGAGCTTGCTCGGGTATAGTGGGAATTTCTTTAGGAATTTTATTCCGACGGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAATTTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCCGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3300 Chironominae sp. water mite diet isolate 3300-BHL032417-GBD23136_6692-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGTATATTAATTCGAACGGAATTAGGACAACCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCAAGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGTTTTGGAAATTGATTATTACCTCTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTAACTTTATTACTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3302 Chironominae sp. water mite diet isolate 3302-BHL032417-GBD16799_22901-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGGGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATAACAACAATCTCTAACATTGTTACTTTCAAGGAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3303 Chironominae sp. water mite diet isolate 3303-BHL032417-GBD12925_6558-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTT-TTTTTGGAGCTTTATCCTGTATAGTTGGAACTTCTTTTTGAATTTTTATCCGGACGGGATTATGTCATCCTGGAACATTTATTGGTGATTACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTAGTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3304 Chironominae sp. water mite diet isolate 3304-BHL032417-GBD15309_19718-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGCATAGTAGGAACTTCTTTTAGAATATTAATCCGAACGGAATCAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTATATTATAATTTTTTTTATAGTAATACCTATTTTAATGGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGATCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCAACTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3307 Psectrocladius sp. water mite diet isolate 3307-BHL032417-GBD24470_7817-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTAGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTTGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAAATGGAGGATTTGGAAATTGATTAGTAACATTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACATTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3308 Chironominae sp. water mite diet isolate 3308-BHL032417-GBD14200_26826-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTTAGAATATTAATTCGAACTGGATTAAGTCATCCTGGAAAATTTATTGGTGATGACCTAATTTATAATGTAATTGTTAATGCTCTTGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTATTTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3310 Chironominae sp. water mite diet isolate 3310-BHL032417-GBD23478_22669-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCGGGTTTAGTAGGAATTTCTTTAAGATTTTTATTCCGACCGGATTTAGGTCATCCTGGAACTTTTTTTGGTGATGACCAATTTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAGTACCTATTTTAATTGGAGGACTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3311 Psectrocladius sp. water mite diet isolate 3311-BHL032417-GBD21743_27496-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATCTGAGCAGAACTCGGCCACGCCGGTTCCTTAATTGGAGATGTTCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTAAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTCTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3312 Chironominae sp. water mite diet isolate 3312-BHL032417-GBD19691_28249-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGTTTTATTGGGAACTTCTTTAAGATTATTAATCCGATCGGAATTAGATCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTATTTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAACTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3316 Chironominae sp. water mite diet isolate 3316-BHL032417-GBD10780_12308-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGGATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGGATTAAGTCATCCTTGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTCTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTAACACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACCTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3317 Chironominae sp. water mite diet isolate 3317-BHL032417-GBD8290_6439-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGGGCTTGATTAGGTATAGTAGGAACTTTTTTAGGAATATTAATCGGAACGGAATAAGGTCATCCTGGAACATTTATTGGTGATTACAAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTCCCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3319 Chironominae sp. water mite diet isolate 3319-BHL032417-GBD5684_11654-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAACTTGATCATGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTGTTTTAATTGAAGGATTTGGAAATTGGTTATTACCACTAATATTAGGATCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCGTACTTTATGACGGTCAAGAAGAATAGGAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3322 Chironominae sp. water mite diet isolate 3322-BHL032417-GBD18780_27772-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGATCTTGATCAGGTATAGTAGTAACTTCTTTAAGATTTTTAATCCGAACGGTATTAGGTCATCCTGGAACATTTATTGGTGATGTCCAAATTTATAATGTATTTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTGCCACGAATAAATAATATAAGATTTTGATTATGACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3323 Chironominae sp. water mite diet isolate 3323-BHL032417-GBD15129_8524-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGATCTTCTTTAAGAATATTAATCCCGGACGGAATTAGGTCACCCTGGAACATTTATTGGTGATAACCAAATTTCTAATGAAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTCGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3326 Chironominae sp. water mite diet isolate 3326-BHL032417-GBD11510_6560-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGTTCAGGAATAGTAGGAACTTCTTTAGGATTATTATTCCAAACGGAATTGGGCCATCCTGGAACTTTTATTGTTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3327 Chironominae sp. water mite diet isolate 3327-BHL032417-GBD26734_16944-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATTCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTTCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGTTTTTCCACGAATAAATAATAAAAGAAATTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTATAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3328 Chironomidae sp. water mite diet isolate 3328-BHL032417-GBD6511_8186-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTT-TTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAAATTATAATGTAATTGTAACTGCTCACGCGTTTGTAATGATTTTCTTCTTAGTAATGCCTGCAATGATTGGAGGTTTTGGTAACTGGTTTGTTCCTTTAATGATTGGAGCTCCTGATATGGCCTTCCCTCGATTAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3331 Chironominae sp. water mite diet isolate 3331-BHL032417-GBD28544_18786-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATATTAATCCGAACGGAATTAGGTCATCCTGGTACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCTTTTTTAATTGGAGGATTTGGAAATTGGTTATTATCACTAATATTAGGAGCCCCTGATATGGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTAGCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3334 Chironominae sp. water mite diet isolate 3334-BHL032417-GBD14662_5883-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGAGCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTTTAACATTTATTGGTTATGACCAATTTTAGAATGTAATTGTTACTTCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACAACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGTATAAATAATATAAGATTTTGATTATTACCCCCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3336 Chironominae sp. water mite diet isolate 3336-BHL032417-GBD17934_28137-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCACTATATTTTTTTTTTGGAGCTTGATCAAGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGTTGATGACCAAATTTATAATGTAATTGTTACGACTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATATCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAA	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3340 Chironominae sp. water mite diet isolate 3340-BHL032417-GBD9274_14376-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTT-TTTTTGGAGCTTGATCAGGGATAGTAGGAACTTCTTTATGAATTTTAATTCGGACGGGATCTGGTCATCCTGGAACATTTATTGGTGATGACTAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3341 Chironominae sp. water mite diet isolate 3341-BHL032417-GBD9111_18503-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGCGCTTGATCAGGTATAGTAGGAACTTATTTAAGTATATTAATCCGAACGGAAGTAGGTCATCCTGGAACATTTTTTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTAAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTATTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3345 Chironominae sp. water mite diet isolate 3345-BHL032417-GBD24510_6161-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAATGATATTAATCCGAACGGAATTAGGTCGTCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGTTCATGCCTTTATTATAATTTTTTTTATAGTAATACCTATTTAAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3348 Chironominae sp. water mite diet isolate 3348-BHL032417-GBD15635_7793-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTT-TTTTTGGAGCTTGATCAGGTATAGTAAGAACTTCTTTTAGAATATTAATCTGAACGGAATTAGGTCATCCTTGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGTTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGTCCCTGATATGACTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3349 Chironominae sp. water mite diet isolate 3349-BHL032417-GBD23330_15444-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTT-TTTTTGGAGCTTAATCAGGTATAGTAGGAACTTCTTTTAGATTATTAATCCGGACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTATTTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGGGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTAGCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3354 Chironominae sp. water mite diet isolate 3354-BHL032417-GBD10051_20282-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGGGCTTGCTCAGGTATAGTAGGAACTTCTTTAAGATTATTAATCCGAACAGATTTAGGTCAACCTGGAACATTTATTGGTGATGACAAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTAGAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGTTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3355 Chironominae sp. water mite diet isolate 3355-BHL032417-GBD17565_3617-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTT-TTTTTGGAGCTTGAGCAGGTATAGTAGGAACGTCGTTAAGAAGATTAAGCCGAACGGAAGTAGGTCATCCTGTTACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3357 Chironominae sp. water mite diet isolate 3357-BHL032417-GBD23077_5544-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGACCTTGATCGGGATTAGTGGGAATTTTTTTAGGATTTTTATTCGGATTGGAATTAGGTAATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3358 Chironominae sp. water mite diet isolate 3358-BHL032417-GBD16667_9319-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCTGGTATAATAGGAACTTCTTTAAGAATATTAATTCGAACGTAATTAGGTCAACCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGTTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3359 Chironominae sp. water mite diet isolate 3359-BHL032417-GBD27929_12250-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTCTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATCCGAACGGACTTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTAATATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCTATGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCAGCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3360 Chironominae sp. water mite diet isolate 3360-BHL032417-GBD27128_17071-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCGGGTTTATTAGGAACTTCTTTAATATTCTCAATCCGATCGGATTTAGGTCATCCTGGAACATTTATTGGTGTTGACCAATTTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTATCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3362 Chironominae sp. water mite diet isolate 3362-BHL032417-GBD22609_21310-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGATTGATCCGGTATAGTAGGAACTTCTTTAAGTATATTAATCCGAACGGGATTAGGTCATCCTGGAACATTTTTTAGTGATTACCAAATTTATAATGTAATTGTTACTGCTCATTCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3363 Chironominae sp. water mite diet isolate 3363-BHL032417-GBD14015_5497-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTTTTGGAGCTTGAGCAGGAATAGTAGGAACTTCTTTAAGAATATTAATCCGAACAGAATGAGGTCATCCTGTAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTTCTCATGCTTTCATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3365 Psectrocladius sp. water mite diet isolate 3365-BHL032417-GBD19218_14903-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCCTGATCCGGTATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGCTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGGTTTTGAATACTTCCCCCGTCATTAACTTTACTATTATCTAGCACGCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3370 Chironominae sp. water mite diet isolate 3370-BHL032417-GBD25019_9127-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATTGTAGGAACTTCTTTATGAATATTAATCCGAACGTAATTAGGTCATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAGTTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTATGAGCCCTTGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCAACTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3371 Chironominae sp. water mite diet isolate 3371-BHL032417-GBD17033_10904-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACAGAATTAGGGCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCTCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGACTATTACCACCATCTCTTACTTTATTACTTTTAAGAAGAATAGTAGAAGATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3373 Chironominae sp. water mite diet isolate 3373-BHL032417-GBD24511_9852-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCGGGTTTAGCAGGAACTTCTTTAAGAATATTAATCCGAACGAAATTGGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTATTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGTCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTAGTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3374 Chironominae sp. water mite diet isolate 3374-BHL032417-GBD25778_7440-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTTTTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTTAGAATATTAATTCGAATGGAATTCTGACATCCTGGAACATTTATTTGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTTTTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3376 Chironominae sp. water mite diet isolate 3376-BHL032417-GBD3147_14368-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGAAGGAACTTCTTTAAGATTATTAATCGGACCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACAAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGAAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCATGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3377 Chironomus riparius water mite diet isolate 3377-BHL032417-GBD22219_12443-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACACTATTTTTTGGGGCTTGATCCGGCATAGTGGGAACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACAACCCGGAACTTTCATTGGAGATGGCCAAATTTATAATGTTGTAGTTACTGCCCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTGCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3379 Chironominae sp. water mite diet isolate 3379-BHL032417-GBD24794_15852-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTAGAGCTTGCTCAGGTATAGTAGGAAATTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGTACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGATCATGCTTTTATTATAATTTTTTTATATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGTAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3381 Chironominae sp. water mite diet isolate 3381-BHL032417-GBD19054_21974-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCGGGTATAGTAGGAACTTCTTTAAGATTATTATTCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTAGTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAACATAAGATTTTGATTATAACCACCATCTCTAACCTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3384 Chironominae sp. water mite diet isolate 3384-BHL032417-GBD3823_13828-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGGGCCTTGATC-GGTATTATTAGGAACTTCTTTAGAATTTTTATTCCGACCGGACTTGGGTCATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3386 Chironominae sp. water mite diet isolate 3386-BHL032417-GBD21659_24487-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTTAGAATATTAATCCGAATGGAATTAGGTCATCCTGGAATATTTTTTGGTGATGACCAAATATATAATGTAATTGTTACTGCTCATGCTTTTATTATAATATTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCGCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3387 Chironominae sp. water mite diet isolate 3387-BHL032417-GBD7203_22455-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTGTTTTGGAGCTTGATCAGGTTTAGTAGGAACTTCTTTAAGAATATTATTACGTACGGAATTGGGTCATCCTGGAACATTTATTGGTGATGCCCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGCTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3389 Chironominae sp. water mite diet isolate 3389-BHL032417-GBD7955_19234-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTT-TTTTTGGGGCTTGATCGGGTATTGTTGGAACTTCTTTTAGAATATTTATCCGGACGGAATTTGGATATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3390 Chironominae sp. water mite diet isolate 3390-BHL032417-GBD22468_12941-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTTTATTTTTTTTTTGGAACTTGATAAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGGACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTTCCACTAATATTAGGAGCCCCTGATATAGCATTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3391 Chironominae sp. water mite diet isolate 3391-BHL032417-GBD18223_3332-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTTTGGAGCTTGAGCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTGTTGCTGATGACCAATTTTAAAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3397 Paratanytarsus sp. water mite diet isolate 3397-BHL032417-GBD29405_17248-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCTCATCGGGAACCCGGCGGCGAGCAAGAAGA-GGGGGGAAAAGGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3400 Chironominae sp. water mite diet isolate 3400-BHL032417-GBD25941_6905-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTAATCAGTAATATAAGTAACTTCTTTATGAATTTTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACGGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3402 Chironominae sp. water mite diet isolate 3402-BHL032417-GBD21516_18025-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGCTCTGGTTTAGTAGTAACTTCTTTTATAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTAACACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGATTAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3405 Chironominae sp. water mite diet isolate 3405-BHL032417-GBD14417_3780-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTTTATTTTTTTTTTTGGAGCTTGAGCAGGGATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACTTTTATTGGTTATGACAAAATTTAGAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3407 Chironominae sp. water mite diet isolate 3407-BHL032417-GBD12587_8360-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGCGCTTGACCAGGATTAGTAGGAATTTTTTTAGGATTTTTATCCGGAAGGGAATTAGGTCTTCCTGGAACATTTTTTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3408 Chironominae sp. water mite diet isolate 3408-BHL032417-GBD8822_14266-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGGGCTTGATCAGGTATAGTAGGTACTTCTTTTAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCCCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTATCACTGATACTAGGAGCCCCTGATATGACTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3409 Chironominae sp. water mite diet isolate 3409-BHL032417-GBD5224_15301-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCGGGTATAGTAGGAACTTCTTTAAGAATTTTAATCCGAACGGAATTAGGTCATCTTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGGTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCATACTTTATTACTTTCAAGAAGACTAGTAGAAAATGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3411 Chironominae sp. water mite diet isolate 3411-BHL032417-GBD27021_18015-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCGGGTATATTAGGAACTTCTTTAAGAATATTAATCTGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3413 Chironominae sp. water mite diet isolate 3413-BHL032417-GBD25208_15643-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTTTTTTAGAATATTAATTCGAACGGAATTAGGTCCTCCTGGAAAATTTTTTGGTGATGACCAAATTTATAATACAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATATGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3414 Chironominae sp. water mite diet isolate 3414-BHL032417-GBD22062_12992-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTTATCAGGTATATTAGGAACTTCTTTAAGAATATTAATCCGAACGGCATTAGGTCATCCTGGAACATTTATTGGTTATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTGTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATGATTACCACCATCGCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3416 Chironominae sp. water mite diet isolate 3416-BHL032417-GBD24757_19609-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATCTTTTTTTTTTTGGAGCTTGATCTGGTTTAGTAGTAACTTCTTTTAGATTTTTAATCCGAACGGAATTAGTTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTAGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTAATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3419 Chironominae sp. water mite diet isolate 3419-BHL032417-GBD26771_10813-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAATTTTTTTAAGAATATTAATCCGTACGGAATTAGGTAATCCTGGAACATTTATTGGTGATGTCCAAATTTATAATGTAATTGTTATTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATGATATAAGATTTTGATTATTACCACCATCTCTTACTTTAGTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3421 Chironominae sp. water mite diet isolate 3421-BHL032417-GBD8508_18900-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTT-TTTTTGGAGGTTGATCAGGTATTGTAGGAACTTCTTTTAGGATTTTTATCCGGACGGGATTAGGGCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGTTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTTTTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACCTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3425 Chironominae sp. water mite diet isolate 3425-BHL032417-GBD26865_23260-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGGATAGGTGGAACTTCTTTTAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATTCCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCCCTAAAATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGAATTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3426 Chironominae sp. water mite diet isolate 3426-BHL032417-GBD7961_4448-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGTTATATTAGGAACTTCTTTAAGAATATTATTCCGAACGGAATTAGGTCATCCTGGAACATTTATTGTGGATGACCAATTTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACTACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTACATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3428 Chironominae sp. water mite diet isolate 3428-BHL032417-GBD17843_28470-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGAAGCTTGATCAGGTATATTAGGATCTTCTTTAAGAATTTTAATCCGACCGAAATTAGGTCATCCTGGAACATTTATTGTTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3430 Chironominae sp. water mite diet isolate 3430-BHL032417-GBD11733_28237-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTG-AGCTTTATCAGGGATTGGAGGGACTTCTTTTAGAATTTTAATCCGGACGGGATTAGGGCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGCTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTATTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTATTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3431 Chironominae sp. water mite diet isolate 3431-BHL032417-GBD8309_23280-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGGTTGGTTAGGGATAGTAGGAACTTTTTTTAAAATATTAATTCGGACGGAATTTGGTCATCCTGGAAAATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATTCCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3432 Chironominae sp. water mite diet isolate 3432-BHL032417-GBD10368_13050-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTATGTCATCCTGTAACATTTATTAGTGATTACTAAATTTATAATGTAATTGTTACTGCTCATGATTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3433 Chironominae sp. water mite diet isolate 3433-BHL032417-GBD21142_23588-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGGAGCTTGTTCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAACTTGGTTATTACCACTAATATTAGGAGCCCATGATATGGCTTTTACACGAATAAATAATATAAGACTTGGATTATTACCACCATCTCTAACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3434 Chironominae sp. water mite diet isolate 3434-BHL032417-GBD28217_19698-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTATTTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTTTTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGTTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCATTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTTACTTTATTACTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3439 Chironominae sp. water mite diet isolate 3439-BHL032417-GBD17311_5573-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTT--TTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAAGTAGGTAATCCTGGAACATTTATTGGTGATGACCAAAGTTATAAGGTAATTGTTACTGCTCAGGCTTTTATTATAAGTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3440 Chironominae sp. water mite diet isolate 3440-BHL032417-GBD25909_11460-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTT-TTTTTGGGGCTTGATCGGGTATAGTAGGAACTTTTTTAGAATTTTAATCCGGAGGGAATTAGGTCATCCTGGAACATTTATTGGTGAAGATCAAATTTATAATGTAATTGTTAATGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3445 Chironominae sp. water mite diet isolate 3445-BHL032417-GBD22186_18681-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGATCGTGATCAAGTATAGTAGGAACTTTTTTAAGAATTTTTATCCGAACGGAATTAGGTCCTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3446 Chironominae sp. water mite diet isolate 3446-BHL032417-GBD9530_14278-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTT-TTTTTGGAGCTTTGTCCGGTATTGTAGGAACTTCTTTAAGGATATTTATCCGGACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACTAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACCATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3447 Chironominae sp. water mite diet isolate 3447-BHL032417-GBD10351_3916-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGACCTTTCTAGGTTATAGTAGGAACTTTTTTAAGAATTTTAATCCGAACGGAATTGGCTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGTTCATGCGTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3448 Chironominae sp. water mite diet isolate 3448-BHL032417-GBD14156_14685-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGGCCTTGATCGGGTTTATT-GGAACTTTTTTTAGGATTATTATTCCGAAGGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTATTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3450 Chironominae sp. water mite diet isolate 3450-BHL032417-GBD6582_8004-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTTTTTTTGGAGCATGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAAAATTTATTGGTGCTGACCAAATTCATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTAGTTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3452 Chironominae sp. water mite diet isolate 3452-BHL032417-GBD27805_21539-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCAGGTATAGTGGGAACTTCCTTAAGAATTTTAATCCGAACGGAATTAGGTCTTCCTGGAAGATTTATTGGTGATGACCAAATTTATAATCTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTACTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAGTAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3456 Chironominae sp. water mite diet isolate 3456-BHL032417-GBD21235_13088-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTCTAGTAGGAACTTCTTTAAGGATATTAATCCGAACGGGATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATCGGAGGTTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCATTTCCACGAATAAATAATATAAGATTTTGATTATTATCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3457 Chironominae sp. water mite diet isolate 3457-BHL032417-GBD12170_12359-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTGTATTTTTTTTTTGGAGTTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGCATTTGGTCATCCTGGAACATTTATTGGTGATGCCTAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACATTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3465 Oligochaeta sp. water mite diet isolate 3465-BHL032417-GBD27955_9532-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGAAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGCATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTGTCCCTCGCCTTAACTATTAAAGATTCTGACTACTCCCACCTTCGCTAATCCTATTAGTTTCTTCTGCTGCCGTATAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL3467 Chironominae sp. water mite diet isolate 3467-BHL032417-GBD22415_10727-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCCTTATATTTTTTTTTTTTGGAGCTTGCTCGGGTATAGTAGGAATTTCTTTAAGTATTTTTATCAGAACGGAATTAGGTCATCCTGGAATATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGTTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3468 Chironomus sp. water mite diet isolate 3468-BHL032417-GBD25248_24587-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTAATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACAAACCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTACTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3470 Chironominae sp. water mite diet isolate 3470-BHL032417-GBD17381_8019-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGTTATAGTAGGAACTTCTTTAAGATTATTAATCCGACCGAAATTAGTTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATTTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGTCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTGTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3474 Chironomus sp. water mite diet isolate 3474-BHL032417-GBD24263_22825-Ldc30 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACACATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTAGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGATATATCTTTCCCCTGAATAAATAATATAAGATTTTAATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3477 Parachironomus sp. water mite diet isolate 3477-BHL032417-GBD15258_22004-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTACCTTGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTAACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3478 Parachironomus sp. water mite diet isolate 3478-BHL032417-GBD4097_10888-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTGATTGGTGATGATCAAATTTACATTGTATTTGTAACGGCACATGCTTTTATTATATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCCGGAATAAAAAATATAAGTTTTTGACTTCTTCCCCATTTCTTTGACTCTTTTACTTTCTAGTTCAAACGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3480 Chironomus riparius water mite diet isolate 3480-BHL032417-GBD24629_11221-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTAAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAATTAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3483 Chironomus entis water mite diet isolate 3483-BHL032417-GBD5765_10837-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTTTTATAGTTATACCTATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGATATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACATACATTACTCCTTTCAAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3484 Cricotopus sp. water mite diet isolate 3484-BHL032417-GBD26906_15875-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTATGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCCTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3489 Chironomus crassicaudatus water mite diet isolate 3489-BHL032417-GBD13318_12482-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTTTATATATTATTTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTAACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3490 Lebertia sp. water mite diet isolate 3490-BHL032417-GBD9348_6499-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAGTTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCGTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCCGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3491 Parachironomus sp. water mite diet isolate 3491-BHL032417-GBD11476_11999-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCAGGAAAAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGAACGATCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAAATGATTAGTTCCTCTTATATTAGGGACTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3492 Orthocladius sp. water mite diet isolate 3492-BHL032417-GBD17861_13203-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAATAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTTATGGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR741487, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3493 Chironomidae sp. water mite diet isolate 3493-BHL032417-GBD4649_19099-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGTATTCCCTCGAATAGATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3495 Chironomus sp. water mite diet isolate 3495-BHL032417-GBD18836_16090-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCCTTCCTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID KR941561, identified in GenBank as Chironomus quinnitukqut. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3496 Parachironomus sp. water mite diet isolate 3496-BHL032417-GBD17946_6287-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTAAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCTCTTACATTACTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3497 Chironomus crassicaudatus water mite diet isolate 3497-BHL032417-GBD22331_15418-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGCCCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCTATCTTTAACTCTTCTTCTTTCTAATTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3498 Chironomus sp. water mite diet isolate 3498-BHL032417-GBD15686_16758-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAACTAGGACGACCCGGAACTTTCATTGGAGATGACCATATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3500 Orthocladius sp. water mite diet isolate 3500-BHL032417-GBD11690_17417-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTGTTATAATTTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAAGTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR291764, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3501 Chironomus sp. water mite diet isolate 3501-BHL032417-GBD14599_15590-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATATTTTATTTTCGGTGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTAGAAAAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3502 Chironomidae sp. water mite diet isolate 3502-BHL032417-GBD12107_15283-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTGTATTCGGAGCCTGATCAGGTATAGTAGATACTTCCCTTAGTAATCTAGTACGAGCTGAATTAGGACACCCCGGGGCATTAATTGGAGACGATCAAATTTATAACGTAATGGTTACAGCTCATGCCTTTGTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGATTAGTATTACTAATATTAGGTGCACCAGATATAGCTTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3503 Parachironomus sp. water mite diet isolate 3503-BHL032417-GBD19403_6588-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTATTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3504 Chironomus sp. water mite diet isolate 3504-BHL032417-GBD14750_10737-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGATATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACTTCCCCCATCACATACATTACTCCTTTCAAGTTCATTTGTAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3505 Chironomus sp. water mite diet isolate 3505-BHL032417-GBD13134_18506-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTCTTTACATTATTTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTTTAAGTATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTATGGGCCCCTGATATAGCTTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.7% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3506 Chironomus sp. water mite diet isolate 3506-BHL032417-GBD18637_9211-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGAGGCTTGATCCGGAATAGTGGGAACTTCATTAACAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACATCTTCCCCCATTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3507 Chironomus sp. water mite diet isolate 3507-BHL032417-GBD15842_20860-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGAACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTAGAAAAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3508 Parachironomus sp. water mite diet isolate 3508-BHL032417-GBD24690_6370-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTCTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3509 Chironominae sp. water mite diet isolate 3509-BHL032417-GBD6723_22997-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTATATTTTATTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTTGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGGAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3510 Glyptotendipes sp. water mite diet isolate 3510-BHL032417-GBD16189_11789-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATATTGGCACATTATATCTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACGTCTTTAAGTATGCTAATTCGAGCAGAAATAGGACGACCTGGAACTTTTATTGGAGATGACCAGATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATATTTTTTTTTTATAGTTATACCTATTTTAATTGGAGGACTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.4% identical to accession ID KP954645, identified in GenBank as Glyptotendipes senilis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3511 Parachironomus sp. water mite diet isolate 3511-BHL032417-GBD18500_27351-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTCTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGTCTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3512 Lebertia sp. water mite diet isolate 3512-BHL032417-GBD19010_6971-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAGTTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3513 Parachironomus sp. water mite diet isolate 3513-BHL032417-GBD11714_17502-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGGACACCCGTAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCAAATAAATAATATAAGTTTTTAACTTCTTCCCCCTTCTTTGACTCTTTAACTTTCTAGTTCAATTGTAGAAAATGGGGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3514 Glyptotendipes sp. water mite diet isolate 3514-BHL032417-GBD3604_17506-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATATTGGCACATTATATCTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACGTCTTTAAGTATACTAATTCGGGCAGAAATAGGACGACCTGGAACTTTTATTGGAGATGACCAGATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATATTTTTTTTTTATAGTTATACCTATTTTAATTGGGGAATTTGGAAATTGATTAGTCCCTCTTATGCTGGGAGCTCCTGATAAGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KP954645, identified in GenBank as Glyptotendipes senilis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3515 Chironominae sp. water mite diet isolate 3515-BHL032417-GBD11005_11236-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTCTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3517 Parachironomus sp. water mite diet isolate 3517-BHL032417-GBD5608_21238-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCAGATCTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCGCATGCTTTTATTCTAGTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTACTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCCTTCTTTGACCCTTTTACTTTCTAGTTCAATTGTAGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3518 Chironominae sp. water mite diet isolate 3518-BHL032417-GBD11636_24831-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3519 Parachironomus sp. water mite diet isolate 3519-BHL032417-GBD3980_12374-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTCTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGACGATCAAATTTATAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACAAGGCTTTCCCTCGAAAAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTATACTTACTAGTTCAATTGTAGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3520 Parachironomus sp. water mite diet isolate 3520-BHL032417-GBD27539_13382-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATAAGGAAAAAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAGTTAGGACGACCCGGAACTTTTATGGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGTATCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3521 Parachironomus sp. water mite diet isolate 3521-BHL032417-GBD19026_19142-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTATGACGACCCGGAACTTTTATTGGTGATGATCAAAATTTACAATGTATTTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAACAATATAAGATTTTGACTTCTTCCCCCTTCTTTGACCCTATTACTTTCTAGTGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3522 Paratanytarsus sp. water mite diet isolate 3522-BHL032417-GBD4956_10784-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGTCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTTAACTAGGATATCCTGGAACTTTTTTTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTGTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3523 Chironomus sp. water mite diet isolate 3523-BHL032417-GBD19879_24164-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACCTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTAGAAAAAATAATATAAGTTTCTGACTTTTACCCCCCTCTTTTACTCCTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3524 Parachironomus sp. water mite diet isolate 3524-BHL032417-GBD22509_13845-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATATAATTGTAACGGCACATGCTTTTATTATAATTTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGGCTCTTTTAC-TTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.4% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3525 Parachironomus sp. water mite diet isolate 3525-BHL032417-GBD28426_19908-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGTATACTTATTCGAGCTTAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAAATGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACTTCGCCTTCCCTCGAATAAATAATAAAAGTTTTTTGACTTCCTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3526 Glyptotendipes sp. water mite diet isolate 3526-BHL032417-GBD3971_20178-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATATTGGCACATTATATCTTATTTTTTGGGCTTGATCCGGAATAGTGGGAACGTCTTTAAGTATGCTAATTCGAGCAAAAATAGGACGACCTAGAACTTTTATTGGAGATGACCAGATTTATAATGTTATTGTAACAGCTCACGATTTTATTATATTTTTTTTTTTATGATTATACCTATTTTAATTGGGGAATTTGGAACTTGATTAGTCCCTCTTATGCTGGGAGTTCCTGATAAGGCTTTCCCCCGAATAAATAATATAAATTCTTGGCTTCTCCCTCCCTCTTTAACTCTTCTTCTTTCTAGTTCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KP954645, identified in GenBank as Glyptotendipes senilis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3527 Chironomidae sp. water mite diet isolate 3527-BHL032417-GBD4812_21676-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCCTTAAGAATTTTAATTCGACTAAAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGAAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3528 Cricotopus sp. water mite diet isolate 3528-BHL032417-GBD9901_15753-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATTTAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3529 Parachironomus sp. water mite diet isolate 3529-BHL032417-GBD28188_10384-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTTATTGTAACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGAAATGGCTTTCCCTCCAAAAAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTACAATTGCAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3530 Parachironomus sp. water mite diet isolate 3530-BHL032417-GBD14721_4807-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACTACCCCTAACTTTTATTGGTTATGATCAAATTTACAATGTAATTGTAACGTCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTACTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTCGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3531 Orthocladius sp. water mite diet isolate 3531-BHL032417-GBD6991_16802-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTATTTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTCTTTGATTGGAGACAACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATATTTTTTTTTATGGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCTCTTACATTACTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR745842, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3533 Phaenopsectra sp. water mite diet isolate 3533-BHL032417-GBD5274_9942-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTATGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGATCATGCATTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3534 Cricotopus sp. water mite diet isolate 3534-BHL032417-GBD7784_16424-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3535 Glyptotendipes sp. water mite diet isolate 3535-BHL032417-GBD5139_23430-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATATTGGAACACTATATTTTATTTTCGGATCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGCGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTTTTATATATTTTTTTTTATAGTTATACCTATTTAAATTGGGGAATTTGGAAATTGATTAGTCCCTCTTATGCTGGGAGCTCCTGATAAGGCTTTCCCCCGAATAAATAATATAAATTCTTGGCTTCTCCCTCCTTCTTTAACTCTTCTTCTTTCTAGTTCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KP954645, identified in GenBank as Glyptotendipes senilis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3536 Chironominae sp. water mite diet isolate 3536-BHL032417-GBD20594_23302-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTTAATTAGGACGACCCGGAACCTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3537 Glyptotendipes sp. water mite diet isolate 3537-BHL032417-GBD23369_14198-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATATTGGAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCAGAAATAGGACGACCTGGAACTTTTATTGGAGATGACCAGATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATATTTTTTTTTTATAGTTATACCTATTTTAATTGGGGAATTTGGAAATTGATTAGTCCCTCTTATGCTGGGAGCTCCTGATAAGGCTTTCCCCCGAATAAATAATATAAATTCTTGGCTTCTCCCTCCTTCTTTAACTCTTCTTCTTTCTAGTTCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KP954645, identified in GenBank as Glyptotendipes senilis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3538 Chironomus sp. water mite diet isolate 3538-BHL032417-GBD15375_11083-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATGTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAAATTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCCTGCATAGCCTTTCCCACAAAAAAATAATATAAGTTTCTGACTTTTACCCCCCTCTATTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3539 Chironomus sp. water mite diet isolate 3539-BHL032417-GBD5801_22284-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATGTTTGGGGCTTGCTCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATATTAAATGGAGGATTCGGAACCTGACATGTCTCCCTAATACTGGGAGCACCTGACATAGCTTTTCTTAGAAAAAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3540 Parachironomus sp. water mite diet isolate 3540-BHL032417-GBD21800_4554-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATCTGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTATTACCCCCATCTTTAACATTACTATTAGCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3541 Chironomus sp. water mite diet isolate 3541-BHL032417-GBD11642_21792-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAGTATTAGGAGCTCCAGATATGGCCTTCCCTCGAATATATAATATAAGTTTTTGAGTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3542 Parachironomus sp. water mite diet isolate 3542-BHL032417-GBD20115_26816-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACTACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAGTAAAAAATATAAGTATTTGACTTATTCCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3544 Chironomus crassicaudatus water mite diet isolate 3544-BHL032417-GBD5656_11986-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAAATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGTAACTTTTATTGGTGATGACCAAATTTATAATGTTGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTTAATATTAGGAGCTCCAGATATGGCCTCCCCTCGAATATATAATATAAGTTTTTGAGTACTCCCCCCATCTTTAACTCTTCCTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.8% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3545 Oligochaeta sp. water mite diet isolate 3545-BHL032417-GBD23398_22247-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACGTGCATTCCTAATAATTTTCTTTCTGGTTATACCCAGTATTTACTGGTGGATTTGGAAATTGACTTCTACTTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACAACTACCACCTTCACTAATCCTATGGGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL3546 Parachironomus sp. water mite diet isolate 3546-BHL032417-GBD11225_16731-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACAACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACGGAACATGCTTTTATGATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTATTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3547 Chironomidae sp. water mite diet isolate 3547-BHL032417-GBD3759_14746-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTGTATTCGGAGCCTGATCAGGTATAGTAGGTACTTCCCTTAGTAATCTAGTACGAGCTGAATTAGGACACCCCGGGGCATTAATTGGAGACGATCAAATTTATAACGTAATGGTTACATCTCATGCCTTTGTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGTGGATTTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACGTTCTAGTTCAATTGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.5% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3548 Parachironomus sp. water mite diet isolate 3548-BHL032417-GBD16715_3959-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTGTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGTAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTGTAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGATCCCGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCACTTGTAGAAAATGGCGCTGGAACCGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3552 Chironomidae sp. water mite diet isolate 3552-BHL032417-GBD12679_28363-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACATGCAGGCTCATTAATTGGAGACAATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCATTATTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3553 Chironominae sp. water mite diet isolate 3553-BHL032417-GBD19367_22405-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCAAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTCAATTGGAGGTTTTGGAAATTGACTTATTCCTTGAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTTTTACGTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3556 Parachironomus sp. water mite diet isolate 3556-BHL032417-GBD4095_9677-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGATTACTTATTCGAGCTGAATTAGGACGACCCGGAAATTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCCCATGCTTTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGACATGGCTTTCCCGCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3560 Chironomus sp. water mite diet isolate 3560-BHL032417-GBD22044_27376-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTCTTTACATTATTTTTTGGTTCTTGATCAGGATTGTTAGGGCCTTCTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGCTTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.0% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3561 Amphichaeta sp. water mite diet isolate 3561-BHL032417-GBD4119_14977-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCATGGAGCCTTTTTAGGAAGAGACCAACTGTATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCCTAGTAATACCAGTTTTTATTGGAGGATTTGGAAGTTGAATTCTACCTTTAATACTTGAGGCACCTGATATAGCATTCCCACGCTTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCGATTAGTTGCATAGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL3562 Chironomus sp. water mite diet isolate 3562-BHL032417-GBD2449_17920-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAAAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAAATTTTAATTGGAGGTTTCGGAAATTGACTTGTACCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATATATAATATAAGTTTTTGAGTTCTCCCCCCATCTTTAACTCTACTTCTGTCTAGTTCAATTGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3563 Parachironomus sp. water mite diet isolate 3563-BHL032417-GBD25936_20183-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCGAATTTACAATGTAATTGTAACGACACATGCTTTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATCTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTTCCCCTTCTTTGACTCTTTTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3565 Chironomus sp. water mite diet isolate 3565-BHL032417-GBD8925_10457-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTGTAGTTACAGCTCACGCATTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.1% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3566 Parachironomus sp. water mite diet isolate 3566-BHL032417-GBD9633_15530-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTTAGAATACTTATTCGAACTGAATTATGACGACCCGGAACTTTTATTGGTAATGATCAAATTTACAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAACTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3567 Orthocladius sp. water mite diet isolate 3567-BHL032417-GBD16020_15829-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTATGGCTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCGGATATAGCTTTCCCTCGAATAAATAATATATGCTTTTGATTATTACCCCCATCTCTAACATTACTATTAGCTAGCTCAATTGTAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3570 Penicillium sp. water mite diet isolate 3570-BHL032417-GBD4074_13327-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTATATTTTATGTTTTCATTATTTTCAGGATTAATAGGAACAGCGTTTTCAGTGTTAATAAGATTAGAATTATCTAGACCAGGTGTTCAATATATTTCAGATAATCAATTATATAATAGTATAATTACAGCTCACGCTATATTGATGATTTTCTTTATGGTTATGCCAGCTTTAATAGGAGGATTTGGTAATTTCTTATTACCTTTATTAGTAGGAGGTCCTGATATGGCATTCCCAAGATTAAATAACATTAGTTTCTGATTATTAGTACCAAGTTTATTCTTATTCATATTCTCAGCTACAATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.1% identical to accession ID KX931017, identified in GenBank as Penicillium sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3573 Orthocladius sp. water mite diet isolate 3573-BHL032417-GBD20650_2859-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAACAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATATTTTTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KR744139, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3574 Cryptochironomus sp. water mite diet isolate 3574-BHL032417-GBD16450_12796-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTGATTCGAGCAGAATTAGGACGACCAGGAACTCTTATAGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCAGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3579 Parachironomus sp. water mite diet isolate 3579-BHL032417-GBD23740_26317-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAACTTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCGTCCCCCTGCTGTGACTCTATTACTTTCTAGTGCAATTGTATAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3583 Parachironomus sp. water mite diet isolate 3583-BHL032417-GBD14634_11291-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGGCTTCTTTAAGAATACTTATTCGAGCTGAATTAGGAGGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCGGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3584 Chironominae sp. water mite diet isolate 3584-BHL032417-GBD25707_16551-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTACGAATATTAATCCGAACGAAATTAGGTCATCCTGAAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATATTTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3585 Cricotopus sp. water mite diet isolate 3585-BHL032417-GBD6108_11701-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTAATTGTAACGGCACACGCTTTTATTATATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCATACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KF000262, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3586 Parachironomus sp. water mite diet isolate 3586-BHL032417-GBD11899_7442-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCTTCTTTGACTCTATTAGTTGCTAGTGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3587 Parachironomus sp. water mite diet isolate 3587-BHL032417-GBD28891_19102-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCCGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAGCTTTTATTGGTGATGATCATATTTACAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATAAAAGTTTTTGACTTCTTCCCCCTTCTGTGACTCTTTTACTTTCTAGTTCAACTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3588 Psectrocladius sp. water mite diet isolate 3588-BHL032417-GBD5515_7527-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTTTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3594 Parachironomus sp. water mite diet isolate 3594-BHL032417-GBD13029_17937-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATTCTTATTCGAGCTGAATTCGGACTACCCGGATCTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGACACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCATTGACTCTATTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3595 Chironomidae sp. water mite diet isolate 3595-BHL032417-GBD24341_24793-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTTATAGCTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3597 Chironomus sp. water mite diet isolate 3597-BHL032417-GBD27724_18131-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGTAACTTTATACATTATTTTTGGGGCTTGATCCGTAATAGTGGTAACTTCATTAACAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAAGTGACTTGTCCCCCTAATACTTGGAGCACTTGACATAGCTTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCGCCCGCTCTTACTCTTCTT-TTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3598 Parachironomus sp. water mite diet isolate 3598-BHL032417-GBD19656_20642-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAATTCTTGGCTTCTCCCTCCTTCTTTAACTCTTCTTCTTTCTAGTTCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3602 Parachironomus sp. water mite diet isolate 3602-BHL032417-GBD24905_25238-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATATTTTATTTTCGGAGCTTAATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACCGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTAGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTATTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3604 Chironomidae sp. water mite diet isolate 3604-BHL032417-GBD15274_25996-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTGTATTCGGAGCCTGATCAGGTATAGTAGGTACTTCCCTTAGTAATCTAGTACGAGCTGAATTAGGACACCCCGGGGCATTAATTGGAGACGATTAAATTTATAACGTAATGGTTACAGCTCATGCCTTTGTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAACTTGATTAGTACCACTAATATTAGGTGCACCAGATATAGCTTTCCCTCGAATAAATAATATATGCTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGTAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3605 Chironomidae sp. water mite diet isolate 3605-BHL032417-GBD24545_7955-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTGTATTCGGAGCCTGATCAGGAATAGTAGGCACTTCCTTTAGTATTTTAGTTCGAGCTGAATTAGGACACCCCGGGGCATTAATTGGAGACGATCAAATTTATAACGTAATGGTTACAGCTCATGCCTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGTGGATTTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3607 Culex pipiens water mite diet isolate 3607-BHL032417-GBD23303_11461-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTCAGGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGGTCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCATTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3608 Cricotopus sp. water mite diet isolate 3608-BHL032417-GBD26048_16790-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCTCTTACATTACTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3615 Chironomus riparius water mite diet isolate 3615-BHL032417-GBD7294_16782-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTGGATCCGGAATAGTGGGAACTTCATTAACAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGATGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTTACCTCCCTATCTTACTCTTCTT-TTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3617 Parachironomus sp. water mite diet isolate 3617-BHL032417-GBD21790_14120-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTAACGACACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTTAATCGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTTTGACTCTTTTACTGTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3618 Chironomidae sp. water mite diet isolate 3618-BHL032417-GBD6301_11917-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGAGTTTTACCTCCCTCTCTTACTCTTCT-TTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.8% identical to accession ID KR621135, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3623 Chironominae sp. water mite diet isolate 3623-BHL032417-GBD8105_11606-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTAGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTAGCAAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3624 Chironominae sp. water mite diet isolate 3624-BHL032417-GBD13032_7693-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTATATTTTATCTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGTCATCCTGAAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3626 Parachironomus sp. water mite diet isolate 3626-BHL032417-GBD15750_6609-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGGTCTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTTAGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCTTTGACTCTACTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3628 Cricotopus sp. water mite diet isolate 3628-BHL032417-GBD12083_5764-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATTCGGGCAGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACAGCACATGATTTTGTTATAATTTTTTTTTATAGTTATACCTATTTTAAATGGTGGGTTTGGAAAATGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTAACTTCTTCCTCCTTCACTTACATTTCTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3629 Parachironomus sp. water mite diet isolate 3629-BHL032417-GBD11260_27441-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTTAGAATACTTATTCGAACTGAATTAGGACTACCCGGAACTTTTATTGTTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTTGAGGATTTGGAGATTGAATAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTTCCCTCGAATAAATAATATAAGTTTTAGACTTCTTCCCCCTTCTTTGACTCTATTACTTTCTAGTTCAATTGTAGAAAATGGAGATGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3634 Parachironomus sp. water mite diet isolate 3634-BHL032417-GBD16213_17977-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTTTTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCTGACATAGCTTTTCCTAGAAAAAATAATATAAGTTTCTGACTTTTGCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3635 Parachironomus sp. water mite diet isolate 3635-BHL032417-GBD5138_11457-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCTTTAAGAATTCTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCCATAGTTATACCTATTTTAATCGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGTGGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCGTTGACTCTTTTACTTTCTAATTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3637 Glyptotendipes sp. water mite diet isolate 3637-BHL032417-GBD17638_3968-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATATTGGCACATTATATCTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACGTCTTTAAGTATGCTAATTCGAGCAAAAATAGGACTACCTTGAACTTTTATTGGAGACGACCTTATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATATTTTTTTTTTATAGTTATACCTATTTTAATTGGGGTATTTGGAAATTGATTAGACCCTCTTATGCTGGGAGCTCCTGATAAGGCTTTCCCCCGAATAAATAATATAAATTCTTGGCTTCTCCCTCCTTCTTTAACTCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KP954645, identified in GenBank as Glyptotendipes senilis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3638 Parachironomus sp. water mite diet isolate 3638-BHL032417-GBD23947_8238-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATTAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGATATTGATTAGTACCACTAATATTAGGTGCACCAGATATAGCTTTCCCTCGAATAAATAATATATGCTTTTGATTATTACCCCCATCTTTAACATTACTATTAGCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3639 Parachironomus sp. water mite diet isolate 3639-BHL032417-GBD20839_28224-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTTTTGGTAATGATCAAATTTATAATGCAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGTTCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTTTGACCCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3640 Parachironomus sp. water mite diet isolate 3640-BHL032417-GBD14218_24523-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCTTTACGAATACTTATTCGAGCTGAATTAGGACGACCCGGAGCTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGTGCTCCAGACATGCCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3643 Parachironomus sp. water mite diet isolate 3643-BHL032417-GBD15620_6935-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGTATAGTAGGGACTTCTTTAAGAATATTTATTCGAGCTGAATTAGGACGCCCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTTGGAAATTGATTAGATCCTCTTATATTAGGAGCTCCTGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3644 Chironomus sp. water mite diet isolate 3644-BHL032417-GBD27543_9742-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGCATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATGCCAATTTAAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGATATAGCTTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3655 Cricotopus sp. water mite diet isolate 3655-BHL032417-GBD27723_12535-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATCCGGGCGAAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACAGCCCATGCTTTTGTTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGCGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAAAAAATAATATAAGTTTTTGACTACTTCCCCCTTCTCTTACATTACTACTATCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3659 Parachironomus sp. water mite diet isolate 3659-BHL032417-GBD27855_21835-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACATTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCCCTTATATTAGGGGCTCCAGACATGGCTTTTCCCCGAAGAAATAAAAAAAGTTTTTGACTTTTTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3661 Parachironomus sp. water mite diet isolate 3661-BHL032417-GBD19461_10040-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGTATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACCGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGCTTAGTTCCTCTTATATTAGGGACTCCAGACATGGCTTTCCCCCGAATAAAAAATATAAGTTTTTGACTTCTCCCCCCCTTCTTTGACTCTTTTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3664 Chironomus sp. water mite diet isolate 3664-BHL032417-GBD24809_18452-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACATCATTAACAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAAATTTATAATGTTGTAGTCACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGTAAACTGACTTGTCCCCTTAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCGGACTTTTACCACCCTCTCTTACTCTTCTT-TTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3667 Orthocladius sp. water mite diet isolate 3667-BHL032417-GBD14719_5298-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTTGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGGAACAGCTCATGCTTTTGTTATAATTTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTCCCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATCGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3668 Parachironomus sp. water mite diet isolate 3668-BHL032417-GBD11006_25666-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGAGCAGGAATAGTAGGAACTGCTTTAAGAATACTTATTCGAGTTAAATTATGACAACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATCTAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3669 Chironominae sp. water mite diet isolate 3669-BHL032417-GBD16346_11577-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGCTATAGTAGGAACTTCGTTATGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAGTGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCCTCGAATAAATAATATAAGGTTTTGATTATTACCCCCTTCAGTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3671 Orthocladius sp. water mite diet isolate 3671-BHL032417-GBD20450_3929-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTATTTGATTGGAGACGAGCAAATTTATAATGTTATTGTTACAGCTCATACTTTTGTTATAATTTTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR758170, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3672 Parachironomus sp. water mite diet isolate 3672-BHL032417-GBD25251_22415-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTTAGAATACTTATTCGAGCTGAAGTAGGACGACCCGAAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGAACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATCGATTAGTTCCTCTTATATTAGAGGCTCCAGACATGGCTTTCCCTCGACTAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTCGTTCAATTGTATAAAATGGCGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3678 Parachironomus sp. water mite diet isolate 3678-BHL032417-GBD16610_3484-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTAATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCACTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCTTTGACTCTTTTATTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3685 Parachironomus sp. water mite diet isolate 3685-BHL032417-GBD14634_23273-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGTCGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTGCCCCCTTCTTTGACTATTTATCAATCTAGTGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3687 Parachironomus sp. water mite diet isolate 3687-BHL032417-GBD6561_8232-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACAACCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTAACGGCTCATGCTTTTATTATAATTTTTTTCATAATTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGACTCCAGACATGACTTTCCCTCGAATAAATAAAATAAGTTTTTGGCTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTATAGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3690 Parachironomus sp. water mite diet isolate 3690-BHL032417-GBD17196_13276-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATATTTTATTTTCGGAGCTTGATCAGGATTAGTAGGGCCTTCTTTAAGAATACTTATTCGAGCTAACTTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3693 Parachironomus sp. water mite diet isolate 3693-BHL032417-GBD20857_24680-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCCTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTTGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACAAGGCCTTCCCCCGGAAAAATAATATAAAGTTTTGACTTCTTCCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3704 Chironomus sp. water mite diet isolate 3704-BHL032417-GBD18105_8907-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTAGTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTCTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCTCCCTCTCTTACTCTTCTT-TTTCTAGTTTTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3710 Parachironomus sp. water mite diet isolate 3710-BHL032417-GBD19313_3715-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACTACCCGGAACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTTGGAAATTTATTAGTTCCTTTTATATTAGGGGCTCCCGACACGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3716 Chironominae sp. water mite diet isolate 3716-BHL032417-GBD16014_4106-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACAGCACATGC-TTTGTTAGAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3719 Chironomus sp. water mite diet isolate 3719-BHL032417-GBD25701_9196-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGCGCTAAATTAGGACGACCCGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCTCCCTCTCTTACTCTTCCT-TTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3722 Parachironomus sp. water mite diet isolate 3722-BHL032417-GBD14959_27443-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGAAACGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTGACTCTCTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3729 Chironomus sp. water mite diet isolate 3729-BHL032417-GBD16875_23485-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATGTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGAATTGTCCCCCTAATACTTGGAGCACCTGACATTACTTTTTCCTCGAAAAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTTTCAAGATCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3731 Oligochaeta sp. water mite diet isolate 3731-BHL032417-GBD25630_22713-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTAAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACACGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL3734 Parachironomus sp. water mite diet isolate 3734-BHL032417-GBD24152_13471-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGGGCTTCTTTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGAGGCTCCAGACATGGCTTTCCCTCGAATAAATAATAAAAGTTTTTGACTTCTTCCCCCTTCTTAGACTCTTTTACATTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3735 Parachironomus sp. water mite diet isolate 3735-BHL032417-GBD14374_28269-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTGATTCGAGCGGAATTAGGACGACCCGTAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACTGCACATGCTTTTATTATAAATTTTTTCATAGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAAACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTTGACTTCTCCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3736 Parachironomus sp. water mite diet isolate 3736-BHL032417-GBD24688_6387-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTCGGAGCTTGATCAGTAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACAACCCGCAACTTTTATTGGTGCTGATCAAATTTACAATGTAATTGTAACGGCACATGTGTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTCGAGTCTTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCAAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3746 Parachironomus sp. water mite diet isolate 3746-BHL032417-GBD21872_27894-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGTCCCGGTAATTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCAAAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGTGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGAATCTTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3752 Orthocladius sp. water mite diet isolate 3752-BHL032417-GBD22723_17271-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCCTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGAACGACCCGGAACTTTCATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTTATGGTTATGCCTATTTTTATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR744139, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3754 Chironominae sp. water mite diet isolate 3754-BHL032417-GBD14469_18616-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGTAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATAATAATCCGAACTGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAATTTTATAATGTAATTGTTACTGCCCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTCTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3761 Parachironomus sp. water mite diet isolate 3761-BHL032417-GBD16792_14064-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGATTTAGGACATGCTGGTTATTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTTATGGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACCTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3763 Orthocladius sp. water mite diet isolate 3763-BHL032417-GBD13561_25373-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTATTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTACGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCCCCAGATATAGCTATCCCTCGAAAAAATAATATAAGGATTTGAATATTACCCCCCTTCATTAACTTTATTATTGCCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3764 Parachironomus sp. water mite diet isolate 3764-BHL032417-GBD10538_3293-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGTCGACCCGGATCTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGAGTGGGAAATTGATTAGTTCCTCATATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3765 Chironominae sp. water mite diet isolate 3765-BHL032417-GBD19249_26225-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATATTAATCCGAACGGAATTACGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAAAATTAGGGGCCCCTGATATGACTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3768 Parachironomus sp. water mite diet isolate 3768-BHL032417-GBD19846_6517-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACGGCACATGC-TTTACTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTTTAACTCTTTTACTATCTAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ166526, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3780 Chironomus sp. water mite diet isolate 3780-BHL032417-GBD28688_11935-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAACAATGCTTATTCGAACAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGTTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCTCCCGCTCTTACTCTTCTT-TTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3786 Parachironomus sp. water mite diet isolate 3786-BHL032417-GBD21936_24440-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGTTGAATTAGGACGACCCGTAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGACTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTAACTCTTTTACATTCTAGTTCAATTGTATAAAATGGAGCTGAAACA	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3789 Parachironomus sp. water mite diet isolate 3789-BHL032417-GBD2583_15531-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGGGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACCTGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTTCCACTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTTTATTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3792 Chironomus sp. water mite diet isolate 3792-BHL032417-GBD24189_11614-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATGTTTGGGGCCTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTAGAAAAAATAATATAAGTTTCTGACTTTTACCCCCCACTCCTACACATCTTCAATCTAGTTCTTTCGTATAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3797 Cricotopus sp. water mite diet isolate 3797-BHL032417-GBD28014_19145-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCACGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGACTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAGATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTATTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3800 Chironomus sp. water mite diet isolate 3800-BHL032417-GBD10151_4671-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGTACTTCATTAACAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTGTACCTCCCGCTCTTACTCTCCTT-ATTCTAGTGCTTGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3805 Chironomus sp. water mite diet isolate 3805-BHL032417-GBD5383_8915-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAACAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGAAATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGACTTTTCCCTCCCTCTCTACCTCTTCTT-TATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3808 Parachironomus sp. water mite diet isolate 3808-BHL032417-GBD6641_25922-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTAGACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGCATTTCACCTCTTCCCCCCTCTTTGACTCTTTTAATATCTAGTGCAATAGTAGAAAATCGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3809 Glyptotendipes sp. water mite diet isolate 3809-BHL032417-GBD10681_24955-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATATTGGCACATTATATCTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACGTCTTTAAGTATGCTAATTCGAGCAGAAATAGAACGACCTGGAACTTTTATTGGAGATGACCAGATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATATTTTTTTTTTATAGTTATACCTATTTTAATTGGAGAATTTGGAAATTGATTAGTCCCTCTAATACTGGGAGCTCCTGATAAGGCTTTCCCCCGAATAAATAATATAAATTCTTGGCTTCTCCCTTCTTATTTAACTCTACTTCTTTCTAGTTCAATTGTCGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KP954645, identified in GenBank as Glyptotendipes senilis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3812 Chironomidae sp. water mite diet isolate 3812-BHL032417-GBD4516_12065-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GACACTTTACTTTATTTTTTGAAGCTTGATCGGGATTAGTAGGACCATCTTTAAGAATATTAATTCGAGCAGAATTAGGCCACCCAGGAACTTTGATTGGGGATGATCAAATTTACAATGTATTTGTAACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGTGGATTTGGAAATTGGCTTTTACCTTTAATACTTGGAGCCCCTGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCATCTATGACATTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KP043758, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3817 Glyptotendipes sp. water mite diet isolate 3817-BHL032417-GBD19561_24552-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATATTGGCACATTATATCTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACGTCTTTAAGTATGCTAATTCGAGCAGAAATAGGACGACCTGGAACTTTTATTGGAGATGACCAGATTTATAATGTTATTGTAACAGCTCACGCTTTTATTATATTTTTTTTTTATAGTTATACCTATTTTAATTGGGGAATTTGGAAATTGATTAGTCCCTCTTATGCTGGGAGCTCCTGATAAGGCTTTCCCCCGAATAAATAATATAAGTTTTTGACTATTACCCCCTTCATTAACT-TTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KP954645, identified in GenBank as Glyptotendipes senilis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3821 Parachironomus sp. water mite diet isolate 3821-BHL032417-GBD10523_3192-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACCTTTATTGGTGATGATCAAATCTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGGGCTCCAAACATGGCTTTCCCTCGAATAAATAACATAAGTTTTTGACTTCTTCCCCCTTCTTTGACCCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3831 Chironominae sp. water mite diet isolate 3831-BHL032417-GBD28554_14749-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTCTATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGTAATTAGGTCATCCTGTAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTCTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3832 Parachironomus sp. water mite diet isolate 3832-BHL032417-GBD29001_12213-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGTATACTTATTCGAGCTGAATTAGGACGACCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAATTCCTCTAATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATGTAAGTTTTTAACTTCTTCCCCCTTCTTTGACTCCTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3833 Parachironomus sp. water mite diet isolate 3833-BHL032417-GBD18034_14623-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGAATTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGGTTTCCCTCCAATAAATAATATAAGGTTTTGACCTCCTCCCCCTTCTTTGACCCTTTTTCCTTCCAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3837 Chironomus riparius water mite diet isolate 3837-BHL032417-GBD21715_20206-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTACTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3838 Parachironomus sp. water mite diet isolate 3838-BHL032417-GBD11281_21576-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGAGACTTTTTTAAGAATACTTATTCGAGCTGAATTAGAACGACCCTGAACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3841 Diptera sp. water mite diet isolate 3841-BHL032417-GBD12290_11440-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACTGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATTATTTTTTTTATAGTAATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID KT382826, identified in GenBank as Anopheles punctulatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3848 Parachironomus sp. water mite diet isolate 3848-BHL032417-GBD22789_15264-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAATTATACTTTTTCGAGCTGATTTAGGACAACCCGGAACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3853 Orthocladius sp. water mite diet isolate 3853-BHL032417-GBD17947_8930-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTATATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTGTTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCGCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR291764, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3857 Orthocladius sp. water mite diet isolate 3857-BHL032417-GBD11319_27521-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTGTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGTTGCTTCATTAAGAATTTTAATTCGAGCTGAAGTAGGACATGCTGGTTCTTTGATTGTAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTAGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTATTGATTATTACCCCCTTCATTAACATTATTATTGTCTAGTTCTATTGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3860 Parachironomus sp. water mite diet isolate 3860-BHL032417-GBD26148_15388-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGTTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAAAAAATAAAATAAGTATTTGAATTCTTCCCCCCTCTTTGACTCTTATACTTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3863 Chironomus sp. water mite diet isolate 3863-BHL032417-GBD10921_15274-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATATTTTATTTTCGGAACTTGATCAGGAAGAGTAGGGACTTCTTTAAGAATACGTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGATGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAAGTGACTTGTCCCCCTAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCTCCCTCTCTTACTCTTCTT-TTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3875 Glyptotendipes sp. water mite diet isolate 3875-BHL032417-GBD13503_20993-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATATTGGTTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGGCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATATTTTTTTTTATAGTTATACCTATTTTAATTGGGGAATTTGGAAATTGATTAGTCCCTCTTATGCTGGGAGCTCCTGATAAGGCTTTCCCCCGAATAAATAATATAAATTCTTGGCTTCTCCCTCCTTCTTTAACTCTTCTTCTTCCTAATTCAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.4% identical to accession ID KP954645, identified in GenBank as Glyptotendipes senilis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3887 Chironomus sp. water mite diet isolate 3887-BHL032417-GBD4115_13246-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTCTTTTTGGGGCTTGATCCGGAATATTGGCTACTTCATTAACAATGCTTATTCGCGCAGATTTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCTCCCTCTCTTACTCTTCTT-TTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3891 Parachironomus sp. water mite diet isolate 3891-BHL032417-GBD4370_12940-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCTTTAAGAATACTTATTCGAGCTGAATTCGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTAAAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTTATATTAGGGGCTCCAGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTATTATTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3895 Chironomidae sp. water mite diet isolate 3895-BHL032417-GBD12198_21326-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTTCATTATATTTTATTTTTGGAGCTTAATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTCCCCCTAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCTCCCTCTCTTACTCT-TCCTTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.7% identical to accession ID GU565719, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3903 Parachironomus sp. water mite diet isolate 3903-BHL032417-GBD27460_19562-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTGTATTTTATTTTCGGATCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGTGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTCGACTTCTCCCCCCTTCTTTGACTCAGTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGAAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3910 Chironomus sp. water mite diet isolate 3910-BHL032417-GBD23700_20901-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAACACTGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCTCCCTCTCAAACTCTTCAT-TTTCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3914 Parachironomus sp. water mite diet isolate 3914-BHL032417-GBD25422_6955-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTTCGGAGCTTGATCAGGAATAGTAGGGCCTTCTTTAAGATTTCTTATTCGAGCTGAATTAGGCCGACCCGGAACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAAATTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGGTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3932 Parachironomus sp. water mite diet isolate 3932-BHL032417-GBD7090_22007-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTCTCGGAGCTTGATCAGGAATCGTAGGTACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCAGAAATTGTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGTGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTGTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3933 Chironomus riparius water mite diet isolate 3933-BHL032417-GBD14122_3958-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAACAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCATATTTATAATGTTGTCGTTACTTCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCACTAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCTCCCTCTCTTACTCTTCTT-TTTCTAATTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3940 Parachironomus sp. water mite diet isolate 3940-BHL032417-GBD28286_16308-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATCTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGATCTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAGCTGCACATGCTTTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCTTTGACTCTATTACTTTCTAGTTAAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3945 Chironominae sp. water mite diet isolate 3945-BHL032417-GBD8027_9050-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGTCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATATTAAGTGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATAACATCCTCCATCTCTATCTCTTATTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3948 Chironomus riparius water mite diet isolate 3948-BHL032417-GBD1923_16237-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAACAATGCTTATTCGAGCAGAATTAGGACGGCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTAATGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATAGCCTTCCCTCGAAAAAAATAATATAAGTTTCTGACTTTTACCTCCCTCTCTTACTCTTCTT-TTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3952 Parachironomus sp. water mite diet isolate 3952-BHL032417-GBD17601_19857-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGTTGAATTAGGACGACCCGGAACTTTTATTGGTAATGATTAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATAGCTTTCCCTCGAATAAACAATATAAGGTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR778259, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3953 Chironomus crassicaudatus water mite diet isolate 3953-BHL032417-GBD26659_7337-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGCCGTCCTGGAACTTTTATTGGTGATGACCAAAATTTATGATGTTGTCGTAAAAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATATATAATATAAGTTTTTGAGTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.8% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3956 Chironomus riparius water mite diet isolate 3956-BHL032417-GBD3570_20385-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTCTACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAACAATGCTTATTCGAGCAGAATTATGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCTCTTGACATAGCTTTTTCTCGAATAAATAATATAAGTTTCTGACTTTTACCTCCCTCTCTTACTCTTCTT-TTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3964 Parachironomus sp. water mite diet isolate 3964-BHL032417-GBD9685_10474-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGTTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTGATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCATTCCCTCGAATAAATAATATAAGTTTTTAACTTCTTCCCCCGTCTTTGACACTATTACTTGCTAGTGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL3967 Orthocladius sp. water mite diet isolate 3967-BHL032417-GBD13312_19842-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACACGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCTCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTGACTTTATTATTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3969 Cricotopus sp. water mite diet isolate 3969-BHL032417-GBD7564_18678-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATCTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTATAAGAATTTTAATCCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACAGTACATGCTTTTGTTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTTACATTACTACTATCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3970 Chironomus sp. water mite diet isolate 3970-BHL032417-GBD26007_18274-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTGTATACATTATTTTTGGGGCTTGATCCGGAATATTGTGAACTTCATTATCAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGTATTCGGAAACGGACTTGTCTCCCTAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCTCCCTCTCTTACTCTTCTT-TTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3971 Parachironomus sp. water mite diet isolate 3971-BHL032417-GBD25745_21732-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGTAGCTTGATCAGGAATAGTAGTTACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTCTTATATTATGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTAACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3979 Drosophila sp. water mite diet isolate 3979-BHL032417-GBD27002_20315-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACATTATATCTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACGTCTTTTAGTATGCTAATTCGAGCAGAAATAGGACTACCCGGAACTTTTATTGGAAATGACCAAATTTATAATGTTATTGTAACAGCTCTATCTTTTATTATATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCGAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.0% identical to accession ID AY750090, identified in GenBank as Drosophila lacertosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3991 Chironominae sp. water mite diet isolate 3991-BHL032417-GBD25281_23953-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGCGCTTGATCAGGTATAGTAGGTACTTCTTTTAGAATATTAATCCGAACGGAATTAGGTTATCCTGGAACATTTATTGGTGATGACTAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGACCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTAATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3994 Parachironomus sp. water mite diet isolate 3994-BHL032417-GBD24227_25955-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTATGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTAACTTCTTCCCCCTGCTTTGACTCTTTTACGTGCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3995 Chironomidae sp. water mite diet isolate 3995-BHL032417-GBD17517_10277-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTGTATTCGGAGCCTGATCAGGTATAGTAGGTACTTCCCTTAGTAATCTAGTACGAGCTGAATTAGGACACCCCGGGGCATTAATTGGAGACGATCAAATTTATAACGTAATGGTTACAGCTCATGCCTTTGTAATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAAGTGACTTGTCCCCCTAATACTCGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCTCCCTCTCTTACTCTTCT-TTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.0% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL3996 Parachironomus sp. water mite diet isolate 3996-BHL032417-GBD22042_24070-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGTTCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCCTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTACTTTGACACTTCTACATTCTAGTTCAATTGTATAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4002 Parachironomus sp. water mite diet isolate 4002-BHL032417-GBD24867_19591-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTTAGAATACTTATTCGAGTTTAATTAGGACGAGCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTACTTGTAACTGCACATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGAATTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4004 Parachironomus sp. water mite diet isolate 4004-BHL032417-GBD24187_24882-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGTATACTTATTCGAGCTTAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCACCAGACATAGCTTTACCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4006 Chironomus sp. water mite diet isolate 4006-BHL032417-GBD26014_11296-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATGTTTGGGACTTGATCCGGAATAGTGGGAACTTCCTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACTAAATTTATAATGTTGTAGTTACTGCTCATGCGTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTCACAGAGCTTTTCCTAGAAAAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4015 Chironomus sp. water mite diet isolate 4015-BHL032417-GBD4704_21915-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGTATGATCCGGAATAGTGGGAACTTCATTAACAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTCCCCCTAATACTTGGAGCACTTGACATAGCTTTTCCCCGAAAAAATAATATAAGTTTCTGACTTTTACCTCCCTCTCATACTCTTCTT-TTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4017 Orthocladius sp. water mite diet isolate 4017-BHL032417-GBD9967_23201-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATTTTTATTTTCGGAGCTTGATCAGGTATAGTAGGGACTTAATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGGAATTGATTAGTACCTTTAATGTTAGGAGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4022 Chironomus sp. water mite diet isolate 4022-BHL032417-GBD12098_13110-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAAATAGGACGACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAAACTGACTTTTCCCCCTAATTCTTGGAGCACTTGATATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4024 Parachironomus sp. water mite diet isolate 4024-BHL032417-GBD27450_20855-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATACTTATTCGAGCTTAATTAGGACAACAAGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAATTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTATTACTTTCTAGTTCAAATGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4025 Orthocladius sp. water mite diet isolate 4025-BHL032417-GBD22370_20588-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGAGCTTGATTAGGAATAGTAGGAACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTATTTGATTGGAGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCCTCATTAACTTTATTATTGTCTAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4030 Chironomus sp. water mite diet isolate 4030-BHL032417-GBD10245_9815-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTCTTTACATTATTTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAGTAGTTACAGCTCACACATTTATTATAATTTTTTTCGTAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAATTCAATTATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4031 Cricotopus sp. water mite diet isolate 4031-BHL032417-GBD28238_19261-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTAAATTGGTGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCTCTTACATTACTACTATCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4034 Chironomidae sp. water mite diet isolate 4034-BHL032417-GBD16537_12656-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.3% identical to accession ID KR085336, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4036 Chironomus sp. water mite diet isolate 4036-BHL032417-GBD28045_14432-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAACAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATTACCAAATTTATAATGTTGTAGTTACTGCACATGATTTTATTATAATTTCTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAACCTGACTTGTCCCCCTAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTCCCTCCCTCTCATACTCTTCTT-TTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4038 Glyptotendipes sp. water mite diet isolate 4038-BHL032417-GBD13950_20859-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATATTGGAACACTATATCTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACGTCTTTAAGTATGCTAATTCGAGCAGAAATAGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATATTTTTTTTTTATAGTTATACCTATTTTAATTGGGGAATTTGGAAATTGATTAGTCCCTTTTATACTGGGAGCTCCTGATAAGGCTTTCCCCCGAATAAATAATATAAATTCTTGGCTTCTCCCTCCTTCTTTAACACTTCTTCTTTCTAGTACAATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KP954645, identified in GenBank as Glyptotendipes senilis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4040 Chironomus sp. water mite diet isolate 4040-BHL032417-GBD19410_16895-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAACAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTCACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGAAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATAGCTTTTCCTCAAAAAAATAATAAAAGTTTCTGACTTTTACCTCCCTCTCTAACTCTTCTT-TTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4052 Parachironomus sp. water mite diet isolate 4052-BHL032417-GBD3073_16531-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTCGGAGCTTGATCAGGAATAGAAGGGACTTCTTAAAGAATACTTATTCGAGCTGAATTAGGACAACCGGGAACTTTTATTGGTGATGATCTAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGTCTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4054 Chironomus sp. water mite diet isolate 4054-BHL032417-GBD10239_23177-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCAGAATAGTGGGAACTTCATTAACAATGCTTATTCGAGCAGCATTAGCACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAAATTTAATTGGAGGATTCGGACACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCTCCCTCTCTTACTCTTCTT-GTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4065 Parachironomus sp. water mite diet isolate 4065-BHL032417-GBD19632_22795-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATAAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACAACCCGAAACTTTTATTGTTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTGTAATTTTTTTCATAGCTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCGTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAATTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4067 Parachironomus sp. water mite diet isolate 4067-BHL032417-GBD24800_23151-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGATCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGACTTCGGTCGACCCGGAACTTTTATTGATGATGATCAAATTTACAATGTAATTGTAACCGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4069 Chironomus sp. water mite diet isolate 4069-BHL032417-GBD27669_14301-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGAGCCGGAATAGTGGGAACTGCATTTACAATACTTATTCGAGCAGAATTAGGACGACCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGTTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCTCCCTCTCTTACTCTTCTT-TTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4073 Chironomus riparius water mite diet isolate 4073-BHL032417-GBD25629_14570-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTATATTACAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGAGATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCCTCTTTCTAGTTTATTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4074 Chironomus sp. water mite diet isolate 4074-BHL032417-GBD8464_12315-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTAGGAACTTCATTAACAATGCTTATTCGAGCAAAATTAGGACGACCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAACTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGAAGCACTTGACATAGCTTTTCCTCGAAAAAATAATATAAGTTTCTGACTTTTACCTCCCTCTCTTACTCTTCTT-TTTCTAGTTCTTTCGTAGAAGATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4077 Parachironomus sp. water mite diet isolate 4077-BHL032417-GBD7221_16077-Ldc31 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGCAGGGACTTCTTTAAGAATACTTATTCGAACTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTGGGGGCTCCAAACATGGCTTTCCCTCGATTAAATAATATAAGTTTTTGACTACTTCCCCCTTCTTTAACCCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR285466, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4080 Chironominae sp. water mite diet isolate 4080-BHL032417-GBD21825_24241-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGATCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACATCTTCCCCCTTCATTAACCCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4081 Culex pipiens water mite diet isolate 4081-BHL032417-GBD9701_8351-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAACGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCCTTTATTATAATTTTTTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4082 Chironominae sp. water mite diet isolate 4082-BHL032417-GBD21806_24229-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGATACTTTTATTGGAAATGAGCAAATTTACACTGTAATTGTCACATCACACGCTTTTATTATAATTTTTTTTTTTTATAGTTATGCCAATTTTAATTGGATGTGTTGGAAATTGACTTATTCCTTTAATGTTAGTAGTCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTACATTAACCCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4083 Chironomidae sp. water mite diet isolate 4083-BHL032417-GBD7355_9561-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGTATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTTAATTGGAGGCTTTGGAAATTGAATAGTACCTTTGATATTAGGGGCTACTGAAATAGCTTTTCCGCGAATAAAAAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAAATCAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4084 Chironominae sp. water mite diet isolate 4084-BHL032417-GBD11233_22139-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATACTAATTCGAGCAAAACTTGGACGACCTGGTACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCTCCCTTCATTAACCCTATTACCATCAAGTTCTATTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4085 Chironomidae sp. water mite diet isolate 4085-BHL032417-GBD14643_23126-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.1% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4086 Chironomidae sp. water mite diet isolate 4086-BHL032417-GBD12344_7371-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTCGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTATCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.6% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4087 Chironomidae sp. water mite diet isolate 4087-BHL032417-GBD17614_14553-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGAGAGCCCCTGATAAAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4088 Chironomidae sp. water mite diet isolate 4088-BHL032417-GBD22155_8474-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTAGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCTTCATTAACCATACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4089 Culex sp. water mite diet isolate 4089-BHL032417-GBD13121_28827-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTTGGGGCTTGAGCTGGAATAGTTGTAACTTCTTTAAGTTTACTAATTCGATCAGAATTAATTCAACCAGGTGTATTTATTGGAAATGGTCAAATTTATAATGTTATTGTAACTGCTCATGCCTTTATTATAATTTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTTGAATAAATAATATAAGTTATTGAATATTACCTCCTTCATTGACACGACAACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4091 Psectrocladius sp. water mite diet isolate 4091-BHL032417-GBD26559_21396-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAACTCGAGCAGAACTCGGCCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTAATACCTATTTTAACTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4092 Chironomidae sp. water mite diet isolate 4092-BHL032417-GBD20294_24360-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAAATCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAAATTATAATGTAATTGTTACAGTTCATGCTTTTGTAATAATTTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAATTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4093 Chironominae sp. water mite diet isolate 4093-BHL032417-GBD13510_15092-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAATTTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4094 Chironomidae sp. water mite diet isolate 4094-BHL032417-GBD3317_12853-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATTAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTCAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGAGGATCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4095 Chironomidae sp. water mite diet isolate 4095-BHL032417-GBD21176_27268-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCCTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCTCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4097 Chironomus riparius water mite diet isolate 4097-BHL032417-GBD9275_5873-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4098 Paratanytarsus sp. water mite diet isolate 4098-BHL032417-GBD22571_7564-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGACTATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATACATTTTTTTCATAGTTATACCTTTTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTATTATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4099 Chironomidae sp. water mite diet isolate 4099-BHL032417-GBD27139_12592-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAGACTTTATGGTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGATTTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATACGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACATTATTATTATCTAGATCAATTGTGGAAAATGGCGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4100 Chironominae sp. water mite diet isolate 4100-BHL032417-GBD20457_11156-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGGCAACCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTGTTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTGTCAGGAAGAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4101 Chironominae sp. water mite diet isolate 4101-BHL032417-GBD18845_18979-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTTATCTGGTATAGTAGGTACTTCTTTTAGTATGCTATTTCGAGCAGGACTTGGACGACCTGGTACTTTTATTGGAGATGACCTAATTTACAATGTAATTGTCACAGCACACTCTTTTATTATTAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4102 Culex sp. water mite diet isolate 4102-BHL032417-GBD14853_8814-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTTGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4103 Chironominae sp. water mite diet isolate 4103-BHL032417-GBD23675_13201-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGGGCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGGAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4105 Chironominae sp. water mite diet isolate 4105-BHL032417-GBD11431_14518-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTGGG-GCTTGATCTGGTATAGTAGGTACTTCTTTTAGTATGCTTATTTGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTTCAATGTTATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4106 Chironomidae sp. water mite diet isolate 4106-BHL032417-GBD23756_4838-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTCATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4107 Macrocyclops sp. water mite diet isolate 4107-BHL032417-GBD5327_13957-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGACTTAGTATTTATTGGCAGGTGCTTGAGCGGGGTTAGTAGGAACTGAACATAGAATGATTATTCGACTTGAGTTAGGTCAGCCGGGCAGCTTATTGGGTGATGATCGAATTTATAATGTAGTAGTAACTGCTCACGCATTTGTGATATTTTTTTTTATAGTTATACCAATTTTAATTGGGGGATTTGGAAACTGGTTAGTTCCCCTAATACTAGGGTCTCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTTCTATTGTCCGCTTTAATCTTATTATTGGCTAGGGGCCTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID MF745282, identified in GenBank as Macrocyclops sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4108 Chironomidae sp. water mite diet isolate 4108-BHL032417-GBD5993_7845-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACACTCAAATTTATAAAGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4109 Chironominae sp. water mite diet isolate 4109-BHL032417-GBD22430_12071-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4111 Chironomidae sp. water mite diet isolate 4111-BHL032417-GBD17124_24610-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAAC---TCTTTTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4112 Chironomidae sp. water mite diet isolate 4112-BHL032417-GBD10347_25633-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATCGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGTTATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTATTGCCCCCATCATTAACTTTATTATTATCTAAAAGAATAGTGGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4113 Cricotopus sp. water mite diet isolate 4113-BHL032417-GBD11836_6511-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACATTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4114 Chironomidae sp. water mite diet isolate 4114-BHL032417-GBD25343_22159-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAATAGGCACTTCTTTAAGAATTTTAATTCGGCTAGAATTAGGACACCCAGGGTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCGTCATTAACCTTACTATTATCGAGATCAATAGTAGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4115 Chironominae sp. water mite diet isolate 4115-BHL032417-GBD27568_19579-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCATGATATGGCTTTTCCACGAATAAAAAATATAAGATTTTGATTATTATCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4116 Culex sp. water mite diet isolate 4116-BHL032417-GBD15617_8741-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAATTTTATAATGTTATTGTAACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4117 Chironomidae sp. water mite diet isolate 4117-BHL032417-GBD16959_25236-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTCTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAAGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCAAATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4119 Chironomidae sp. water mite diet isolate 4119-BHL032417-GBD11002_8400-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCCGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGATATACCAATCTTAATTGGAGGATTTGGAAAATGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTAACCACGAAAAAACAATATAAGTTTGTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4120 Culex sp. water mite diet isolate 4120-BHL032417-GBD20967_18197-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGTTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.1% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4121 Orthocladiinae sp. water mite diet isolate 4121-BHL032417-GBD13418_10063-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGATGATCAAATTTATAATTTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGAGTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATACAAGATTTTGATTGTGGCCCCCAGCATTAACTTTATTATTAACCAGATCAATTGTGGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4122 Chironominae sp. water mite diet isolate 4122-BHL032417-GBD11601_18613-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGTGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCGAATTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4123 Culex sp. water mite diet isolate 4123-BHL032417-GBD27748_15948-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGATCTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACACTACTACTATCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.4% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4124 Chironomidae sp. water mite diet isolate 4124-BHL032417-GBD13949_15306-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCAAGCAGAACTTGGACGACCTGGTACTTAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGTGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4126 Chironomidae sp. water mite diet isolate 4126-BHL032417-GBD23394_4367-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACTTGCAGGAGCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTCTCCCACGAATAAAAAATATAAGTGTTTGATTGTTGCACCTATCATTAACTTTATTATTATTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4128 Chironominae sp. water mite diet isolate 4128-BHL032417-GBD25914_23144-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATCTTATTTT-GGAGCTTGATCTGGTATTGTAGGTACTTCTTTTAGTATGCTAATTCGAGCATGACTTGGACGACCTGGTACTTTTATTGGAGATGTCCAAATTTACAATGTAATTGTCACAGCACACGCTTTTTTTATAATTTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACCTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4129 Phaenopsectra sp. water mite diet isolate 4129-BHL032417-GBD24391_17826-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCAGCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4132 Chironominae sp. water mite diet isolate 4132-BHL032417-GBD25275_17118-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTTTAGTATGCTAATTCGAGCCGAACTTGGACGACCTGGTACTTTTATTGAAGATGACCAAATTTACAATGTAATTGTTACAGCACACGCTTTTTTTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCTAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGCTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4133 Chironomidae sp. water mite diet isolate 4133-BHL032417-GBD24529_11607-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGTTCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAAAATTAGGACACCCAGGCTAATTAATCGGAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGAGAATAAATAATATAAGATTTAGATTATTACCCCCTACATTAACCTTACCTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4134 Culex sp. water mite diet isolate 4134-BHL032417-GBD23342_6315-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAGGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTACCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.1% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4135 Chironomidae sp. water mite diet isolate 4135-BHL032417-GBD26155_22248-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGTATAGTTGGTACTTCTTTAAGTATTCTAATTCGAGCAAAATTAGGACATGCAGGCTCATTAATTGGAGAAGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTATTTCCTTTAATATTAGGAGCCCCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4136 Chironominae sp. water mite diet isolate 4136-BHL032417-GBD13990_10566-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACACAGGCTCATTAATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4138 Chironominae sp. water mite diet isolate 4138-BHL032417-GBD4692_8302-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4139 Chironomidae sp. water mite diet isolate 4139-BHL032417-GBD9071_23600-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGTAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGATTTTTAATTCGACTATAATTAGGACACCCATGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGACTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCTCTTCATTAACCTTACTTTTATCAAAATCAATAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4140 Chironomidae sp. water mite diet isolate 4140-BHL032417-GBD8111_10692-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGTGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTAAAGCACATGCTTTTGTAATAATTTTTTTTATAATGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTGGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTAACCCCATCATTAACCTTACTTTTATCAAAAACAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4142 Chironomidae sp. water mite diet isolate 4142-BHL032417-GBD21675_22348-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGTTCCGGAATAGTTGGAGCTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACATGCAGGCTCATTAATTGGAGACGAACAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATATTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAAAATAAGTTTTTGATTGTTGCCAGCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4143 Orthocladius sp. water mite diet isolate 4143-BHL032417-GBD24514_11442-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTATTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4146 Chironomidae sp. water mite diet isolate 4146-BHL032417-GBD9182_18618-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTAATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGGCATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAAAAATATAAGTTGTTGATTGTAGACCCAATCATTAACGTTATGATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4147 Orthocladiinae sp. water mite diet isolate 4147-BHL032417-GBD7306_9447-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGTAATAGTTGGAACTTCTTTAAGAATTCTAGTTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGGTCAAATTTATAATGTAATTGTTACAGCTCGTGCTTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4148 Chironominae sp. water mite diet isolate 4148-BHL032417-GBD3687_12883-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCGTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTCACAGCACACGCTTTTTTTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCCTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4149 Diptera sp. water mite diet isolate 4149-BHL032417-GBD29526_16087-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTATTTAAGTTTGCTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGGTCAAATTTATAATGTTATTGTAACTGCTCATGTCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTAAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATGTTGATTATTACCCCCTTCATTAACCTTACTTTGATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4150 Chironominae sp. water mite diet isolate 4150-BHL032417-GBD4358_11006-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTCAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATAGGAGATGACCAAATTTACAATGTAATTGTCACTGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTCTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCATCATCAACTCCTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4151 Chironominae sp. water mite diet isolate 4151-BHL032417-GBD18428_23145-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACATTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTCGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCATTAACTCTTTTACTTTCATGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4152 Orthocladiinae sp. water mite diet isolate 4152-BHL032417-GBD25768_14012-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTTTATTTTATTTTCGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACATGCAGGCTCATTTATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTCCCACGAATAAATAATATAAGATTTTGACTGTTGCCCCCATCATTAACTTTATTATTATCTAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4155 Chironominae sp. water mite diet isolate 4155-BHL032417-GBD15261_20729-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAAATTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4156 Chironominae sp. water mite diet isolate 4156-BHL032417-GBD7152_24487-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTCAAGTATGCTTATTCGAGCAGGACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTTATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGTACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGAATTCTTCCCCCCTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4157 Culex sp. water mite diet isolate 4157-BHL032417-GBD26185_12157-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAACTTTATAATGTTATTGTAACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4158 Chironominae sp. water mite diet isolate 4158-BHL032417-GBD11839_5048-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATGTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTTATGTATGCTAATTCGAGCAGAACTTGGACGAACTGGTACTTTTATTGGAGATGACTAAATTTACAATGTACTTGTCACAGCACACGCTTTTATTATAAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGAGTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4160 Culex sp. water mite diet isolate 4160-BHL032417-GBD28075_13570-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCACAAAGATATTGGAACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGATCAGAATTAAGTCAACCAGGTGTATTTTTTGGAAATGGTCAAATTTATAATGTTATTGTAACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTTGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACACTACTACTATCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.1% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4163 Chironominae sp. water mite diet isolate 4163-BHL032417-GBD26176_19272-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATCCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACCCTTTTTCTATCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4164 Chironomidae sp. water mite diet isolate 4164-BHL032417-GBD17292_17228-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGATGATTTGGACACTGACTAGTTCCTTTAATATTAGGAGCACCTGATACGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGAACCAATCATTAACTTTATTATGATCTAGATCAATTGTGGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4165 Chironominae sp. water mite diet isolate 4165-BHL032417-GBD20293_8021-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGGTCTGGTATAGTAGGTACTTCTTTAAGTATGCTTATTCGAGCATGACTTGGACTATCTGGTAATTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4168 Chironomidae sp. water mite diet isolate 4168-BHL032417-GBD26751_23831-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTGTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCCGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGAATAGTTCCTTTAATATTAGGAGCACCTGATATGGCCTTCCCACGAAAAAATAATATAAGTTTTTTGATTGTGGCCCCCATCATTAACTGTATTATTATCTAGAGCAATTGTGTAAAATGGAGCCGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4169 Chironominae sp. water mite diet isolate 4169-BHL032417-GBD13392_3799-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTCTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTTGTACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAAATCTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGTCTTCTTCCCCCTTCATTAACCCTTTTACTTTCAAATTCTATTGTAGAAAATGGCGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4171 Chironominae sp. water mite diet isolate 4171-BHL032417-GBD7035_18152-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCTTTAAGTATGCTAATTCAAGCAGAACTTGGACGACCTGGCACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACCCTTTTACTTTCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4172 Chironomidae sp. water mite diet isolate 4172-BHL032417-GBD4603_10826-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAACTTTATTTTATTTTCGGAGCTTGATTAGGAATAGTTGGAACTTCTTTAAGTATTCTAATTCGAGCAGAAGTAGGACATGCAGGTTCATTAATTGGAGACGATCAAATATATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTCGCCCCCATCATCAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4173 Chironomidae sp. water mite diet isolate 4173-BHL032417-GBD11199_16107-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTAATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4174 Orthocladiinae sp. water mite diet isolate 4174-BHL032417-GBD22221_23525-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGATCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATAATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTATGAGCACCTGATATGGCTTTCCCACGAATAAATAACATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGAACAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4175 Chironominae sp. water mite diet isolate 4175-BHL032417-GBD15428_3929-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTT-GGAGCTTGAGCGGGTATAGTAGGTACTTCTTTAAGTATGCTAAGTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGACATGACCAAATTTACAATGTAATTGTCACAGCACACGCCTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4176 Culex sp. water mite diet isolate 4176-BHL032417-GBD9613_4848-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGATTAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCCTTTATTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTTCATTAACCTTACTTTTATCAAGATCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.7% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4178 Culex sp. water mite diet isolate 4178-BHL032417-GBD20522_17496-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGAGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAACAGAATTACGTCAACCAGGTGTATTTATTGGAAATGGTCAAATTTATAATGTTATTGTAACTGCTCATGCCTTTATTATAATTTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCACCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATAGTGGAAAATGGAGCTGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4179 Chironomidae sp. water mite diet isolate 4179-BHL032417-GBD15208_21611-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTCATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCACGAATAAATAGTATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTACCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4181 Chironomidae sp. water mite diet isolate 4181-BHL032417-GBD29162_12552-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTGAGTATACTTATTCGAGCAGAATTAGGACGCCCAGGAACTTTTATTGGAGATGATCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGTTTCTTCCACCGTCTCTAACTCTTCTACTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR287035, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4182 Chironominae sp. water mite diet isolate 4182-BHL032417-GBD2283_13429-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTTATTCGTGCTGCACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACAAGCATTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4186 Chironominae sp. water mite diet isolate 4186-BHL032417-GBD21320_16430-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGGACTTGGACGAACTGGTACTTTTCTTGGAGATGACCAAATTTACAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGGGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4188 Chironominae sp. water mite diet isolate 4188-BHL032417-GBD12325_10079-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGGACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTCTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCACCATCATTAACTCTATTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4189 Chironomidae sp. water mite diet isolate 4189-BHL032417-GBD9350_10455-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTACGTCAACCAGGTGTATTTATTGGAAATGGTCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTGGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4191 Cryptochironomus sp. water mite diet isolate 4191-BHL032417-GBD7556_13712-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCATGCTGTTATTATAATTTTTTTCATGGTTATACCATTTTTTAATTGGAGGATTTGGAAATTGATTAGAACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4192 Chironominae sp. water mite diet isolate 4192-BHL032417-GBD9253_26626-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTAGTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATATTTTTTTTTATAGTTATGCCCATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTTTATTATTATCTAGATCAATTGTGTAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4193 Chironominae sp. water mite diet isolate 4193-BHL032417-GBD15740_11691-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGCATAGTAGTTACTTCTTTATGTAGGCTAATTCGAGCAGTACTTGGACGACCTGGTACTTTTATAGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCCTATTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4195 Chironomidae sp. water mite diet isolate 4195-BHL032417-GBD21267_13600-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATATCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4196 Chironominae sp. water mite diet isolate 4196-BHL032417-GBD12802_14667-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGGATGCTAATTCGGGCAGAACTTGGACGACCTGGTATTTTTATTGGAGATGACCAAATTTACAATTTAATTGTCACAGCACACGCTTTTTTTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAAAGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4199 Chironomidae sp. water mite diet isolate 4199-BHL032417-GBD26380_23966-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTTATCGGAGACGAACAAATTTATAATGTAATTGTTACGGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGGCTTTCCGCGAATAAGAAATAAAAGATTTTGAATAATACCCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4200 Chironominae sp. water mite diet isolate 4200-BHL032417-GBD22965_22978-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATTGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGGACTTGGCCAAACTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACACTTTTCTTATAATTTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTTTTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4201 Chironomidae sp. water mite diet isolate 4201-BHL032417-GBD28475_17908-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAAACGATCAAATTTATAATGTAATTGTTACATCACATGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGCAAATTGATTAGTACCTTTGATATTTGCGTCTCCTGATATAGCTTTTCCGCGAATAAAAAAAATAAGATTTTGATTACTACCACCTGCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4203 Lebertia sp. water mite diet isolate 4203-BHL032417-GBD20766_16101-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGGACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTGCCTCCATCCTTAACTCTACTACTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4207 Chironomidae sp. water mite diet isolate 4207-BHL032417-GBD28755_13649-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAAACGATCAAATTTATAATGTAATTGTTACAGCACATGATTTTATAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATAGATTAGTACCTCTGATATTAGGGGCTCCTGATATAGCTTTTCCGAGAATAAATAATATAAGATTTAGATTATTACCCCCTTCATTAACCTAACTTTTATCAAGATCAATAGTATAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4209 Chironomidae sp. water mite diet isolate 4209-BHL032417-GBD4988_20172-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGTAGCATTCGGACCCCCAGGCTCATTAATCAGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCCTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTGACTTTTATCAAAATCAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4210 Chironominae sp. water mite diet isolate 4210-BHL032417-GBD17574_5542-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTT-GGAGCATGATCGGGTATAGTAGGTACTTCTTTAAATATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCATATTTACAAGGTAATTGTCACAGCACACGCTTTTATTATAGTTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4211 Chironomidae sp. water mite diet isolate 4211-BHL032417-GBD27854_14784-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTTATCAATCAGAAAAGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTGTATAGTGATGCCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTGATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4212 Chironomidae sp. water mite diet isolate 4212-BHL032417-GBD22320_11802-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTTTATTTTATTTTCGGAGCTTGATCAGGAATATTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAAAAATTTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTGTGAATGTTGCCCCCATCATTAACATTATAATAATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4213 Chironominae sp. water mite diet isolate 4213-BHL032417-GBD12053_28219-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTTATGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTCATTGTCACAGCACACGCTTTTATTATATTTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGAAATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCCATTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4214 Culex sp. water mite diet isolate 4214-BHL032417-GBD15012_24515-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTCTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTATATTTATTGGAAATGGTCAAAATTTATAATGCTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATATTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCCGATATGGCCTTTCCTCGAATAAATAATATAAGTTCCTGACTACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4216 Chironomidae sp. water mite diet isolate 4216-BHL032417-GBD6224_9584-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATGTTATTTTTGGAGCTTGAGCGGGTGTAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAAGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATGTTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTATAGCAAGATCAATAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4217 Chironomidae sp. water mite diet isolate 4217-BHL032417-GBD27479_13720-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCCAATTCGAGCAGAATTATGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAAGATTTGGAAACTGACTAATTCCTTTAATATTAGGAACACCTGATATGGCCTTCCCCCGAATAAAAAAAATAAGTATTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4221 Chironominae sp. water mite diet isolate 4221-BHL032417-GBD20577_27212-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATTGTAGGTACTTCTTTCAGTATGCTAATTCGAGCTGAACTTGGACGAACTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGCCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTGCTAATGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4222 Chironominae sp. water mite diet isolate 4222-BHL032417-GBD14279_8298-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATAGGAGATGACCAAATTTACAATGTAATTGTCACAGCACAAGCTTTTCTTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGATTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCATCATTAACCCTTTTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4223 Chironominae sp. water mite diet isolate 4223-BHL032417-GBD7622_19708-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACCGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCCATCATTAACTTTATTATTATCTAGATCAATCGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4226 Chironominae sp. water mite diet isolate 4226-BHL032417-GBD5653_11905-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTTTTTAAGTATGCTAATTCGAGCAGGAATTGGACGACCTGGGACTTTTATTGGAGATGACTAAATTTACAATGTAATTTTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAATCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4228 Chironomidae sp. water mite diet isolate 4228-BHL032417-GBD17490_2254-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTGTATTTTATTTTCGGAGCTTGATAAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACAGTCAGTCTCATTAATTGGAGACGATCTAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGAGTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCTCCTGATATGGCTTTCCCACGTATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4233 Chironominae sp. water mite diet isolate 4233-BHL032417-GBD3800_17669-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCAAGCAGAACTTGGTCGGCCTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACCCTACTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4234 Chironominae sp. water mite diet isolate 4234-BHL032417-GBD24079_12597-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATTGTAGGTACTTCTTCAAGTATGCTAATTCGAGCAGAACTCGGACGACCTGGTACTTTTATTGGAGATAACCAAATTTACAATGTAATTGTCACAGCACACGCTTTCATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGCTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4236 Chironomidae sp. water mite diet isolate 4236-BHL032417-GBD18927_28322-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGATCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTATTACCCCCTTCATTAACC---CTTTTACTTTCAAGTTCTATTATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4238 Chironominae sp. water mite diet isolate 4238-BHL032417-GBD16243_3532-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTT-GGAGCTTGAACGGGGATAGTAGGTACCTCTTTAAGGATGCTAAATCGAGCAGAACTTGGACTACCTGGTACCTTTATTGGAGATGACCAAATTTACAATGTAATTGTGACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATTCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4241 Orthocladiinae sp. water mite diet isolate 4241-BHL032417-GBD14758_28404-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGAAACTTCTTTAAGAATTTTAATTCGAGTAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTAGCTCCTTTAATATTAGGAGCACCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCTTCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4242 Chironomidae sp. water mite diet isolate 4242-BHL032417-GBD23933_23185-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGGGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAAAAATATAAGATTTTGATTATTACCCCCTTCATTAACCTAACATAAAGCAAGAGCAAGAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4245 Chironomidae sp. water mite diet isolate 4245-BHL032417-GBD23751_6977-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTCGAATTATGACACCCAGGCTCATTCATCGGAGAAGATCAAATTTATAAGGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAAATTTTGATTATTACCCCCATCATTAACCTTACTTTTATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4248 Culex sp. water mite diet isolate 4248-BHL032417-GBD15883_3344-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGGCAACAAATCATAAAGATATTGGAACAGTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTGTACTAATTCGAGCAGAATTAAGTCAACCAGGTTTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTTGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCTTATATGGCCTTTCCTCGAATAAATAATATAAGTTCTTGAATTCTTCCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGCGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4249 Culex sp. water mite diet isolate 4249-BHL032417-GBD9051_18803-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTGCTAATTCGAGCAGAACTAGGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATTATAAATGGAGGATCTGGAAATTGATTAGTTTCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACCCTTCTACTTTCAAGTAGTTTAGTAGAAAATGGAGCCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4251 Lebertia sp. water mite diet isolate 4251-BHL032417-GBD3733_11845-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAGTAGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTATAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGGTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCACCATCCTTAACCCTACTACTAACAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4252 Chironomidae sp. water mite diet isolate 4252-BHL032417-GBD17771_20934-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTGTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGGATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4253 Chironominae sp. water mite diet isolate 4253-BHL032417-GBD24349_4631-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGCATAGTAGGTACTTCATTCTGTATGCTAATTCGAGCAGTACTTGGACGACCTGGTCCTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTATGACTTCTTCCCCCTTTCAGTAACTCTTTTACTTTCAAGTTCTAGTGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4256 Chironominae sp. water mite diet isolate 4256-BHL032417-GBD2571_14541-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTATTCCTTTCAGTATGCTAATTCGAGCAGTACTTGGACGACCTGGTACCTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATGTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4259 Chironominae sp. water mite diet isolate 4259-BHL032417-GBD18774_5992-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTT-GGAGCTTGATCGGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACAACCTGGTACTTTTATTGGAGATGACCAATTTTACAATGTACTTGTCACAGAACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTGTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4261 Chironominae sp. water mite diet isolate 4261-BHL032417-GBD4418_17602-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTTATCTGGTATAGTAGGTACTTCTTCATGTATGCTAATTCGATCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATATTATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCCTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4265 Chironomidae sp. water mite diet isolate 4265-BHL032417-GBD18953_22344-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGTATAGTTGGAACTTCTTTAAGAATTCTTATTCGAGCAGAATTAGGACATGCAGGCACATTCATTGGAGACGATCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTGTTATAATTTTTTTTATAGTTATACCAATCTTAATTTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGAATGTTGCCCCCGTCATTAACTTTATTAATATCTAGATCAATTGTGGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4267 Chironomidae sp. water mite diet isolate 4267-BHL032417-GBD19024_13913-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATAGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCTAATAAATAATATAAGATTTTGATTATAAACCCCTGCAAGAACCTGACGTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4272 Chironominae sp. water mite diet isolate 4272-BHL032417-GBD25366_19754-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCCTGATCTGGCATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGGACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCACACGCTTTTATTATTATTTTTTTTATAGTTATTCCAATTTTAATTGGAGGGTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4273 Chironomidae sp. water mite diet isolate 4273-BHL032417-GBD10716_12049-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTAAAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAAGAGAAGTTTTTGATTGTTGTCCCCATCATTAACATTATAATAAGCTAGAGCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4274 Chironominae sp. water mite diet isolate 4274-BHL032417-GBD20223_14750-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCAAGCAGAACTTGGACGACCTGGTACTTTTATTGTAGATGAGCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAAC---CTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4276 Paratanytarsus sp. water mite diet isolate 4276-BHL032417-GBD12235_27067-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAACTGAACTAGGACATCCCAGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTTCTATCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4277 Chironomidae sp. water mite diet isolate 4277-BHL032417-GBD20283_20201-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTCTGGAAATTGATTAGTACCTTTGATATTAGAGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTAATACCCCCTACATTAACCTAGCCATTAGCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4278 Chironomidae sp. water mite diet isolate 4278-BHL032417-GBD25689_9957-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATATTTCTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTAACTTTGATATTAGGGGCTCCCGATATAGCTTTTCCGCGAATAAAAAAAAAAAAAATTTTGAATATTACCCCCTTCATTAACCTTACCTTTAACAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4279 Chironomidae sp. water mite diet isolate 4279-BHL032417-GBD26464_23870-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAAAAATAAAAGTTGTTGATTGTTGCCCCCATCAGTAACTTAATGATAATCTAGAACAATTGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4280 Orthocladiinae sp. water mite diet isolate 4280-BHL032417-GBD8276_25773-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAATTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCAGGCTCATTAATTGGAGAAGATCAAATTTAAAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTATTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4284 Chironomidae sp. water mite diet isolate 4284-BHL032417-GBD24358_20181-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTTAGAATTTTAATTCGACTAGAATTAGGACATCCAGGATAATTAATTGGAGACGATCAAATTTATAATGTTATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4285 Chironomidae sp. water mite diet isolate 4285-BHL032417-GBD17315_19502-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATACTAATTCGAGTAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAAATTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATATTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCAGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACTTTATTAATATCTAGAGCAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4286 Chironominae sp. water mite diet isolate 4286-BHL032417-GBD18603_28215-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGCTCTGGGATAGTTGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTTGCCGAACTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGAATTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4292 Chironomidae sp. water mite diet isolate 4292-BHL032417-GBD16414_14139-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTGAGAATTCTAATTCTAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTGTGATCGTGGCCCCCATCATTAACATTATAATAATCTAGAGCAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4293 Chironominae sp. water mite diet isolate 4293-BHL032417-GBD22355_10278-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTTTTGTATGCTAATTGGTGCAGAACTTGGATGACCTGGTACTTTTATTGGAGATGACCAAATTTTCAATGTAATTGTCACAGCACACGCTTTTATTATATTTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACATCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4294 Chironomidae sp. water mite diet isolate 4294-BHL032417-GBD13758_24302-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAATATTTTGGTTATAACCCACTTCATTAAACTGACGTTGATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4295 Culex sp. water mite diet isolate 4295-BHL032417-GBD26655_10728-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAAAATTATATTTATTTTTGGGGCTTGAGCTGGAATAGCTGGAACTTCTTTAAGTTTACTAATTCTGGCAGAATTAAGTCAACCAGGTGTATTTTTTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTTATTCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCATTTCCTCGAATAAATAATATAAGTTCTTGAATACTACTTCCTTCATTGACACTACTAATTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4301 Culex sp. water mite diet isolate 4301-BHL032417-GBD5187_7977-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTTGGGGCTTGAGCTGGATTAGTTGGACCTTCTTTAAGTTTACTATTTCGAGCAGAATTGAGCCAACCAGGTGTATTTATTGGAAATGGTCAAATTTATAATGTTATTGTAACTGCTAGTGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTTGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACACTACTACTATCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4304 Chironominae sp. water mite diet isolate 4304-BHL032417-GBD4117_18922-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTACTTTATTTTTGGAGCTTGATCCGGAATAGTAGGAACATCTTTAAGAATACTAATTCGAGCAGAATTAGGACATCCAGGAACATTGATTGGGGATGATCAAATTTACAACGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTTAATTGGTGGGTTTGGAAATTGACTTTTACCTTTAATACTTGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCATCTATTTCATTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR759090, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4305 Chironominae sp. water mite diet isolate 4305-BHL032417-GBD3366_20182-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGGTCTGGTATTGTAGGTACTTCTTTAAGGATGCTAATTCGAGCAGGACTTGGAAGACCTGGTACTTTTAATGGAGATGAACAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGAAATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4306 Chironominae sp. water mite diet isolate 4306-BHL032417-GBD25655_17704-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTTATCTGGTATAGTAGGTACTTCTTCTAGGATTCTTATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACTATGTAATTTTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTACATTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4308 Chironominae sp. water mite diet isolate 4308-BHL032417-GBD9579_12556-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTTATGTATGCTAATTCGATCAGACCTTGGACGACCTGGTACTTTTAATGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCGTCGAATAAATAATATAAGTTTTTGACTTCGTCCCCCTTCATTAACTCTTTTACTTTCAAATTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4309 Chironomidae sp. water mite diet isolate 4309-BHL032417-GBD4597_21353-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGATAACCTGATATGTCTTTCCCACCAATAAATAATATAATTTTTTGATTGTTGACCACATCATTAACTTGATTATTATCTAGATCAATTGTGGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4310 Chironominae sp. water mite diet isolate 4310-BHL032417-GBD16138_2258-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTT-GGAGCTTGATCGGGGATAGTAGGTACTTCTTTAAGTATGCTAAGTCGAGCAGAACTCGGACGACCTGATACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATTATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCCTTTACATTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4314 Chironominae sp. water mite diet isolate 4314-BHL032417-GBD26624_19816-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGATATAGTAGGTACTTCTTTAAGTATGCTAATTCAAGCAGAACTTAGACGACCTGGTACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATGCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTGCGTCCCCCTGCATTAACCCCTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4317 Chironominae sp. water mite diet isolate 4317-BHL032417-GBD28575_11593-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTT-AGCTTTATCTGGTATTGTAGGTACTTCTTTAAGTATTCTTATTCGGGCAGGACTTGGACGACCTGGGACTTTTATTGGAGATGACCAAATTTACAATGTTATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAATTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4324 Culex sp. water mite diet isolate 4324-BHL032417-GBD28547_15508-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTTTATTTATTGGAGATGGTCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAGATTAATTACTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTTGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACACTACTACGATCAAGTAGTTTAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4325 Chironominae sp. water mite diet isolate 4325-BHL032417-GBD20867_16359-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTTTTTTAGTATGTTAATTTGAGCAGGACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTATTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4328 Chironominae sp. water mite diet isolate 4328-BHL032417-GBD26895_20256-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATCGTAGATACTTCTTTTAGTATGCTTATTCGAGCAACACTTGGACGACCTAGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAATCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4330 Chironominae sp. water mite diet isolate 4330-BHL032417-GBD26542_19942-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTTTAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTTCAATGTAATTGTTACAGCACACGCATTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTACTCCTTTAATGTTAGGAACCCCATATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4336 Chironominae sp. water mite diet isolate 4336-BHL032417-GBD8739_12069-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGATACTTTTATTGGAGATGACCAATTTTACAATGTAATTGTCACAGTACACGCTCTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTATTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4337 Culex sp. water mite diet isolate 4337-BHL032417-GBD22215_21800-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCCGGAATTGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGGTCAAATTTATAATGTTATTGTAACTGCTCAAGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGACCTTTCCTTGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACACGACTACGTTCAAGTAGTCTAATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4338 Chironominae sp. water mite diet isolate 4338-BHL032417-GBD26731_15702-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGAAGACCAAATTTACAATGTAACTGTCACAGCACACGATTTTATTATAATTTTTTTTAGAGTTATGCCAATTTTAATTGGAGGTTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4339 Chironominae sp. water mite diet isolate 4339-BHL032417-GBD14451_2745-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTT-GGAGCTTGATCGGGTATAGTAGGTACTTCGTTAAGTATGCTAAGTCGAGCAGAACTTGGACGACCGGGGACTTTTATTGGAGATGACCAATTTTACAAGGTAATTGTAACAGAACACGCTTTTATTATAATTTTTTTTATAGTTATTCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTCCTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4341 Chironominae sp. water mite diet isolate 4341-BHL032417-GBD23294_7002-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCCTGGTCTGGTATTGTAGGTACTTTTTTTTGTATGCTTATTTGGGCCGGACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4343 Chironomidae sp. water mite diet isolate 4343-BHL032417-GBD5468_21034-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATAAGTTCCTTTGATATTAGGAGCTCCTGATATAGCTTTCCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACGTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4345 Chironomidae sp. water mite diet isolate 4345-BHL032417-GBD4387_9381-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTATTTTATGTTCGGAGCTTGATCAGGATTAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGAACAAGTTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACTTTATTACTATCTAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4346 Chironomidae sp. water mite diet isolate 4346-BHL032417-GBD16841_13456-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATACTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAAGATTTGGAAACTGACTAGTTCCTTTAATATTAGGATCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTAGACCACATCATTAACATTATGATGATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4347 Chironominae sp. water mite diet isolate 4347-BHL032417-GBD12086_7201-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTTTAGTATGCTATTTTGAGCATAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATATACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTACTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTGTCAAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4352 Chironominae sp. water mite diet isolate 4352-BHL032417-GBD18629_13331-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGGTCTGGTATAGTTGGTACTTCTTTAAGTATGCTAATTTGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACTATGTAATTGTCACAGCACACGCTTTTATTGTTATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTAAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4356 Chironominae sp. water mite diet isolate 4356-BHL032417-GBD28214_18086-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTAATTCTTTTAGTATGCTAATTTGAGAAGAAATTGGACGATCTGGTACTTTTATTGGAGATGACTAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCCATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4358 Chironominae sp. water mite diet isolate 4358-BHL032417-GBD5996_12474-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTCCTTTAAGTATACTAATTCGAGCAGAACTTGGACAACCTGATACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4359 Chironomidae sp. water mite diet isolate 4359-BHL032417-GBD10482_10059-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTTGGGTTTGAGCTGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTCTGATTGTTGCCCCCATCATTAACTTTATGATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4361 Chironomidae sp. water mite diet isolate 4361-BHL032417-GBD3096_9772-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCCCACGCCTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCTTCATTAACCTTATTTTTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4363 Chironomidae sp. water mite diet isolate 4363-BHL032417-GBD25258_20118-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATGCAGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAAATTTTTTTAGAGTTATACCAATCTTAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAAAAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4367 Chironominae sp. water mite diet isolate 4367-BHL032417-GBD5286_20807-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTAATCTGGTATAGTAGGAACTTCTTTAAGAATGTTAATCCGAACGGAATTAGGTCATCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4372 Chironominae sp. water mite diet isolate 4372-BHL032417-GBD13807_4452-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTT-GGATCTTGATCGGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTAACAGCACACGCCTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTACTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGACCAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4373 Chironomidae sp. water mite diet isolate 4373-BHL032417-GBD25875_13992-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTATTAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTAATTAACCTTACTATTATCAAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4378 Chironominae sp. water mite diet isolate 4378-BHL032417-GBD10053_4983-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTAGGATAGTAGGTACTTCTTTTAGTATGCTAATTCGGGCAGAAATTGGACGACCTTGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACATCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAATCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4381 Chironominae sp. water mite diet isolate 4381-BHL032417-GBD14875_5473-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTT-GGAGCTTGAACGGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGGACCTTTATTGGAGATGACCAAATTTACAATGTAATTGTGACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTGTTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTCTTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4382 Chironomidae sp. water mite diet isolate 4382-BHL032417-GBD3761_19280-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTCTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAAAAGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAAGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATAAAGCTTTTCCCCGAAAAAAAAAAAAAAATTTTGATTATTAACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4384 Chironominae sp. water mite diet isolate 4384-BHL032417-GBD12660_9284-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATACTTTATTTTTGGAGCTTGATTTGGTATAGTAGGTACTTCTTTAAGTATGCTTATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAGCAAATTTACAATGTAATTCTCACAGCCCACCGTTTTATTATAATTTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAAAAAATAATATAAGTTTTCGACTTCTTCCCCCTTCATTAACCCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4385 Orthocladiinae sp. water mite diet isolate 4385-BHL032417-GBD8394_3512-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAAGTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGTAGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCTTCATTAACTCTTTTTCTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4386 Chironominae sp. water mite diet isolate 4386-BHL032417-GBD18691_2457-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTT-GGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGTACGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCATATTTACAAGGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAAC---TTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4387 Chironominae sp. water mite diet isolate 4387-BHL032417-GBD13304_4933-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTT-GGAGCTTGAGCGGGGATAGTAGGTACTTCTTTAAGTATGCTAAATCGAGCAGAACTTGGACGATCTGTTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTAACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCTCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4389 Chironominae sp. water mite diet isolate 4389-BHL032417-GBD14532_3997-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTT-GGAGCTTGAGCGGGGATAGTAGGTACTTCTTCAAGGATGCTAAATCGAGCAGAACTTGGACGACCTGGGACTTTTATTGGAGATGACCAAACTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTCTTGTAGAAAATGGAGCTGGACCAG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL439 Oligochaeta sp. water mite diet isolate 439-BHL040517-GBD16207_16981-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTGCCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTTCTAATTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL4397 Chironominae sp. water mite diet isolate 4397-BHL032417-GBD5494_13735-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTCAAGTATGCTAATTCGAGCAGAACTTAGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAATCAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTGACTTTCAAGTTCTATTGTAGAAAACGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4398 Chironominae sp. water mite diet isolate 4398-BHL032417-GBD4148_21416-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGGGCAGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATGGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCGCGAATAAATAATATAAGTTTTTGACTTCTTCCCCACTTCATTAACTCTTTTACTTTCAAGTTCTATTCTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL440 Chironomus riparius water mite diet isolate 440-BHL040517-GBD25857_19453-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTAACTTGT-CCCATAATACTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGGCTTTTACCCCCCTCTCATACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4400 Chironominae sp. water mite diet isolate 4400-BHL032417-GBD22934_3794-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGGTCTGTTATAGTAGGTACTTCTTTTAGTATGCTAATTCGAGCAGGACTTGGACGACCTGGGACTTTTATTGGAGATGACCAAATTTACAATGTTATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAAGAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4402 Chironominae sp. water mite diet isolate 4402-BHL032417-GBD29220_13073-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATTGTAGGTAATTCTTTTAGTATGATAATTCGAGTAGGAATTGGGCGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCACAAGCTTTTATTATAATTTTTTTTATAGTTATGCCCATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCTTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4406 Chironominae sp. water mite diet isolate 4406-BHL032417-GBD11095_3860-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGATACTTCTTTAAGTATGCTAATTCGAGCAGTACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACCCGCTTTTATTATAATTTTTTTTATAGTTAGGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTCTACCTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4410 Chironominae sp. water mite diet isolate 4410-BHL032417-GBD13865_29088-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATTGTAGGTACTTCTTTTTGTATTCTAATTTGAGCTGTACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCACACGCTTTTATTATTATTTTTTTTTATAGTTATGCCGATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGATCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4412 Chironominae sp. water mite diet isolate 4412-BHL032417-GBD14563_4489-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTT-GGAGCTTGAGCGGGTATAGTAGGTACTTCTTTAAGTATGCTAAGTCGAGCAGAACTTGGACGACCTGGAACATTTATTGGAGATGACCAAATTTACAATGTAAGTGTAACAGAACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTTGAAATTGACTTATTCCTTTAATGTTAGGAACCCCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4416 Chironomidae sp. water mite diet isolate 4416-BHL032417-GBD13384_13541-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTGAAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTCTAATATTAGGAGCTCCTGATATAGCTTTTCCGAGAATAAATAATATAAGATTTTGATTATTACCACCATCACTAACCTTACTTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4417 Chironomidae sp. water mite diet isolate 4417-BHL032417-GBD18314_3303-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTGTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATGCGAGCAGAAGTAGGACATTCAGGCTCATTAATTGGAGACGATTAAATTTATAATGAAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4418 Chironominae sp. water mite diet isolate 4418-BHL032417-GBD20663_19484-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTTCAATGTAATTTTCACAGCACACGCCTTTATTATAATTTTTTTTATAGTTATATCAATTTTAATTTGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4419 Chironominae sp. water mite diet isolate 4419-BHL032417-GBD26165_16834-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTTAATTATGCTACTTCGAGCAGAACTTGTACGACCTGATACTTTTATAGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATTGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGATTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTGTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4420 Chironominae sp. water mite diet isolate 4420-BHL032417-GBD1860_16036-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTG-AGCTTTATCTGGTATTGTAGGTACTTCTTTTAGTATTCTAATTCGAGCAGAACTTGGACTACCTTGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACCGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATTTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTATTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4422 Culex sp. water mite diet isolate 4422-BHL032417-GBD29220_13524-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGATCATTATATTTTATTTTTGGTGCTTGAGCAGGAACAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGAGTATTTATTGGAAATGATCAAAATTATAATGTTATTGTAACTGCTCATGCCTTTATTATAGTTTTTTTTCATAGTAATACCAATTATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTCTTGAATACTACCTCCGTCATTGACACTACCACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4425 Chironominae sp. water mite diet isolate 4425-BHL032417-GBD21564_26970-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTTGTATAGTAGGTACTTCTTTTAGTATTCTCATTCGAGCAGTACTTGGACGAACTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAACACACGCTTTTTTTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL443 Amphichaeta raptisae water mite diet isolate 443-BHL040517-GBD13594_21742-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL4430 Chironominae sp. water mite diet isolate 4430-BHL032417-GBD25041_7491-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTGTAGTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCTGTACTTGGACTACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4431 Chironominae sp. water mite diet isolate 4431-BHL032417-GBD22556_4317-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGTACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTCCCCTCGACTAAATAATATAAGTTTTTGACTTCTTCCCCCTTCAATAACGCGTTTACGTTCAAGTTCTATTGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4433 Chironomidae sp. water mite diet isolate 4433-BHL032417-GBD24193_13325-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGTCACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAATGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGAATATTGCCCCCTTCATTAACCTTACATTAATCAAGAGCAATAGTAGAAAATGGAGCTGGAGCAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4436 Chironomidae sp. water mite diet isolate 4436-BHL032417-GBD27499_21286-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGTAATAGTAGGCACTTCTTTAAGAATTTTAATTCTACTAAAATTAGGATACCCAGACTCATTAATCGGAGGCGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTTTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGTCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACCTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4437 Orthocladiinae sp. water mite diet isolate 4437-BHL032417-GBD6698_22931-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCATAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATTATGTAATTGTTACAGCTCATGCTTTTGTAACAATTTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGGGCTCCTGGTATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL444 Chironomus crassicaudatus water mite diet isolate 444-BHL040517-GBD8557_10954-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAGTTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAATTCATTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4440 Oligochaeta sp. water mite diet isolate 4440-BHL032417-GBD28362_14870-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATTAACTATATAATACTCTAGTAACTGCACATGCATTCATAATAATTTTCTTTCTGGTTATACCAGTTCTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTCCCCACGACTTAACAATTTAAGATTCTGACTACTACCCCCTTCACTAATCCGATTAGTGTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL4443 Chironomidae sp. water mite diet isolate 4443-BHL032417-GBD2062_16765-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGGGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTGATATTAGGGGCCCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCCTCATTAACCCTACTTTTATCAACAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4444 Culex sp. water mite diet isolate 4444-BHL032417-GBD26889_23232-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGATCATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTATTAATTCGAGCAGAATTAAGTCAACCAGGTGCATTTATTGGAAATGGTCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATAGCCTTTCCTTGAATAAATAATATAAGTTCTTGAATACTTCCTCCTTCATTGACACTACTACTATCAAGTAGTTTAGTAGAAAATGGAGCTCGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4446 Chironominae sp. water mite diet isolate 4446-BHL032417-GBD13501_27368-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTTTAGTATGCTAATTCGAGCAGTACTTGGACGACCTGGTACTTTTATTTGAGATGACCAAATTTTCAATGTAATTGTCACAGTACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCGTCCCCCTTCATTAACTCTTTTACATTCAAATTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL445 Chydorus brevilabris water mite diet isolate 445-BHL040517-GBD21444_21434-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCAGTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCCCGTCTTAATAAATTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTGGGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4451 Chironominae sp. water mite diet isolate 4451-BHL032417-GBD24477_14967-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTTTAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTCTTTTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTCTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTCCATTAACTCCTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4452 Chironominae sp. water mite diet isolate 4452-BHL032417-GBD25893_11765-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATACTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTTATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACTGCACACGCTTTTATTATAATTTTTTCTTATAGTTATGCCAATTTTAATTTGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCCTCATTAACCCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4455 Chironomidae sp. water mite diet isolate 4455-BHL032417-GBD11782_26085-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTTGACTAGAATTAGGACACCCAGGCTCATTAATCTGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTATAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGAGTCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTGCCTTTATCAAGAACAATAGTAGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4456 Chironominae sp. water mite diet isolate 4456-BHL032417-GBD14113_26866-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATTCTAATTAGAGCAGAACTTGGATGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATTTTAGGAACCCCAGATATGGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL446 Oligochaeta sp. water mite diet isolate 446-BHL040517-GBD18933_16680-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACCCTATACTTAATTTTAGGAGTTTGAGCCGGAATAATTGGAACCGGAACTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTCCTAGGGAGAGATCAGCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTTTTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTATTACTTGGAGCACCAGATATGGCCTTCCCACGACTTAACAATTTAAGATTTTGACTTCTACCACCTTCACTAATCCTACTAGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL4462 Chironominae sp. water mite diet isolate 4462-BHL032417-GBD15698_8907-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTATAGTATGCTAATTCAAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAGTAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTTTTACTTTCAAATTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4469 Chironominae sp. water mite diet isolate 4469-BHL032417-GBD24999_22899-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATTGTAGGTACTTCTTTTAGTAAGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAACAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATCGACTTATTCCTTTAATATTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTATTACTTTCAAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL447 Chironominae sp. water mite diet isolate 447-BHL040517-GBD12740_19749-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATTAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTACTCATGCATTTATTATATTTTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTCTCAAGTTCGATTGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4470 Chironominae sp. water mite diet isolate 4470-BHL032417-GBD8228_21785-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTCAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTAACAGCACACGACTTTAATATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTCTTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4471 Culex sp. water mite diet isolate 4471-BHL032417-GBD21733_17088-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTTGGGCTTTGAGTTGGATTAGTTGGAATTTCTTTAGGTTTACTATTTCGAGCGGATTTAAGTCAACCAGGTGTATTTATTGGAAATGGTCAAATTTATAATGTTATTGTAACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTTGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4475 Chironomidae sp. water mite diet isolate 4475-BHL032417-GBD4145_18437-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGAAGCTTGATCGGGAATCGTAGGCACTTCTTTACGAATTTTAATTCGACTAGATTTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTGTGCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACATTAATCAAGAGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4477 Chironominae sp. water mite diet isolate 4477-BHL032417-GBD3661_12738-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGGTTAGTCTGGTATAATAGGTACTTCTTTTAGTATGCTAATTCGGGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATCTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCGTCATTAACTCTTTTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL448 Chironomus crassicaudatus water mite diet isolate 448-BHL040517-GBD8480_7376-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATATTATTTTGGTGCTTGCTCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAGTTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGATCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTCTTGACTTCTCCCCCCATCCTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.1% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4481 Chironominae sp. water mite diet isolate 4481-BHL032417-GBD14499_24094-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAACTTGATCTGGTATTGTATGTACTTCTTTAATTATTCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGATATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATTTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4482 Chironomidae sp. water mite diet isolate 4482-BHL032417-GBD11789_7695-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTACTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGAACATGCTTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTATCTTTGATATTAGGGGATCCTGATATAGCTTTTACGCGAATAAGTAATATAAGATTTTGATTATTACCCACTTCATTAACCTGACGTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4488 Chironominae sp. water mite diet isolate 4488-BHL032417-GBD8099_12213-Ldc32 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGAATAGTAGGTACTTCTTTAAGTATGCTAATTCGTGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACACTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTATCAAGCAAGTGCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL449 Chironomidae sp. water mite diet isolate 449-BHL040517-GBD21573_16830-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCGTGATCGGGAATAGTAGGAACTTCTCTTAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAAATTTAATTGGAGATGATCAAATTTATAATGTTATTGTAACAGGCCATACTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTGCCATTAATATTAGGAGCACCTGATATGGCATTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCTTCCTTAACATTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR754220, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4492 Paratanytarsus sp. water mite diet isolate 4492-BHL032417-GBD20586_22054-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCCATAGTTATACCTATTTTATTTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAACAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4495 Chironomus crassicaudatus water mite diet isolate 4495-BHL032417-GBD7793_7003-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTTGGTGCTCGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCAAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATATCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTTGAATAAATAATATAAGTTTTGGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4496 Drosophila sp. water mite diet isolate 4496-BHL032417-GBD7230_9083-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCC--CTCTTTAACTCTTTTACTTTCAAGTAGAATAATGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.4% identical to accession ID DQ471587, identified in GenBank as Drosophila karakasa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4497 Paratanytarsus sp. water mite diet isolate 4497-BHL032417-GBD9091_17910-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGTGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCGCCAGATATAGCGCTTCCTCGAATAAATAAAATAAGATATTGACTTCTTCCCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4498 Paratanytarsus sp. water mite diet isolate 4498-BHL032417-GBD14519_23025-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATATTGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.7% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4499 Chironomidae sp. water mite diet isolate 4499-BHL032417-GBD27976_18560-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGTACATCTTTAAGAATTTTGATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTATTTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL450 Lebertia sp. water mite diet isolate 450-BHL040517-GBD22359_12472-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGAAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTAAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATTAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCCTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4500 Chironomidae sp. water mite diet isolate 4500-BHL032417-GBD7799_23013-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAAAACTCGGTCACGCTGTTTCTTTAATCGGAGACGATCAAATTTATAATGTATTTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGGGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGAGAGCCCCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4501 Chironomidae sp. water mite diet isolate 4501-BHL032417-GBD12807_8855-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.6% identical to accession ID KM102730, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4502 Paratanytarsus sp. water mite diet isolate 4502-BHL032417-GBD28554_14155-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTCATAGTTATACCTCTTTTAATTGGAGGATTTGGCAACTGATTATTGCCTTTAATAATAGGAGCCCCAGATATAGCTTTTCCCCCAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACACTTTTACTTTCAAGGAAAATAGTGGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4503 Oligochaeta sp. water mite diet isolate 4503-BHL032417-GBD14968_5431-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCA--AGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.2% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL4504 Paratanytarsus sp. water mite diet isolate 4504-BHL032417-GBD18871_8367-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGGCATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTTGGGAGCTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACGCTTCTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4505 Paratanytarsus sp. water mite diet isolate 4505-BHL032417-GBD16131_25888-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATCTGGGAACTGATTATTGCCTTTAAAATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGAGTTTGACTTCTCCCCCCCCTCGTTAACTCCGTTACTTTCAAGTAGAAAAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4507 Chironomus sp. water mite diet isolate 4507-BHL032417-GBD9598_15020-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCAAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATATCAATCTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCCTCTTTAACGCTTTTACTTTCAAGTAAAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4508 Chironomus sp. water mite diet isolate 4508-BHL032417-GBD29650_15048-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCAAGCAGAATTATGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATATCAATTTTAATTGGAGGTTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTGGACTTCTCCCCCCAGCTTTAACTCTTCTTCTTTTTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4509 Paratanytarsus sp. water mite diet isolate 4509-BHL032417-GBD11694_20874-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGCTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCTAATAAATAATATAAGATTTTGACTTCTTCCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL451 Chydorus brevilabris water mite diet isolate 451-BHL040517-GBD22839_25659-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTCTTTGGAATTTGAGCTGGTATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATAAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTCTTAGTAGGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4511 Paratanytarsus sp. water mite diet isolate 4511-BHL032417-GBD26960_21806-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCTAGATATAGCTTTTCCTCGAAAAAATAATATAAGATTTTGACATCTTCCCCCCTCGTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4512 Paratanytarsus sp. water mite diet isolate 4512-BHL032417-GBD21855_23388-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGAATTGGGAACTGGTTATTGCCTTTAATATTAGGTGCCCCAGAAATAACTTTTCCTCGAATAAAAAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTCTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4513 Paratanytarsus sp. water mite diet isolate 4513-BHL032417-GBD17489_1927-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGCACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATCATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.4% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4514 Paratanytarsus sp. water mite diet isolate 4514-BHL032417-GBD8032_23543-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATATTGACTACTACCCCCCACTTTAACACTATAACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4515 Paratanytarsus sp. water mite diet isolate 4515-BHL032417-GBD15658_10215-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCAAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR770273, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4516 Paratanytarsus sp. water mite diet isolate 4516-BHL032417-GBD23056_16983-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTATTTTCGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACTTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGTATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4517 Paratanytarsus sp. water mite diet isolate 4517-BHL032417-GBD19175_23877-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTTGGAGCCTGAGCAGGAATAGTAGGAACTGCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGAACAAATTTATAATGTAATTGTTACAGCTCATGCATTCATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4519 Parachironomus sp. water mite diet isolate 4519-BHL032417-GBD22290_22570-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGACTAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL452 Chironomus sp. water mite diet isolate 452-BHL040517-GBD22697_19494-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTCTAGGGGCTTCACCCGGAATAGTGGTAACTTCATTAAGAATGCTTATTCGAGCAGATTTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCAACTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4520 Paratanytarsus sp. water mite diet isolate 4520-BHL032417-GBD14501_25232-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACCTTATTTTTGGTGCTTGATCCGGAATAGTAGGAACTTCCTTAAGAATATTTATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCATGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4522 Paratanytarsus sp. water mite diet isolate 4522-BHL032417-GBD19402_27449-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTGTAGTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTTAAGATTATTAATTCGAGCTGAGCTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAGTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGTAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4523 Paratanytarsus sp. water mite diet isolate 4523-BHL032417-GBD7181_18950-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGTCTGATCAGGAATAGTAGGCACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGAACAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTGCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4526 Chironomus riparius water mite diet isolate 4526-BHL032417-GBD27025_15113-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATGGGAGATGAACAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTCTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4527 Paratanytarsus sp. water mite diet isolate 4527-BHL032417-GBD11452_16353-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTCGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGATCCCCAGATATAGCTTCTCCTCGAATAAATAATAAAAGATTTTGACTTCTTCCCCCACTCTTTAAATCGTTGACTTTCAAGTAGAATAGGGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4529 Paratanytarsus sp. water mite diet isolate 4529-BHL032417-GBD19484_27083-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGCGTCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL453 Oligochaeta sp. water mite diet isolate 453-BHL040517-GBD27297_11431-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAAGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTTCCTAATAATTTTCTTTATGGTTATACCAGTATTTATTGGAGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATAAACAATTTAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL4530 Paratanytarsus sp. water mite diet isolate 4530-BHL032417-GBD10681_25226-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTGGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGACTTTAATATTAGTAGTCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTGCTTCCCCCCCTCTTTAACTCTTTTACTGTCAAGTAGAATAGTGGAAAATGGATCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4531 Paratanytarsus sp. water mite diet isolate 4531-BHL032417-GBD11781_28721-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCATAAGAATATTAATTCGAGCTAAACTAGGACATCCTGGAACTTTTATTGGAGATGACAAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGTATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTGCTTCCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4532 Chironominae sp. water mite diet isolate 4532-BHL032417-GBD25675_12287-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTGTTGGAGCTTGATCAGGTATTGTAGGAACTTCTTTAAGTATTTTAATCCGAACGGTATTAGGTCATCCTGGAACATTTATTGGTGATGACCAATTTTATAATGTAATTTTTACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4534 Paratanytarsus sp. water mite diet isolate 4534-BHL032417-GBD23545_15282-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCTGAACTATGACAACCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTTTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4535 Chironomidae sp. water mite diet isolate 4535-BHL032417-GBD21727_11125-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTTATTTTTGGGGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTTATTCGAGCTGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGAACAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4539 Chironomidae sp. water mite diet isolate 4539-BHL032417-GBD24435_11195-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGATGATTAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4541 Cricotopus sp. water mite diet isolate 4541-BHL032417-GBD3061_14077-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGACCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCAGATAAAGCATTCCCTCGAATAAATATCATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4544 Paratanytarsus sp. water mite diet isolate 4544-BHL032417-GBD25486_9151-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGATGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGTGAACTGATTATTGCCTTTAATATTAGGGGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4546 Paratanytarsus sp. water mite diet isolate 4546-BHL032417-GBD26771_17740-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATACTAATTCGAGCTAAACTAGGACATCCTGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGTATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCCTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCGTTAACTCTTTTACTTTCAAGGAGAATAGTGGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4547 Paratanytarsus sp. water mite diet isolate 4547-BHL032417-GBD12336_8827-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTCTATTGGAGATGACCAAATTTATAATGTAATTGTGACAGCTCATGCATTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCTTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCGTTAACACTTTTACTTGCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4548 Diptera sp. water mite diet isolate 4548-BHL032417-GBD21852_15593-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCCTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.7% identical to accession ID HM022405, identified in GenBank as Anopheles peryassui. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL455 Chironomus riparius water mite diet isolate 455-BHL040517-GBD26041_14341-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACGTTATACATTATTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTGTTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAATTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTCGTCCCACTAATACTTGGAGCACCTGACGTAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTGTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4551 Paratanytarsus sp. water mite diet isolate 4551-BHL032417-GBD21540_10183-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATACTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAATCTTCATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTACCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4552 Chironominae sp. water mite diet isolate 4552-BHL032417-GBD21440_23893-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCAAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAGCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGATTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTGCCCCTTTCATTAACCCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4553 Chironominae sp. water mite diet isolate 4553-BHL032417-GBD7136_18089-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGAACAAATTTATAATGTTATTGTAACAGCTCATGTTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATACAAGATTCTGATTACTTCCCCATTCTTTATCACTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4556 Amphichaeta sp. water mite diet isolate 4556-BHL032417-GBD25414_22051-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTTAATAATTTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.1% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL456 Chironomus sp. water mite diet isolate 456-BHL040517-GBD12626_17340-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTGTTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTCGTCCCCCTAATACTTGGAGCACCTGACGTAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4560 Paratanytarsus sp. water mite diet isolate 4560-BHL032417-GBD14726_8318-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCTTTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTCATAGTTATACCTTTTTTAATTGGAGGATTTGGAAACTGATTAATGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4562 Paratanytarsus sp. water mite diet isolate 4562-BHL032417-GBD24859_22624-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCTTTTTTGGTGCCTGATCAGGTATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCGGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATATAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTCATAGATATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4563 Paratanytarsus sp. water mite diet isolate 4563-BHL032417-GBD11799_20708-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTACCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTTGAGGATTAGGGAACTGATTATTGCCTTCAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACGTCGTCCCCCATCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4566 Paratanytarsus sp. water mite diet isolate 4566-BHL032417-GBD15273_4379-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTAAACTAGGACATCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGGAGCTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTTACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4567 Phaenopsectra sp. water mite diet isolate 4567-BHL032417-GBD27992_17399-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTTGGAGCTTGATCAGGATTATTAGGAACTTCTTTAAGTTTATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCATTACGTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACGGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4569 Paratanytarsus sp. water mite diet isolate 4569-BHL032417-GBD26420_9520-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTAAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTTGGGAACTGATTATTCCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACACTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL457 Chironominae sp. water mite diet isolate 457-BHL040517-GBD21071_15972-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAAGAATGGTAGGAACTTCTTTAAGTATACTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAACGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGGCTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4571 Chironomidae sp. water mite diet isolate 4571-BHL032417-GBD2429_16059-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTTGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTTTAGTGAAACCTATTTTAATTGGAGGATTTGGAAATTGATTAGGTCCTTTAATATTGGGAGCCCCTGATATAACCTTCCCTCGAATAAAAAATATAAGGTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4573 Paratanytarsus sp. water mite diet isolate 4573-BHL032417-GBD5195_9080-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTAAAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTTATTATTGCCTTTAATATTAGGAGCCCCAGAAAAAGCTTTTCCTCGAATAAATAATAAAAGATTTTGACTGCTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4574 Paratanytarsus sp. water mite diet isolate 4574-BHL032417-GBD28571_14434-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTCTAAGTATATTAATTCGAGCTGATCTAGGACATCCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGAGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCATTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4577 Paratanytarsus sp. water mite diet isolate 4577-BHL032417-GBD4441_22304-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGAAGACCAAATTTATAATGTGATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCGGATATAGCTGTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCCCTCTTTAACTCGTGTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4578 Paratanytarsus sp. water mite diet isolate 4578-BHL032417-GBD13647_2298-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATATATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAAGAAATAATATAAGATTTTGACTTCTTCCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACCGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL458 Chironomus sp. water mite diet isolate 458-BHL040517-GBD23817_10486-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCCGGAAATTTCATTGGCGATGACCAAATTTATAATGTTGTAGTTACTGCACATGGTTTTATTATAATTTTTCTCATAGTTATACCAATTTTAATTGGAGGGTTCGGAAACTGACTTGTCCCCCTAAGACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGCTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4583 Paratanytarsus sp. water mite diet isolate 4583-BHL032417-GBD13618_5034-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCGAAGAATATTAATTCGAGCTGAACTAGGACATCCTTGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTCATAGTTATAACTACTTTAAATGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4586 Chironominae sp. water mite diet isolate 4586-BHL032417-GBD25946_9128-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGACATCCTGGAACATTTATTGGTAATGAACAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACCTTATTAATTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4589 Paratanytarsus sp. water mite diet isolate 4589-BHL032417-GBD28305_18849-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTTGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCATATATAGCTTTTCCCCGAATAAAAAAATAAAATTTTGGCTTCTTCCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL459 Chironomus sp. water mite diet isolate 459-BHL040517-GBD25338_25324-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGGGGCTTCATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACTAAATTTATAATGTTGTAGTTAGTGCACATGCTTTTATTATAATTTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4590 Orthocladius sp. water mite diet isolate 4590-BHL032417-GBD13561_11975-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTCGGAGCTTGATCAGGAATCGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTCTTTGATTGGAGAAGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTATTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4594 Chironomidae sp. water mite diet isolate 4594-BHL032417-GBD18276_9639-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTAGTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGACTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGGGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4595 Paratanytarsus sp. water mite diet isolate 4595-BHL032417-GBD4467_23240-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATCCGAGCTGAACTAGGCCATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGAGTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAATAGAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4599 Paratanytarsus sp. water mite diet isolate 4599-BHL032417-GBD5711_14842-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTATGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATGATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATAAAACTTTTCCCCCAATAAATAATATAAGAATTTGACTTCTTCCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL460 Psectrocladius sp. water mite diet isolate 460-BHL040517-GBD21527_25221-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTCATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAGTAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4600 Paratanytarsus sp. water mite diet isolate 4600-BHL032417-GBD17474_12777-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTATTTGTTACCGCTCACGCTTTTGTAATTAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTCCCCCCCTCTTTAACCCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4602 Amphichaeta raptisae water mite diet isolate 4602-BHL032417-GBD24310_21704-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGAACAGGAACAAGACTATTAATTCGAATTGAATTAAACCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTTATTAGTAATACCATTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL4604 Paratanytarsus sp. water mite diet isolate 4604-BHL032417-GBD26306_18170-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTAGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGTGCCCCAGATATAGCTTTTCCTCGAATAAATAATAGAAGATGTTGACTGCTGCCCCCCTCTTTAACGCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4605 Chironomidae sp. water mite diet isolate 4605-BHL032417-GBD9613_17467-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATAAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCAGGTTCTTTAATCGGACACGATTAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTAAAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGTTTAGTTCCTTTAATATTGAGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTAGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4607 Paratanytarsus sp. water mite diet isolate 4607-BHL032417-GBD16333_26996-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGAACAAATTTATAATGTAATTGTTACAGCTCATGCATTTTTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGAATTATTCCCCCCATCTTTAACCCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4609 Paratanytarsus sp. water mite diet isolate 4609-BHL032417-GBD16058_11709-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTACATCTTTGGTGTCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGATCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTGTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCCTTTACATTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL461 Phaenopsectra sp. water mite diet isolate 461-BHL040517-GBD6357_19314-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR723136, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4610 Chironomidae sp. water mite diet isolate 4610-BHL032417-GBD15092_5584-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGATGGTACAGGAACAAGACTATTAATTCGTATTGAAATAACCCATCCTGGAGCCTTTTTAGGAAGAGCCCAACTATATAATACCTTCGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTGATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4614 Chironominae sp. water mite diet isolate 4614-BHL032417-GBD17272_27552-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCATGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCATGACTAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4616 Paratanytarsus sp. water mite diet isolate 4616-BHL032417-GBD15119_3639-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTAGGACATCCTTGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTCGAATAGTGTAAACTGGAGCTGCTACAG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4619 Paratanytarsus sp. water mite diet isolate 4619-BHL032417-GBD8496_17863-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTTTAGGATTTGGGAATTGATTATTGCCTTTAATATTAGGAGCCCAAGATATAGCCTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCCTCTTTAACTCTTTTACTTTCAAATAGAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL462 Chironominae sp. water mite diet isolate 462-BHL040517-GBD10784_18612-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4622 Phaenopsectra sp. water mite diet isolate 4622-BHL032417-GBD7980_19578-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTAAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGTTGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTAACTTTACTTCTTTCTAGTGCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4624 Chironomidae sp. water mite diet isolate 4624-BHL032417-GBD14959_21828-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATATTAATTGGAGGATTTGGAAACTGACTAGTTCCATTAATATTAGGAGCACCAGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCACCATCATTAACTTTATTATTATCTAGAGTAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4627 Chironominae sp. water mite diet isolate 4627-BHL032417-GBD21614_3993-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTACTTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAAATTATAATGTTCTTGTAACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTACCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL463 Chironominae sp. water mite diet isolate 463-BHL040517-GBD22958_6691-Ldc35 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTAGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTCCCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4630 Lebertia sp. water mite diet isolate 4630-BHL032417-GBD25081_13452-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAACTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAAATGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGCTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4632 Paratanytarsus sp. water mite diet isolate 4632-BHL032417-GBD6820_8824-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATAGTTCATTTTTGGTGCCTGATCAGGAATAGTAGGTACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTATTCCCCCCTCTTTAACTCATTTACTTGCATGTAGAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4634 Paratanytarsus sp. water mite diet isolate 4634-BHL032417-GBD20779_17356-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTATGAATATTAATTCGAGCTTAACTAGGACATCCTGGAACTTTTATTGGAGATGACTAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGTACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCAGTTACTTTAAAATAGAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4636 Lepidoptera sp. water mite diet isolate 4636-BHL032417-GBD9454_12900-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTTCATTATACTTCATTTTTTGGTGCCTGATCAGGACTAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCA--GTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.1% identical to accession ID KR780074, identified in GenBank as Oligia apameoides. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4641 Chironomidae sp. water mite diet isolate 4641-BHL032417-GBD7070_23149-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTAAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTAATACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.3% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4643 Paratanytarsus sp. water mite diet isolate 4643-BHL032417-GBD4286_18221-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATTAGTAGGAACTTCCCTAAGATTATTATTTCGAGCTGAACTAGGACATCCTGGTACTTTTATTGGAGATGACCAGATTTACAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTATTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4645 Paratanytarsus sp. water mite diet isolate 4645-BHL032417-GBD11950_2986-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTT-GGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCCTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTTCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.4% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL465 Psectrocladius sp. water mite diet isolate 465-BHL040517-GBD10133_16274-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4654 Paratanytarsus sp. water mite diet isolate 4654-BHL032417-GBD19052_25420-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTGTACTTCATTTTTGGTGCCTGATAAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGATATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGACTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTGTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCGCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL466 Psectrocladius sp. water mite diet isolate 466-BHL040517-GBD23398_24598-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTATTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTTAGTATTTTAATTTGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGCCGGTCAAATTTATAATGTAATTGTTTCCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCACTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4661 Paratanytarsus sp. water mite diet isolate 4661-BHL032417-GBD9937_12417-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAATTGTACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACAGCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAACAATATAAGATTTTGACTTCTTCCCCCCTCTTCAACTCTGGTACTTGCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4667 Paratanytarsus sp. water mite diet isolate 4667-BHL032417-GBD7170_17091-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCCTAGAATATTAATTCGAGTTGAACTATGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAACAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4669 Paratanytarsus sp. water mite diet isolate 4669-BHL032417-GBD26937_23138-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGTTGAACTAGGACAACCTGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTATTGCCTTTAATATTAGGGGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTGCTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL467 Chironominae sp. water mite diet isolate 467-BHL040517-GBD10224_21600-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4679 Paratanytarsus sp. water mite diet isolate 4679-BHL032417-GBD5612_24585-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATAGTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCAGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL468 Psectrocladius sp. water mite diet isolate 468-BHL040517-GBD4643_12586-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCCTTTGTAATAATTTTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGGGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4680 Paratanytarsus sp. water mite diet isolate 4680-BHL032417-GBD27715_16118-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAGCTTACCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACTAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCATTTACTTGCAAGTAGAATAGTTGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4682 Paratanytarsus sp. water mite diet isolate 4682-BHL032417-GBD18667_26843-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTACCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATAACTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATAAAGCCTTTCCCCGAAAAAAAAAAAAAGATTTTGACCTCTGCCCCCCCTCTTTAACACTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4685 Paratanytarsus sp. water mite diet isolate 4685-BHL032417-GBD17985_24208-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGAACAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGAATATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCCAATAAATAAAATAAGATTTTGACTTATTCCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4687 Culex pipiens water mite diet isolate 4687-BHL032417-GBD22490_4642-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGGTCAAATTTATAATGTTATTGTAACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTTGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCGTTGACACTACTACCTTTAAATAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4688 Paratanytarsus sp. water mite diet isolate 4688-BHL032417-GBD26958_9412-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCTGGAATAGTAGGAACTTCTCTAAGGATATTAATTCGAGCTGAACTAGGACATCGTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTCGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTTCTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL469 Chironomidae sp. water mite diet isolate 469-BHL040517-GBD13980_25874-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GACACTTTACTTTATTTTTGGAGCTTGATCCGGAATAGTAGGAACATCTTTAAGAATATTAATTCGAGCAGAATTAGGGCACCCAGGAACATTGATTGGGGATGATCAAATTTACAATGTAATTGTAGCAGCCCATGCTTTTATTATAATTTTTTTTTTATAGTTATACCAATTTTAATTGGTGGATTTGGAAATTGGCTTTTACCTTTAATACTTGGAGCCCCTGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCATCTATTTCATTACTTCTTTCTAGATCAGTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KP043758, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4698 Paratanytarsus sp. water mite diet isolate 4698-BHL032417-GBD25218_22063-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATACTTCATTTTTGGTGCCTGATCAGGTATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGGTTTTCCCCGAAAAAAAAAAATAAGATTTTGACTTCTTCCCCCCGCTTTAACTCTTTTACTTACAAGTAGAATAGTGTAAAAAGGAGCTGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL470 Psectrocladius sp. water mite diet isolate 470-BHL040517-GBD16275_11421-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAAAACTCGGTCACGCTGGTTCTTTAATCGGAGAAGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGAAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTATCTGATTACTTCCCCCGTCATTAACCTTACTATTATCTAGCTCACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4703 Paratanytarsus sp. water mite diet isolate 4703-BHL032417-GBD24499_22519-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGTTGAATTAGGACACCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTATAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCATTAACTCTACTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL471 Chironomidae sp. water mite diet isolate 471-BHL040517-GBD29111_14695-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATGTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCGCGTGCTTTTGTAATACTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGAGTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATTATAAGAGTTTGATTATGACCCCCTTCATTAACCAAACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4710 Paratanytarsus sp. water mite diet isolate 4710-BHL032417-GBD23007_5784-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGATGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTAATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCTAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAATAGAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4713 Paratanytarsus sp. water mite diet isolate 4713-BHL032417-GBD2801_11640-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACTTCCTGGAACTTTTATTGGAGATGAACAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTAGAGGATTTGGGAACTGAATATTGCCTTTAATATTAGGAGACCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTTTTTTACTTTCAAGTAGAATAGTGGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL472 Chironomidae sp. water mite diet isolate 472-BHL040517-GBD8121_13455-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTTAATTCGACTAGAATTAGGCCACCCAGTCTCATTACTCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGATTTTGTAATAATTTTTTTAATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGATTAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4722 Paratanytarsus sp. water mite diet isolate 4722-BHL032417-GBD19691_15717-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGTTACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATAAAAGAAATTGACTTCGTCCCCCCGCTTTAACACGATAACTTTCAAGTAGAAGAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL473 Chironominae sp. water mite diet isolate 473-BHL040517-GBD16258_28374-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTAATTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGGGATGACCAAATTTACAATGTAATTGTCATAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAAGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4737 Paratanytarsus sp. water mite diet isolate 4737-BHL032417-GBD20897_27469-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATACTAATTCGAGCTGAACTAGCACATCCTGGAACTTTTTTTGGAGATGAACAAATTTTATAATGTAATTGTTACAGCTCATGCACTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTCCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4738 Parachironomus sp. water mite diet isolate 4738-BHL032417-GBD22915_15987-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGTAGCTTGATCAGGAATAGTAGGAACTTCTTTTAAATATACTTATTCGCGCTACTTTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTTGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL474 Chironomidae sp. water mite diet isolate 474-BHL040517-GBD17964_27135-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAACTTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTAATAGTGATACCTATTTTAATTGGAGGCTTTGCAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTGCTGTTATCAAGATCAATAGTAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4740 Paratanytarsus sp. water mite diet isolate 4740-BHL032417-GBD11559_13690-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGATTATACCTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAGGAATATTAATTCGAGCTGAACTAGGACAACCTGGAACTTTTCTTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTGGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCGTCCCCCCTCTTTAACACTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4741 Drosophila sp. water mite diet isolate 4741-BHL032417-GBD12690_2982-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCC------ATCACTAATTCTA-TTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.6% identical to accession ID KJ841772, identified in GenBank as Scaptodrosophila riverata. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL475 Chironominae sp. water mite diet isolate 475-BHL040517-GBD2808_17425-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAAAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAATTTTACAATGTAATTGTCACAGTACATGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTATTACTAGCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4754 Paratanytarsus sp. water mite diet isolate 4754-BHL032417-GBD23505_14909-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGCTCAGGAATAGTAGGTACTTCCCCTAAGCTTATTAAATCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTCTACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTGTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4758 Paratanytarsus sp. water mite diet isolate 4758-BHL032417-GBD11490_17654-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATAACTATTTTAATTGGAGGATTTGGCAACTGATTATTGCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTAAATCACCCCACTTTAACACTGTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGCAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4759 Paratanytarsus sp. water mite diet isolate 4759-BHL032417-GBD27134_11638-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATAGTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAGCTTCCCTAAGACTATTAATTCGAGCTGAACGAGGACATCATGGAACTTTTATTGGAGATGACCAAAGTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCATTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL476 Chironomidae sp. water mite diet isolate 476-BHL040517-GBD7923_23575-Ldc36 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTACTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAAGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTCAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGAGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAAATCAATAGTAGAAAATGGAGCTGGATCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4760 Paratanytarsus sp. water mite diet isolate 4760-BHL032417-GBD17558_3696-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGTGCATGAGCAGGAATAGTAGGAACTTCCCTAAGAATATTAATGCGAGCTGAACTAGGACATCCTGTAACTTTTATTGGAGATGACCAAATTTAGAATGTAATTGTTACAGCACATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCACAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4762 Paratanytarsus sp. water mite diet isolate 4762-BHL032417-GBD26595_7091-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGAAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTATTTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTGGCCTCGAATAAATAATATAAGATATTGACTTCTTCCCCCCTCTTTAACTCTATTACGTACAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4763 Paratanytarsus sp. water mite diet isolate 4763-BHL032417-GBD27464_15354-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACGAGGAGATCCTGGAACTTTTATTGGATATGACCAAATTTATAATCTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTCGAGGATTTGGGAACTGATTATCGCCTTTAATATTAGGAGCCTCAGATATAGCTTTTCCTCGCATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGTAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4764 Paratanytarsus sp. water mite diet isolate 4764-BHL032417-GBD28484_10127-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGTCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTAGAGCTGAACTAGGACAACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATATGTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCTTTTACTTTCAAGTGGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4765 Paratanytarsus sp. water mite diet isolate 4765-BHL032417-GBD18560_14373-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTGTCGTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTATGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTTTAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCATAGTTAACTCTGTCACTTGCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4766 Paratanytarsus sp. water mite diet isolate 4766-BHL032417-GBD16392_9516-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATAATTCATTTTTGGTGCCTGATCAGGAAATAGTAGGAACTTCCCTAAGAATATTAATTCGCGCTGAACTAGGACATCCTGTAACTTTTATTGGAGATGTCCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCTTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACCTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4767 Paratanytarsus sp. water mite diet isolate 4767-BHL032417-GBD2937_10290-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACAGAAATTTTGGAGACTGATAAGGAATAGTAGGAACTTCACGAAGAATATTAATTCGAGAGGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4771 Paratanytarsus sp. water mite diet isolate 4771-BHL032417-GBD3790_9327-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACATCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCGGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGATCATGCATTTATTATAATTTTTTTCATGGTTATACCTATTTTAATTGGAGGATTTGTGAACTGATTGTTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR286418, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4782 Paratanytarsus sp. water mite diet isolate 4782-BHL032417-GBD14963_3363-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATAAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGTAACTTTTATTGGAGATGACCAAATTTATAATGGAATTGTTACAGCGCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAAATGGAGGAATTGGGAACTGATTATAGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4784 Paratanytarsus sp. water mite diet isolate 4784-BHL032417-GBD18195_28222-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAATTATACTTCATTTTTGGTGCCTGATCAGGAATAGGAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGCTTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCACTGTAACTCTTTGACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL479 Chironomidae sp. water mite diet isolate 479-BHL040517-GBD7699_10293-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCGGGAATAGTTGGAACTTCTTTAATAATTCTACTTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTATAGTTATACCAATCTTAATTGTAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAAAAATATAAGTTTTTGATTGTTGCCACCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4793 Paratanytarsus sp. water mite diet isolate 4793-BHL032417-GBD24925_6799-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTG-TGCCTGATCAGGAATTGTAGGAACTTCCCTTAGAATTTTATTTCGAGCTGGACTAGGACATCCTGGAACTTTTATTTGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTTTTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAAATCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4795 Paratanytarsus sp. water mite diet isolate 4795-BHL032417-GBD27151_18413-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGTATATTAATTCGAGCTGAACTAGGACATCCTGGAACTCTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTTTTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACGTCTTCCCCCCTCATTAACTCTTTTACCTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL480 Chironomidae sp. water mite diet isolate 480-BHL040517-GBD5913_8239-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTATTTTCGGAGCATGATCAGGAATAGTTGGAACTTCTTTAAGCATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAATTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4800 Paratanytarsus sp. water mite diet isolate 4800-BHL032417-GBD7517_7429-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGAGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACGTCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCACTTTAACTATTTTTCTTTCTAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4801 Paratanytarsus sp. water mite diet isolate 4801-BHL032417-GBD8863_12229-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGAGCCTGACCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTAAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCATTAACTCTTTTACTATCAAGATGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4808 Paratanytarsus sp. water mite diet isolate 4808-BHL032417-GBD8264_15393-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTGTAGTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTATGAATATTAATTCGCGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTATGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCGTTAACTCTTTTACTTTCAAGTAGAATAGTGGGAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL481 Chironomidae sp. water mite diet isolate 481-BHL040517-GBD22485_20125-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTATGAATTCTAATTCGAGCATAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGGTTTTGATTGTTGCCCCCATCATTAACTTAATTATTATCTAGAACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4810 Paratanytarsus sp. water mite diet isolate 4810-BHL032417-GBD16209_27598-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGGATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGTAGATGACCAAATTTAGAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL482 Chironomidae sp. water mite diet isolate 482-BHL040517-GBD21096_26448-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GACACTTTACTTTATTTTTGGAGCTTGATCCGGAATAGTAGGAACATCTTTAAGAATATTAATTCGAGCAGAATTAAGACATCCAGGAACATTGATTGGGGATGATCAAATTTACAATGTAATTGTAACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGGCTTTTACCTTTAATACTCGGGGCCCCTGATATAGCCTTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCATCTATTTCATTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KP043758, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4820 Paratanytarsus sp. water mite diet isolate 4820-BHL032417-GBD8406_25490-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATTTTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTTTTTTAATTGGAGGATTTGGAAACTGATTATTCCCTTTAATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTATTACTGTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4823 Paratanytarsus sp. water mite diet isolate 4823-BHL032417-GBD17285_17476-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCAAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTCTAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4825 Paratanytarsus sp. water mite diet isolate 4825-BHL032417-GBD10083_25008-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTATTATTAGGAGCCCAAGATATAGCTTTTCCTCGAATAAATAATAAAAGATTTTGACTTAATCACAACTCTTTAACACGTTGACTTACAAGTAGAATAGTGGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL483 Psectrocladius sp. water mite diet isolate 483-BHL040517-GBD17417_27780-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATAATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAACTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4830 Paratanytarsus sp. water mite diet isolate 4830-BHL032417-GBD16999_27279-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGATTAAATTTATAATGTAATTGTTAAAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGTAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTGTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4831 Paratanytarsus sp. water mite diet isolate 4831-BHL032417-GBD21030_15617-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTATGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTAGAATAAATAATATAAGATTGTGACTTCTACCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4832 Paratanytarsus sp. water mite diet isolate 4832-BHL032417-GBD11052_2957-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATAGTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCCGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCCAATAAATAATAATAAG-TTTTGACTTCTTCCCCCCTTCTTTAACTCTTTTACTTTCAAGTAGAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4834 Chironominae sp. water mite diet isolate 4834-BHL032417-GBD25716_13444-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCATATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTGCCACTAATATTGGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4838 Drosophila sp. water mite diet isolate 4838-BHL032417-GBD8273_22116-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTATTTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTGGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.7% identical to accession ID EU493592, identified in GenBank as Drosophila pulaua. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL484 Chironomidae sp. water mite diet isolate 484-BHL040517-GBD14338_5579-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTTTTTTTATTTTCGGAGCTTGAGCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATGCGAGCAGAATGAGGACATGCAGGCTCATTAATGGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAACTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGACTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4845 Paratanytarsus sp. water mite diet isolate 4845-BHL032417-GBD4264_19014-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTATGAACTTCCCTAAGAATATTAATTCGAGCTTAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTGATACCCATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGTATCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGGTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCACGCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.0% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL485 Chironomidae sp. water mite diet isolate 485-BHL040517-GBD14864_3524-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTGGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGAGAGTCAGTCTCATTAATTGGAGACGATCCAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4856 Paratanytarsus sp. water mite diet isolate 4856-BHL032417-GBD29008_13651-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTACGAATATTAATTCGAGCTGAACTCGGACATCCTGGATCTTTAATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTACACCTATTTTAATTGGAGGATTTGTGAACAGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4857 Paratanytarsus sp. water mite diet isolate 4857-BHL032417-GBD10654_6060-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAACTTTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGAATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGAAAAAGCTTTTCCGAAAAAAAAAAAAAAAAGATTTCGACTTCTTCCCGCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL486 Chironomidae sp. water mite diet isolate 486-BHL040517-GBD24037_9921-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL487 Chironomidae sp. water mite diet isolate 487-BHL040517-GBD7404_15316-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGATGGAACTTCTTTGAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATAATAATTTTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGATCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATATTATAAGTTTTTGATTGTTGCCCCCATCATTAGCTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4874 Paratanytarsus sp. water mite diet isolate 4874-BHL032417-GBD24253_12810-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTATGGTGTCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCACAGTTATACCTATTTTAATTGGAGGATTTTGGGAACTGGTTATTGCCTTTAATATTAGGAGCCTCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCGCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4877 Paratanytarsus sp. water mite diet isolate 4877-BHL032417-GBD18977_20943-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATCGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCGTGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGCAATTGATTATTGCCTTTAATGTTAGGAGTCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCATCACCCCTCTTTAACTCGTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL488 Orthocladiinae sp. water mite diet isolate 488-BHL040517-GBD12927_17322-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTATTTTCGGAGCTTGTTCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCTGGCTCATTAATTGATGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTCCCACGAATAAATATTATAAGATTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4886 Paratanytarsus sp. water mite diet isolate 4886-BHL032417-GBD20581_25170-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATCCTTCATTTTTGGTGCCTGATCAGGAATAGTAGTTACTTCCCTATGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACTAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATATTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGACTTTAATATTAGTAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCATTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4888 Paratanytarsus sp. water mite diet isolate 4888-BHL032417-GBD27570_12349-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTGTAGTTCATTTTTGGTGCCTGATCAGGAATAGTAGGTACTTCCCTACGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCACTTTAACTCATTTACTTTCAAGTAGAATAGTGGAAAATCGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL489 Chironomidae sp. water mite diet isolate 489-BHL040517-GBD17891_8769-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGATCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGATCATGCTTTTGTAATAATTTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAGACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATGGTGGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4898 Paratanytarsus sp. water mite diet isolate 4898-BHL032417-GBD3283_13949-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTGTAGTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGAGATCCTGGAACCTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTAGTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTGTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4899 Paratanytarsus sp. water mite diet isolate 4899-BHL032417-GBD9476_18954-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATAAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTAGAGGATTTGGGAACTGAGTATTGCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTAATCCCCACTCTGTAACACTTTTACGTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL490 Orthocladiinae sp. water mite diet isolate 490-BHL040517-GBD22183_5037-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTTTACTTTATTTTCGGAGCTTGATCCGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGAAGAATTAGGACATGCAGGCTCATTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAAATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4902 Paratanytarsus sp. water mite diet isolate 4902-BHL032417-GBD27962_9903-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCACTATACTTCATTTTCGGTGCCTGATAAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTGCTGCCCCCCTCTTTAACTCTATTACTATCAAGAAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4906 Paratanytarsus sp. water mite diet isolate 4906-BHL032417-GBD25074_23065-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGTTGAACTAGGACATCCTGGCACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGTATTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGCTATGGGAACTGATTATTGTCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACCCTTTTACTATCAAGTAGAATAGTGGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4907 Paratanytarsus sp. water mite diet isolate 4907-BHL032417-GBD26339_14752-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGGGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATAGTAGGAGCCCCAGATATAGCTTGTCCTCGAATAAATAATATAAGAGGTTGACTTCATCCCCCCACGTTAACTCATGTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL491 Chironomidae sp. water mite diet isolate 491-BHL040517-GBD16572_27930-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACAGTTTATTTTATTCTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGTATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATATTGTAATTGTTACAGATCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGATCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4910 Paratanytarsus sp. water mite diet isolate 4910-BHL032417-GBD13303_11019-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTTTATTTCATTTTCGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATTTTAATTCGAGCTGAATTAGGACATCCTGGCACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTAGACTGCTGCCCCCCTAATTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL492 Chironomidae sp. water mite diet isolate 492-BHL040517-GBD21940_11493-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTATAGTTATTCCAATCTTAATTGGAGGATTTGGAAACTGACTTGTTTCTTTAATATTTGGAGCAACTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL493 Chironomidae sp. water mite diet isolate 493-BHL040517-GBD19359_4888-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTGTATTTTATTTTCGGAGCTTGATCAGGAATAGGTGGAACTTCTTTAAGAAATCTAATTCGAGCAGAATTATGACATGCAGTCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGAAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACATTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL494 Chironomidae sp. water mite diet isolate 494-BHL040517-GBD15788_5465-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATAAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAAGTTATAATGTAATTTGTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTATTTCCTCTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4940 Paratanytarsus sp. water mite diet isolate 4940-BHL032417-GBD27681_13500-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATAATTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGTACTAGGACGTCCTGGAATTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATAACTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTTGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4945 Paratanytarsus sp. water mite diet isolate 4945-BHL032417-GBD24253_23879-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTT-GGTGCCTGATCAGGGTTTGTAGGAACTTCCCTTAGAATTTTAATTCGAGCTGAACTAGGACCTCCTGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4951 Paratanytarsus sp. water mite diet isolate 4951-BHL032417-GBD10328_21546-Ldc33 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGATGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGAAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCCCCAGATATAGC-TTTCCTCGAATAAATAATGTAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4953 Cricotopus sp. water mite diet isolate 4953-BHL032417-GBD12537_24885-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4955 Paratanytarsus sp. water mite diet isolate 4955-BHL032417-GBD7835_14409-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAACTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4956 Oligochaeta sp. water mite diet isolate 4956-BHL032417-GBD21433_19082-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATAATCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATATCAGTATTTATTGATGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCATTAATCCTATTAGTTTCTTCTTTCTAATTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL4957 Chironomus sp. water mite diet isolate 4957-BHL032417-GBD15410_21117-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAACGCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4959 Chironomidae sp. water mite diet isolate 4959-BHL032417-GBD21306_14968-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTTTTATAGTTACACCTATTTTAATTGGAGGATTGGGAAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTATACCCTCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL496 Chironomidae sp. water mite diet isolate 496-BHL040517-GBD15409_11823-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTAATTAATTGGGGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATATTTTTTTTTATAGTTATACCAATCTTAATTGAAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAAAATTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM994396, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4960 Lebertia sp. water mite diet isolate 4960-BHL032417-GBD4836_7671-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCCATAATAATTAGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCTGCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4963 Chironomidae sp. water mite diet isolate 4963-BHL032417-GBD9698_22713-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGACCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTATAGTTATACCAATCTTAATTGGATGATCTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4966 Chironomidae sp. water mite diet isolate 4966-BHL032417-GBD21910_19017-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCGTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCCTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCTATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4967 Chironomidae sp. water mite diet isolate 4967-BHL032417-GBD9105_13851-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAACTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4968 Cricotopus sp. water mite diet isolate 4968-BHL032417-GBD27300_7805-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATATGGAATAGTGGGAACCTATCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTACTTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATACTATTACCAAGTCTAATTGGAGGAGTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCTAATAAATAATATAAGATTTTGATTATTACCATCTTCTTTAACATTATTATTATCAAAATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4969 Paratanytarsus sp. water mite diet isolate 4969-BHL032417-GBD28059_20298-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCCGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCAAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTCATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGAAGGATTTGGGAACTGTTTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATGATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL497 Chironomidae sp. water mite diet isolate 497-BHL040517-GBD12709_2802-Ldc61 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAAAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAGTTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCAACTGATATGGCGTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCACCATCAGTAACTTTATCATTATCGAGATCAATTGTGGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4971 Parachironomus sp. water mite diet isolate 4971-BHL032417-GBD19531_24598-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACTCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTTTTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCATACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4972 Paratanytarsus sp. water mite diet isolate 4972-BHL032417-GBD24324_19057-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGAAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACCCTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID KR757714, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4973 Paratanytarsus sp. water mite diet isolate 4973-BHL032417-GBD25592_5542-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4975 Chironomidae sp. water mite diet isolate 4975-BHL032417-GBD26011_14287-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTCTAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTTCCCCTGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTATCTTTACTTCTTTCTAGTTCAAATGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4976 Chironominae sp. water mite diet isolate 4976-BHL032417-GBD3004_12380-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAATAATATTAATCCGAACGGAGTTAGGTCATCCTGGAACATTTGTTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACGTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4977 Paratanytarsus sp. water mite diet isolate 4977-BHL032417-GBD6344_18043-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCGGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGTAACTTTTATTGGAGATGACCAAACTTATAATGTATTTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4978 Paratanytarsus sp. water mite diet isolate 4978-BHL032417-GBD16809_12543-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACCTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAAGATTTGGGAACTGATTATTGCCTTTAATATTAGGTGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTACCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4979 Chironomus riparius water mite diet isolate 4979-BHL032417-GBD7289_13154-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGCAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAAAGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCCCCTAATACTTGGAGCACCTGAGATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4980 Cricotopus sp. water mite diet isolate 4980-BHL032417-GBD16337_11106-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTCTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4981 Chironominae sp. water mite diet isolate 4981-BHL032417-GBD12311_4918-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAAAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4982 Chironomus sp. water mite diet isolate 4982-BHL032417-GBD15897_13252-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACCTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTTGGAGCGCCAGATATGGCCTTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAAC-ATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4984 Chironomidae sp. water mite diet isolate 4984-BHL032417-GBD6412_9271-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGTCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4985 Chironomidae sp. water mite diet isolate 4985-BHL032417-GBD24234_13265-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATCAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGATCCCTCTTATATTAGGTGCCCCAAACATAGCTTTCCCCCGTATAGATAATATAAGTTTTTGGCTTTTACCCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4986 Paratanytarsus sp. water mite diet isolate 4986-BHL032417-GBD24701_8905-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATATTATTTTTGGTGCTTGATCAGAAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAAATAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGAAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4987 Phaenopsectra sp. water mite diet isolate 4987-BHL032417-GBD3928_14158-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGGTTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTGCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4988 Chironomus riparius water mite diet isolate 4988-BHL032417-GBD6003_11248-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGTCTTGTCCCCCATAATACTTGGAGCACCTGACATAGCTTTTCCTCGACTAAATAATATAAGTTTCCGACTTCTACCCCCCTCTCTTACCCTACTTCGTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4989 Chironominae sp. water mite diet isolate 4989-BHL032417-GBD21295_3835-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATCTTTTTTTTTTGGATCTTGATCAGGTATAGTAGGAACTTCTTTAATAATATTAACCCGAACGGAATTAGTTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGAAGGATTTGGAAATTGGCTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTGCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4991 Paratanytarsus sp. water mite diet isolate 4991-BHL032417-GBD9990_17220-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACTTTTTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATACAGCTTTTCCTCGAATAAATAATATAAGATTTTGACATCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4992 Paratanytarsus sp. water mite diet isolate 4992-BHL032417-GBD25215_21217-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTACTTCGAACTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTCATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGATCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL4994 Chironomus sp. water mite diet isolate 4994-BHL032417-GBD19701_10651-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTCGGTGCTTGATCAGAAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4996 Chironomidae sp. water mite diet isolate 4996-BHL032417-GBD19317_16032-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTACATTTTATTTTTGGAGCTTGATCTGGAAAAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTGGGAAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGTAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID KM990292, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4998 Cricotopus sp. water mite diet isolate 4998-BHL032417-GBD2637_17040-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.0% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL4999 Chironomidae sp. water mite diet isolate 4999-BHL032417-GBD21896_8545-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTTGTAGTTATACCTATTTTAATTGGAGGATTGGGAAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL500 Chironomidae sp. water mite diet isolate 500-BHL040517-GBD26508_23547-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTACTTGTTACTGCACATGCTTTCATTATAATTTTTTTTTTATAGTTATACCAATTTTAATTGGAAGATTTGGTAATTTACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAAATAATATAAGATTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5000 Paratanytarsus sp. water mite diet isolate 5000-BHL032417-GBD19592_6230-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATTACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAAATAACTTAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5001 Oligochaeta sp. water mite diet isolate 5001-BHL032417-GBD25732_17965-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAACCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAGGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATAATAGCTTTCCCACGACTTAACAATGTAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.4% identical to accession ID LN810268, identified in GenBank as Chaetogaster diaphanus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL5002 Chironomidae sp. water mite diet isolate 5002-BHL032417-GBD11934_6519-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCTCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5003 Paratanytarsus sp. water mite diet isolate 5003-BHL032417-GBD16748_4921-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTACCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACCTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAAATTGTTTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5004 Chironomus sp. water mite diet isolate 5004-BHL032417-GBD10037_13732-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAATTTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCGCCAGATATGGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTATACCCTCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5005 Cricotopus sp. water mite diet isolate 5005-BHL032417-GBD4994_16105-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGATGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGACTTCTCCCCCCCATCTTTAACTCTTCTTCTT-TCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5006 Cricotopus sp. water mite diet isolate 5006-BHL032417-GBD16138_20113-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCTTCATTATCTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5007 Lepidoptera sp. water mite diet isolate 5007-BHL032417-GBD17646_27370-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAGTTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATATTTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 82.6% identical to accession ID HQ184266, identified in GenBank as Spindasis takanonis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5009 Chironomidae sp. water mite diet isolate 5009-BHL032417-GBD3732_11503-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTAAACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGTCCCAGACATAGCTTTCCCCACGTATAAATAATATAAGTTTTTGGCTATTACCCCCGTCATTAACTTTACTTCTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL501 Chironomidae sp. water mite diet isolate 501-BHL040517-GBD4450_19868-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAACTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTAATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5010 Paratanytarsus sp. water mite diet isolate 5010-BHL032417-GBD14583_17269-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCTGTGCCTGATCAGGAATAGTGGGAACTTCCCTAGGAATATTAATTCGAGCTGAATTAGGACATCCCAGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCCATAGTTATACCTATTTTATTTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5012 Oligochaeta sp. water mite diet isolate 5012-BHL032417-GBD9022_13406-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGATGGATTTGGAAATTGACTTCTACCTCTAATACTCGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID JQ519822, identified in GenBank as Nais communis/variabilis complex sp. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL5013 Oligochaeta sp. water mite diet isolate 5013-BHL032417-GBD8292_5478-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAAATATCTCAACCAGGAACATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATATTTGGAGCACCAGATATAGCTTTCCCACGACTTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTAGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL5014 Orthocladius sp. water mite diet isolate 5014-BHL032417-GBD24046_23282-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCCTTTGTTATAATTTTTTTTTATGGTTATACCTATTTAAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCAATTGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5015 Chironomidae sp. water mite diet isolate 5015-BHL032417-GBD17230_27445-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTGTATTTTATTTTTGGCGCCTGATCTGGGATAATCTGGACTTCTTTAATAATGCTTATTCGAGCAGAATTAGGACGACCCGGAATTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5017 Diptera sp. water mite diet isolate 5017-BHL032417-GBD6804_15306-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTATATTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACTTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCCTCTTTAACATTATTATTATCAAAAACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.6% identical to accession ID KM455055, identified in GenBank as Philophylla caesio. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5018 Cricotopus sp. water mite diet isolate 5018-BHL032417-GBD12384_6420-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGATATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTT-TCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5019 Chironomus sp. water mite diet isolate 5019-BHL032417-GBD18784_10066-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTACATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACGGG	Using NCBI BLASTN in June 2018, this sequence was 95.6% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL502 Psectrocladius sp. water mite diet isolate 502-BHL040517-GBD21769_17306-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTTGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCTCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5021 Culex pipiens water mite diet isolate 5021-BHL032417-GBD24572_13541-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTGTTTATTGGAAATGATCAAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.6% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5022 Chironomidae sp. water mite diet isolate 5022-BHL032417-GBD4567_18890-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTCTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5023 Chironomidae sp. water mite diet isolate 5023-BHL032417-GBD11587_28437-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTATATTTTATTTTTGACGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATGACGTCATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATTGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5027 Chironomidae sp. water mite diet isolate 5027-BHL032417-GBD2936_10605-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATAGGGACTTCTCTAAGAATGCTTATTCGAGTAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGCCCCTCTTATATTAGGAGCCTCAGACATAGCTTTCCCCCCGTATAAATAATATAAGTTTTTGGCCTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5028 Paratanytarsus sp. water mite diet isolate 5028-BHL032417-GBD26304_19561-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGCGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTAAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGAAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCATTAACACTTTTACTATCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5029 Paratanytarsus sp. water mite diet isolate 5029-BHL032417-GBD13243_24886-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCCGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGCACTAGGACATCCCTGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGATCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGAATGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAAAAATATAAGATTTTGACTTCTTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL503 Paratanytarsus sp. water mite diet isolate 503-BHL040517-GBD7676_6950-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTCGGAGCTTAGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAACAGAATTAGGCCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGAAATTGTTACAGCTCATTCCTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGTGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCGTCTTCTATCAAAAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5030 Amphichaeta sp. water mite diet isolate 5030-BHL032417-GBD16526_15202-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTAACCCATCATGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAGTTGAATTCTACCTTTAGTACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.7% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL5032 Paratanytarsus sp. water mite diet isolate 5032-BHL032417-GBD21223_5375-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAACTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR759769, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5033 Lebertia sp. water mite diet isolate 5033-BHL032417-GBD14231_22634-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAATCCTAATTCGACTTAAATTAGGACAACCAGCCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAAATGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAAAAATATAAGATTTTGACTTCTTCCTCCATCCTTAACCCTACTTCTAACAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5034 Hydrachnidiae sp. water mite diet isolate 5034-BHL032417-GBD19349_18060-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAGCTGCTCATGCTTTCGTTATAATTTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.1% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5035 Cricotopus sp. water mite diet isolate 5035-BHL032417-GBD22133_20260-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTGGAATTTTAATTCGAGCAGAATTAGGTCATGCGAGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGAATAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTTCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5036 Cricotopus sp. water mite diet isolate 5036-BHL032417-GBD14740_29114-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTGTAATAATTTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGTATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCATCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5038 Cryptochironomus sp. water mite diet isolate 5038-BHL032417-GBD7544_13698-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCTCATGCTGTTATTATAATTTTTTTCATGGTTATACCATTTTTTAATTGGAGGATTTGGAAATTGATTAGAACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5039 Paratanytarsus sp. water mite diet isolate 5039-BHL032417-GBD6298_11040-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCTGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATATGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL504 Chironomidae sp. water mite diet isolate 504-BHL040517-GBD12386_18630-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTTCATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGTTCTTCCTTATGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGCGCCCCAGATATAGCCTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTGCAAAAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR283178, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5041 Paratanytarsus sp. water mite diet isolate 5041-BHL032417-GBD27072_10427-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAAATCGAGCATAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTCAATATTAGGAGTCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.4% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5042 Oligochaeta sp. water mite diet isolate 5042-BHL032417-GBD22092_26112-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAAATTTCTTTCTTAGTAACACCATTTTTTATTGGAGGATGTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL5043 Chironomus sp. water mite diet isolate 5043-BHL032417-GBD20574_23451-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATCTTAATTCGCGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATATTTTTCTTTATAGTTATACCAATTTAAATTGGAGGTTTCGAAAAATGATTTTTCCCTTTAATATTAGGAGCTCCAGATATGACCTTCCCTCGAATAAAAAATATAAGGTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5044 Chironominae sp. water mite diet isolate 5044-BHL032417-GBD24881_21878-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAACGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATGGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID MG449442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5046 Paratanytarsus sp. water mite diet isolate 5046-BHL032417-GBD29558_14474-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATATTATTTTTGGTGCTTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTCTAATATTAGGAGCCCCAGATATAGCTTTTCCTTGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279360, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5047 Paratanytarsus sp. water mite diet isolate 5047-BHL032417-GBD6574_9116-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTAAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTAACTATTACCCCCATCACTAATTCTATTAGTTGCA--TCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5048 Paratanytarsus sp. water mite diet isolate 5048-BHL032417-GBD15459_23646-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTCATAGTCATACCTATTTTAATTGGAGGATTTGGAGACTGATTATTGCCTTTAATATTAGGAGCCCCAGATACAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTATTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL505 Cricotopus sp. water mite diet isolate 505-BHL040517-GBD28560_14228-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTGCCTTAGAATCTTAATTCGAGCTGAATTAGGACATGCCGGATCGTTAATTGGAGATGATCAAGTTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCATCGAATAAATAATATAAGTTTTTGATTATTACCACCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR960636, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5051 Chironomidae sp. water mite diet isolate 5051-BHL032417-GBD19275_15494-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAATCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.0% identical to accession ID KP039729, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5055 Chironomus crassicaudatus water mite diet isolate 5055-BHL032417-GBD15603_2107-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTTGTTACAGCTCACGCATTTATTCTAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGCTTTGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATGTAAGTTTTTGACTTCTCCCCCCCATCTTTAACTCTACTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.8% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5056 Chironominae sp. water mite diet isolate 5056-BHL032417-GBD15875_13546-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTATTTTTGGAGTCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGAACAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCACCTTCATTAACCCTTCTACTTTCTAGTGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5058 Chironomidae sp. water mite diet isolate 5058-BHL032417-GBD24269_14743-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATATCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATTACTTTCCCACGAATAAATAATATAAGTTTTTGATTGTGGCCCCCATCATTAACTTTATAGTTATCTAGATCAATTGTGGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL506 Chironomidae sp. water mite diet isolate 506-BHL040517-GBD4317_11080-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTATCAGGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5060 Lebertia sp. water mite diet isolate 5060-BHL032417-GBD18176_8369-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACACCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAAAAATAATTGGAGGTTTTGGAAACAGATTAGTTCCACTAATAATCAGATCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTACCCCAACCTTAACCCTACTTCTAACAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5062 Chironomidae sp. water mite diet isolate 5062-BHL032417-GBD15128_23165-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTATTTTTGGCGCCTGATCTGGGATAGTCGGTACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGTCGACCCGGATCTTTCATTGGTGACGAACAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTAATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5064 Chironomidae sp. water mite diet isolate 5064-BHL032417-GBD16080_5286-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTATTTTTGGCGCCTGATCGGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCCGAACTTTCATTGGTTACGACCAAATTTATAACGCAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGCTTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5065 Lebertia sp. water mite diet isolate 5065-BHL032417-GBD26735_10091-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAATCCTAATTCGACTTGAATTAGGACGACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTTGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGGGGGTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAAAAATATAAGATTTTGACTTCTTCCTCCATCCTTAACCCTACCTCTATCAAGGTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5067 Lebertia sp. water mite diet isolate 5067-BHL032417-GBD28893_13198-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTTGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGGTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATAGAGCCTTTCCACGAAAAAAAATATAAGATTTTGACTTCTTCCCCCATCCTTAACGCTACTTCTAACAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5069 Chironomidae sp. water mite diet isolate 5069-BHL032417-GBD21250_20873-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACAAAATTTATTTCGTAACTGTTACAGCCCATGCTTTTATTATAAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL507 Chironominae sp. water mite diet isolate 507-BHL040517-GBD13679_15359-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTCATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR285570, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5072 Oligochaeta sp. water mite diet isolate 5072-BHL032417-GBD26150_22184-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTTATCTTAGGAGTTTGAGCTGGAATAATTGGAACACTAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTACTAATAATTTTCTTTCTGATTATACCAGTATTTATTGGTGGATTTGGAAAATGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACGTAACAAGTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCGGAGGCCGTAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL5077 Chironomidae sp. water mite diet isolate 5077-BHL032417-GBD2555_10956-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCTCCCATCTTTAACTCTTCTTCTGTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5079 Lebertia sp. water mite diet isolate 5079-BHL032417-GBD29674_16075-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTACTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGTACAAATTTACAATACAATTGTAACTGCTCATGCTTTTGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAAAATAAGATTTTGAATTATTCCTCCATCCTTAAATCTACTTCTAACAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL508 Chironominae sp. water mite diet isolate 508-BHL040517-GBD9281_24258-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTAAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCTCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR765094, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5080 Paratanytarsus sp. water mite diet isolate 5080-BHL032417-GBD9730_23797-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTTATTTTTGGTGCTTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTACCCCCCTCTCTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5081 Chironomidae sp. water mite diet isolate 5081-BHL032417-GBD17260_25462-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATCTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACTGACCATGCCTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCCATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5088 Psectrocladius sp. water mite diet isolate 5088-BHL032417-GBD11316_27049-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL509 Chironomidae sp. water mite diet isolate 509-BHL040517-GBD9664_23104-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTGAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTTATAGTTATCCCAATTTTAATTGGAGGATCTGGTAATTGACTTTTGCCTTTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGGTTTTGATTATTACCCCCATCTCTAACATTACTACTGTCAAAAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5090 Chironomidae sp. water mite diet isolate 5090-BHL032417-GBD8761_6982-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.5% identical to accession ID GU565715, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5093 Chironomidae sp. water mite diet isolate 5093-BHL032417-GBD14805_3190-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAAGTAGGACGACCCGGAACTTTCATTGGGGACGACCTAATTTATAACGTAATTGTTACAGGCCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTGGGAAATTGATCGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5094 Chironomidae sp. water mite diet isolate 5094-BHL032417-GBD27325_15111-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTATTTTTGGCGCCTGATCTGGGACAATCGGGACTTCTCTAAGAATGCTTATTTGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTATTACAGCCCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTCTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTATAAAATGGCGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5095 Lebertia sp. water mite diet isolate 5095-BHL032417-GBD28449_20511-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTACTTTGCTTTTGGAGCATGATCCGGTATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCCCATGCTTTCGTTATAAATTTTTTCATAGTAATACCAATAATAATTGGAAGGTTTGGAAACTGATTAGTTCCACTAACAATCAGAGCCCCAGATATAGCTTTTCCACGAAAAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGGTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5099 Cricotopus sp. water mite diet isolate 5099-BHL032417-GBD24905_22363-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCTAATAAATAACATAAGATTTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL510 Cricotopus sp. water mite diet isolate 510-BHL040517-GBD23551_20448-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCTCGATCAGGGATAGTAGGTACTTCCCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGGTCATTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGTTCCTGTTATAGCTTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTTACCTTATTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5106 Chironomidae sp. water mite diet isolate 5106-BHL032417-GBD7794_23265-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGAACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGAAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGTCCCAGACATAGCCTTCCCCCGTATAAATAATATAAGTTTTTGGTTTTTACCCCCGTCATTAACTTTACTTCTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL511 Drosophila sp. water mite diet isolate 511-BHL040517-GBD5130_20340-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAAAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.5% identical to accession ID KJ841763, identified in GenBank as Scaptodrosophila sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5112 Lebertia sp. water mite diet isolate 5112-BHL032417-GBD7792_20339-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTATACTTAATTTTAGGAGTTTGAGCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGTTATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5116 Chironomidae sp. water mite diet isolate 5116-BHL032417-GBD17385_27499-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATGCTTATTCGAGCAGAATTAGGACTACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTTTTCCAGCCCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.4% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5118 Chironomidae sp. water mite diet isolate 5118-BHL032417-GBD16996_20466-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTTGAGCAGAGTTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATGGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTACTTTCCAGTGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5119 Paratanytarsus sp. water mite diet isolate 5119-BHL032417-GBD16854_24083-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATCTTTTTTTTTCATAGTTATACCTATTTTATTTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCCTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5126 Paratanytarsus sp. water mite diet isolate 5126-BHL032417-GBD24933_21777-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTAAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGGCTTTTACCCCCGTCATTATCTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID KR759769, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5128 Lebertia sp. water mite diet isolate 5128-BHL032417-GBD29248_13762-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTTGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAATGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTTGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGGTTTGGAAACTGATTATTTCCACTAATAATCAGAGCCCCAGATATAGACTTTCCACGAAAAAATAAAATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGGTCCTTTACAAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL513 Paratanytarsus sp. water mite diet isolate 513-BHL040517-GBD2508_17067-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGGATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR672858, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5132 Lebertia sp. water mite diet isolate 5132-BHL032417-GBD4103_7866-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTTAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTCCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGTTTTTGGCTTATACCCTCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5137 Paratanytarsus sp. water mite diet isolate 5137-BHL032417-GBD18188_4553-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCTGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTAATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTTCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAACTGGAGCTGGCACCGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5138 Paratanytarsus sp. water mite diet isolate 5138-BHL032417-GBD24550_17200-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAACTCATGTATTTATTCTAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTATGAGCCCCAGATATAGCTTTTCCTCGAATAAATAAGATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACCTTCAAGTAGAATAGTGGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL514 Paratanytarsus sp. water mite diet isolate 514-BHL040517-GBD1814_13737-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCATGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCCTTTCCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID KR753366, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5141 Lebertia sp. water mite diet isolate 5141-BHL032417-GBD9994_25189-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTACTTTGCTTTTGGAGCATGCTCCGGAATAATTTGAGCTAGATTAATAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAAAAATTGGAGGTTTTGGAAACTGATTAGTACCACTAATAATCAGAGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCGTTACAGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5147 Cricotopus sp. water mite diet isolate 5147-BHL032417-GBD14854_8513-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGCCCCGGATCTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCATCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAGAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.1% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL515 Chironomidae sp. water mite diet isolate 515-BHL040517-GBD28169_11297-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTGGGAACTTTCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAACGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTATTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTATTACCCCCGTCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5154 Cricotopus sp. water mite diet isolate 5154-BHL032417-GBD5953_12598-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATCTTCGGAGCATGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATCCGGGCCAAATTAGGACATGCCGGATCATTAATTGGTGACAATCAAATTTACAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCTCTTACATTACTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL516 Diptera sp. water mite diet isolate 516-BHL040517-GBD3710_19453-Ldc62 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTGATACCTATTTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.6% identical to accession ID JX913759, identified in GenBank as Hemipyrellia ligurriens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5161 Paratanytarsus sp. water mite diet isolate 5161-BHL032417-GBD26524_8982-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCCGATCAGGAATAGTGGGAACTTCCCTACGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCACTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGAAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCCCCTGTAACGCCTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5162 Lebertia sp. water mite diet isolate 5162-BHL032417-GBD6690_4672-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCCTTTGGAGCATGATCCGGAATAATTGGAGTTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCACAATCCTAGGAAGTGACCAAATTTACAAAACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGATCCATTAATAATCAGATCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTTTTCCTCCATCCTTAACGCTACTTCTATCAAGTTCCTTTTCAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5163 Chironomidae sp. water mite diet isolate 5163-BHL032417-GBD14764_25662-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATCTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACGTGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCTCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5166 Paratanytarsus sp. water mite diet isolate 5166-BHL032417-GBD13974_19607-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGTATTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGAATTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5169 Lebertia sp. water mite diet isolate 5169-BHL032417-GBD28093_17444-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTTAGAACTCTAATTCGACTTTAATTAGGTCAACCAAGCTCACTCCTAGGAAGTGACCAAATTTACAAATACATTTGCAACTGCTCATGCTTCCGTTATAATTTTTTTCATAGCAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL517 Paratanytarsus sp. water mite diet isolate 517-BHL040517-GBD23404_13329-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTTGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAATAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5171 Chironomidae sp. water mite diet isolate 5171-BHL032417-GBD27450_18741-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTATATTTATTTTTGGCGCCTGATCTGGTATAATCGGTACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACCACCCGGAACTTTAATTGGTAACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGAATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5173 Chironomidae sp. water mite diet isolate 5173-BHL032417-GBD23217_25933-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTTGGCGCATGATCTGGGATACTCGGGACTTCTCTAAGATTGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGATGACGACCAAATTTATAACGTAATTATTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAATTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5179 Chironomidae sp. water mite diet isolate 5179-BHL032417-GBD26574_19148-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTTAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCTGACATAGCCTTCCCCCGTAAAAAAAATAAAAGGATTTGGCTTTTACCCCCAGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5180 Chironomidae sp. water mite diet isolate 5180-BHL032417-GBD11708_28156-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTCTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCCCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTATTTGGCTTTTACCCCCGTCATTAACCTTACTTCTTTCTAAGTCAATTGGAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5183 Chironomidae sp. water mite diet isolate 5183-BHL032417-GBD20469_26651-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGAACTTCTTTAATAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGCATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGTAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5184 Oligochaeta sp. water mite diet isolate 5184-BHL032417-GBD21819_26520-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGATGGATTTGGAAACTGACTTCTACCTCTAATACTTGGAGCGCCAGGTATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTATAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.8% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL5188 Chironominae sp. water mite diet isolate 5188-BHL032417-GBD9153_14396-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGATATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATTTGGACAACCCGGTACTTTTATTGGAGATGTCCAAATTTACAATGTAGTTGTCACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL519 Chironomus riparius water mite diet isolate 519-BHL040517-GBD5684_16352-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATACTTATAACAATTTTAATTGGAGGATTCGCAAACTGACTTGTCCCCCTAATATTTGGAGCACCTGACATAGCTTTTCCTCTAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5191 Amphichaeta sp. water mite diet isolate 5191-BHL032417-GBD25482_24144-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGACCAAGACTATTAATTCGTATTGAATTAACCCATCATGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAGTTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATAAAATAATATAAGGTTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL5192 Chironomidae sp. water mite diet isolate 5192-BHL032417-GBD9183_21947-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCTGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGACATTAACTTAACTTCAATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5195 Amphichaeta sp. water mite diet isolate 5195-BHL032417-GBD8549_17250-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAAGACATCCTGGAGCCTTTTTAGGAATAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTATAATAATTTTTTTCTTAGTAAAACCAGTTTTTATTGGAGGATTTGGGAATTGAATTCTACCTTTAATACTGGGGACACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGAATATTACCCCCATCACTAATTCTATTAGTTGCATCCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.7% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL5199 Oligochaeta sp. water mite diet isolate 5199-BHL032417-GBD2338_16260-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTGCCCACGACTGAACAAATAAAGATACTGACTACTACCGCCTGCACTAAACCTATAAGTGTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL520 Chironomus riparius water mite diet isolate 520-BHL040517-GBD3480_11706-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCTCCCTCTCTTACTCTTCTTCTTTCTAGATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5203 Oligochaeta sp. water mite diet isolate 5203-BHL032417-GBD17801_17643-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAACTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAACACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCA--AGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL5207 Chironomidae sp. water mite diet isolate 5207-BHL032417-GBD9573_27591-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAATTTTCATTGGTGACGAACAAATTTATAACGTAATTGTTACAGCCCATACTTTTATTATAATTGTTTTTATAGTTATATCTATTTTAATTGGAGGATTTGGGAATTGATTGGTACCTCTAATATTAGGAGCCCCTGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5208 Lebertia sp. water mite diet isolate 5208-BHL032417-GBD3670_14742-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTCTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAATGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTTGTTATAATTTTTTTCATTGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAAAAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACCCTACTTCTAACAAGGTACTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL521 Cricotopus sp. water mite diet isolate 521-BHL040517-GBD11965_4828-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATATTGGAACATTATATTTTATTTTCGGGGCTTGATCAGGGATAGTAGGTACTTCCCTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTCATAGTTATACCTATTTTAATTGGGGGGTTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTGTTACCCCCTTCTCTTACCTTATTACCTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR961360, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5210 Psectrocladius sp. water mite diet isolate 5210-BHL032417-GBD26536_14738-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTGAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGTTTTGGAATTTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCGTCATTAACCTTACTATTATCAAGCTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5211 Lebertia sp. water mite diet isolate 5211-BHL032417-GBD29066_13420-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATACGGAATAATTGGAGCTTGATTAAGAACCCTTATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGGTTTGGAAACTAATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAACAAATAAAATAAGATTTTGACTTCTTCCCCCACCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5212 Chironomidae sp. water mite diet isolate 5212-BHL032417-GBD21783_5668-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CCCTATATTTTATTTTTGGAGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTCTAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTAATATTAGGAGCCCCAGACACAGCTTTCCCCCGAATAAATAATATAAGTTTTTGGCTATTACCCCCGTCATTAACTTTACTTCTTTCTAATTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5213 Lebertia sp. water mite diet isolate 5213-BHL032417-GBD29405_16593-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTCGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAGTAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAAATATAGCTTTTCCACGAATAAATAAGATAAGAGTTTGACTTCTTCCTCCATCCTTAACGCTACTTCTAAAAAGGTCCTTTACAGGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5216 Lebertia sp. water mite diet isolate 5216-BHL032417-GBD7364_11930-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACACCCAGGCTCACTCCTAGGAAGTGACCAAATTTATAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCCTTTCCCCCAAAAAATAATATAAGAATTTGACTTCTTCCCCCATCCTTAACTCTACTTCTAACAAGTACCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5219 Amphichaeta sp. water mite diet isolate 5219-BHL032417-GBD3975_10668-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGATCAAGACTATTAATTCGTATTTAATTAACCCATCATGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTTGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAGTTGACTTCTACCTTTAATACTTGGAGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAACTCTATTAGTAGCAACGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL5220 Chironomidae sp. water mite diet isolate 5220-BHL032417-GBD27837_21566-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGTAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAAGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCCTGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTGCCCCCATCACTAATTCTATT	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5221 Chironomus sp. water mite diet isolate 5221-BHL032417-GBD21126_4268-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACCTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCTTTTATTATAATTTTCTTTATAGTTGTACCCTTTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGAATTCCCCCCCCCCATCTTTAACTCTTCTTCTTTCTAATTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL523 Paratanytarsus sp. water mite diet isolate 523-BHL040517-GBD13797_4955-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGTAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATATTTTTTTTCATAGTTAAACCTATTTTAATTGGAGGGTTTGGGAACTGATTATTGCCTTTAATATTTGGAGCCCCCGATATAGCTTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTGCCCCCTCTTTAACTCTTTTTCTTTCAAGTAGAATAGTGGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5233 Chironominae sp. water mite diet isolate 5233-BHL032417-GBD22129_9956-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGAAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATAATAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTAATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL524 Psectrocladius sp. water mite diet isolate 524-BHL040517-GBD19326_7125-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTGTATTTTATTTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCTAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCACCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5242 Paratanytarsus sp. water mite diet isolate 5242-BHL032417-GBD5498_20874-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTATTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCCCGAATAAATAATATAAGAATTTGACTTCTTCCCCCCTCTTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5245 Lebertia sp. water mite diet isolate 5245-BHL032417-GBD28102_11982-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTTGATTAAGAACCCTAATTCGACTTGACTTAGGACAACCAGGCTCACTACTAGGAAGTGTCCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAAATTTTTTCATAGTATTACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAAAAATATAAGATTTTGACTTCTTCCCCCATCCTTAACTCTACTTCTATCAAGGTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5247 Paratanytarsus sp. water mite diet isolate 5247-BHL032417-GBD22579_8989-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCGTGCGGGTTCTTTAATTGGAGATGATTAAATTCATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGAAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR279360, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5249 Chironomidae sp. water mite diet isolate 5249-BHL032417-GBD22405_12750-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTTAGAATACTAATTCGAGTTGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGAGCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL525 Paratanytarsus sp. water mite diet isolate 525-BHL040517-GBD14404_25629-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTAATGCTTTTATTATAA-TTTTTTCATAGTTATACTTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGCTATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCCCTCTTTAACTCTTTTACTTCCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL526 Chironomus riparius water mite diet isolate 526-BHL040517-GBD26742_8633-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTACTTTTGGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACTCGAGCAGAATTAGGACAGACCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCGTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5262 Cricotopus sp. water mite diet isolate 5262-BHL032417-GBD19686_3818-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTAATCTTAGGAGTATGAGCAGGGATAGTTGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAGTAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5265 Chironomidae sp. water mite diet isolate 5265-BHL032417-GBD16599_23795-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGTTAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAACTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTTATATTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGTTCCCTCTTATATTAGAAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCCGTCATTATCTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL527 Chironomus riparius water mite diet isolate 527-BHL040517-GBD11415_16645-Ldc63 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTCATCCGGAAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGAGGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTCTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACCTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTATCTTACTCTTCTTCTATCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5284 Oligochaeta sp. water mite diet isolate 5284-BHL032417-GBD6992_21407-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCATGGAGCCTTTTTAGGAAGGGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAGTTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCATGATTAAATAATATAAGATTTTGACTATTACCCCCATCATTAACTCTACTTCTATCA--AGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.2% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL5285 Lepidoptera sp. water mite diet isolate 5285-BHL032417-GBD20549_25513-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCATGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTC-TTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.5% identical to accession ID KM576860, identified in GenBank as Glyphodes pyloalis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5289 Chironomidae sp. water mite diet isolate 5289-BHL032417-GBD13846_21828-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAGTTTATAACATAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCACTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATGAACTTTACTTCTTTCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL529 Chironomus riparius water mite diet isolate 529-BHL040517-GBD8370_16831-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAGTTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGATCACCTGACATAGCTTTTCCTCGAATAAATATTATAAGTTTCTGACTTTTACCCCCCCCTCTCTTACTCTTCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5292 Oligochaeta sp. water mite diet isolate 5292-BHL032417-GBD15641_7914-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTACCTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCCCCAAATAAAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCCCCAGCCTTAACTCTTCTTCTAACAAGGTCCTTTACAG-----GAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 81.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL5294 Paratanytarsus sp. water mite diet isolate 5294-BHL032417-GBD27376_17700-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATTTTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGAAGAACAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTACTGCCTTTAATATTAGGAGCCCCAGATATAGCCTTTCCTCGAACAAATAAAATAAGATTTTTACTTCTTCCCCCCCTCATTAACTCTTTTACTTTCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL530 Cryptochironomus sp. water mite diet isolate 530-BHL040517-GBD28851_17243-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACAACCAAATTTATAATGTAATTATAACAGCTCATGCTTTTATTATAATTTTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGAGTTTGACTTCTACCCCCATCCTTGACTCTTCATCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5304 Chironomus sp. water mite diet isolate 5304-BHL032417-GBD19434_13371-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAATTTTTTAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGCTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTATTGAATTCTCCCCCCATCTTTAACTCTACTTCTTTCTAGTACATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5305 Chironomidae sp. water mite diet isolate 5305-BHL032417-GBD15325_4504-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATAGGTGACGACCATATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTTATAGTTATAACTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCACTTGTAGAAAATGGCGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL531 Chironomus riparius water mite diet isolate 531-BHL040517-GBD5405_10411-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAATTATAATTGGAGGATTCGGAAATTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAGCAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL532 Chironomus riparius water mite diet isolate 532-BHL040517-GBD18495_13015-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCCTTTATTATAATTTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGTTTTTCCTCGAATAATTAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5320 Cricotopus sp. water mite diet isolate 5320-BHL032417-GBD13162_22597-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5329 Chironomus sp. water mite diet isolate 5329-BHL032417-GBD8256_19267-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGTACTTTTATCGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCGCCAGATATGGCCTTCCCCCGAATAAATAATATAAGTTTTTTGACTTCTCCCCCCATCTTTAACTCTACTTCTATCTAGTCCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5330 Chironomidae sp. water mite diet isolate 5330-BHL032417-GBD8151_10287-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTCATAGTTACACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.6% identical to accession ID GU565708, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL534 Chironomidae sp. water mite diet isolate 534-BHL040517-GBD23796_24167-Ldc64 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGCTCGGGATTAGTAGGCGCTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACATCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAATGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTATGGGGCTCCTGATATAGCTTTTCCGCGAATAAAAAATATAAGAATTTGATTATTACCCCCTACATTAACCGTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5343 Cricotopus sp. water mite diet isolate 5343-BHL032417-GBD26356_9153-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTTGGAACCTCTCTTAGACTTTTAATTCGAGTTGAATTAGGTCATGCGGGTTCTTTATTTGGAGAAGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTATATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATAATTATTATCAAGAACGATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5346 Chironomidae sp. water mite diet isolate 5346-BHL032417-GBD17149_2136-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAATTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTCTTATATTAGGAGCCCCAGACATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KM992253, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5350 Chironomidae sp. water mite diet isolate 5350-BHL032417-GBD22486_24773-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGTTGAACTAGGACATCCTGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTATCTAGTTCAATTCTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KM990292, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5351 Lebertia sp. water mite diet isolate 5351-BHL032417-GBD17705_12835-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGTTTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAAGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAAATATAGCTTTTCCCCCAATAAATAATAAAAGATTTTGACTTCTTCCCCCATCCTTAACTCTACTGCTATCAAGGTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5361 Chironomidae sp. water mite diet isolate 5361-BHL032417-GBD13360_21956-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTAGTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTGTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGCTACAGCTCATGCTTTTGTAATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTAATTAGTTCCTTTAATATTAGGAGCACCTGGTATGGCTTTCCCACGAATAAATAATATAAGTTTTTGAGTGTTGCCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5364 Paratanytarsus sp. water mite diet isolate 5364-BHL032417-GBD2734_19931-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGAACAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGTTTTGGGAACTGATTAGTGCCTTTAATATAAGGAGCCCCTAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTCTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5370 Chironomidae sp. water mite diet isolate 5370-BHL032417-GBD4928_20857-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGATCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTATAATTTTTTTTTATAGTAATACCAATTCTAATTGGAGGGTTTTGAAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTCCCCCCGTATAAATAATATAAGTTTTTGGCTTATACCCTCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.0% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5373 Paratanytarsus sp. water mite diet isolate 5373-BHL032417-GBD20462_5598-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTACATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATACCTTTCCCCCGAAAAAAAAAAAATAAGA-TTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL538 Paratanytarsus sp. water mite diet isolate 538-BHL040517-GBD24621_23344-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTTCTTTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGTCATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATCGTTACAGCTCATGCATTTATTATAATTTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATTTTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCTTTAACTCTTTTACTCTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR292109, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5381 Paratanytarsus sp. water mite diet isolate 5381-BHL032417-GBD6256_23994-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAACATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATTTCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5388 Chironomidae sp. water mite diet isolate 5388-BHL032417-GBD7686_11204-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTAGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGTTCATGCTTTTGTAATAAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL539 Paratanytarsus sp. water mite diet isolate 539-BHL040517-GBD3383_20930-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATGTGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGTAGATGATTAAATCTATAATGTTATTGTTATAGCTAATGCTTTTATTATATTTTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5392 Lebertia sp. water mite diet isolate 5392-BHL032417-GBD21278_15410-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTTGATTAAGAACCTTAATTCGACTTGAATTAGGACAACAAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTTACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATTTTAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAAAAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAAATTTTGACTTCTTCCTCCATCCTTAACCCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5395 Chironomus sp. water mite diet isolate 5395-BHL032417-GBD27251_19535-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGTTTATTCGAGCAGAGTTAGGACGACCCGGAACTTTTATTGGTTATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTGTTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGATTTGTTCCTTTAATATTAGGAGCTCCAGATATGACCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTATAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL540 Chironomus sp. water mite diet isolate 540-BHL040517-GBD9596_12919-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTACTTTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTGTTGGCGACGACCAGATTTATAATGTAATAGTTACAGCTCACGCATTTATTATAATTTTTTTTTCATAGTTATGCCAATTTTAATTGGTGGTTTTGGAAATTGACTTGTACCTTTAATACTAGGGGCCCCTGACATAGCTTTCCCCCGAATAAATAATATAAGTTTCTGATTACCTCCCCCATCACTTACATTACTCCTTTCAAATTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID GU013581, identified in GenBank as Chironomus entis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5401 Nais sp. water mite diet isolate 5401-BHL032417-GBD24814_12820-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATCTAATTTTAGGAGTATGATCAGGAATAGTAGGAACTGGAACAAGATTACTAATTCGAATTGAACTCTCATAACCAGGATCATTCCTTGGAAGAGATCAATTATATAATACTCTTGTTACAGCACATGCACTTTTAATAATTTTTTTCATAGTAATACCTATATTAATTGGAGGATTCGGAAACTGATTACTTCCACTAATACTAGGTGCTGCTGATATAGCATTCCCACGAATAAATAATCTAAGATTTTGATTACTTCCACCATCATTAATTCTACTAATATCTTCTGCAGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID JQ519861, identified in GenBank as Nais barbata. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL5404 Paratanytarsus sp. water mite diet isolate 5404-BHL032417-GBD11436_17060-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCCGATCAGGAATAGTGGGAACTTCCCTAAGAATATTTATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCTTAGTTATACCTTTTTTAATTGAAGGATTTGGGAAATGATTATTGCCTTTAATATTAGGAGCCCCAGATCTAGCTTTTCCTCGAATAAAAAAAATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5405 Chironomus sp. water mite diet isolate 5405-BHL032417-GBD14166_16995-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTTTATATTTTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCTTAATTATGACCTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCGCCAGATATGGCCTTCCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5407 Chironomidae sp. water mite diet isolate 5407-BHL032417-GBD15936_7647-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTCATTGGTGACGACCAAATTTATACCGTATTTGTTACAGCCCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTT-AATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCGGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KM990292, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL542 Chlorodendraceae sp. water mite diet isolate 542-BHL040517-GBD20370_9724-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTACATTATATTTTATTATTCGGTGCATTTGCTGGGGTATTAGGGACGTGTTTTTCCTTAGTTATTCGAATGGAATTAGCACACCCTGGACAACAGATTTTAAATGGAAACCACCAATTATATAATGTCATTATTACAGCCCACGCATTCCTGATGATCTTCTTCATGATAATGCCAGTCTTAATCGGAGGTTTTGGTAACTGGTTTGTACCAGTCATGATTGGTGCACCGGACATGGCGTTTCCACGACTAAACAACATTAGTTTTTGGTTACTGCCACCTTCGCTTTTCTTACTGTTAAGTTCTGCTTTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 80.4% identical to accession ID b|Z47795, identified in GenBank as Tetraselmis subcordiformis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL543 Leptocera erythrocera water mite diet isolate 543-BHL040517-GBD6844_9102-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTATATTTGGAGCTTGAGCGGGAATAGTAGGAACTTCTCTTAGTATTTTAATTCGAGCAGAATTAGGACATCCAGGTGCTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTATAGTAATACCTATTATAATTGGAGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATGAATAATATAAGTTTTTGATTACTACCTCCTTCTCTTACCTTACTTTTAGTAAGCAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR394103, identified in GenBank as Leptocera erythrocera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5434 Oligochaeta sp. water mite diet isolate 5434-BHL032417-GBD17122_26856-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTACCTTAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTACACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAGTTGAATTCTACCTTTAATACTTTGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL5439 Chironomidae sp. water mite diet isolate 5439-BHL032417-GBD19305_24417-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTTGGTGATGCCCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATATTTTTTTTTATAATTATACCTATTTTAATTGGAGGATTTTGGAATTGATTGATCCCTCTAATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTATCTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL544 Paratanytarsus sp. water mite diet isolate 544-BHL040517-GBD10619_7980-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAAGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATATATTTTTTTCTTAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCTCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5441 Paratanytarsus sp. water mite diet isolate 5441-BHL032417-GBD21523_22789-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCCCTAAGAATATTAATTCGAGCTTAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAATTTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGTCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACCCTTTTACTTTCAAGTAGAATAATGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID KR757714, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL545 Paratanytarsus sp. water mite diet isolate 545-BHL040517-GBD28139_13137-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATCAGGACACCCTGTAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACATCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGATCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTAACAAGAAGATTGGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5451 Lebertia sp. water mite diet isolate 5451-BHL032417-GBD19373_21727-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTGCTTTTGGAGCATGATCTGGAATAATTGGTGCTTGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTTGTTATAATTTTTTTCATAATAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAAAAATAAAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCATTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5452 Paratanytarsus sp. water mite diet isolate 5452-BHL032417-GBD6933_15178-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTGTAGTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTTAACTAGGACAACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGAGTTTGACTTCTTCCCCCCTCGTTAACTCTGGTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5453 Paratanytarsus sp. water mite diet isolate 5453-BHL032417-GBD12503_2450-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATAGTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTACCTTTAATATTAGGAGCCCCAGATATAGCTGTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTGTAACTCTTTCACTTTCAAGTAGAAGAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5458 Amphichaeta sp. water mite diet isolate 5458-BHL032417-GBD26217_7634-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTGGAGCTTGATCTGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTAATGCATATGCATTTTTAATAATTTTTTTCTTAGTAACACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL546 Chironomus riparius water mite diet isolate 546-BHL040517-GBD16351_25219-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTATCCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5466 Chironominae sp. water mite diet isolate 5466-BHL032417-GBD21719_10428-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTCATAATAATACCTATTTTGATTGGAGGATTTAGAAATTGGTTATTACCACTAATATTTAGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL547 Chironominae sp. water mite diet isolate 547-BHL040517-GBD15269_28595-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAAAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACATCTCACTCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCCCACTGATATAGCTTTTCCGCGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCATTAACTCTACTTCTTTCTAACTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5477 Oligochaeta sp. water mite diet isolate 5477-BHL032417-GBD29180_12754-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTTTATACTTAATCTTAGGAGTTTAAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCTGATATAGCTTTCCCTCGAATAAACAATATAAGTTTCTGACTACTACCCCCTTCACTAACCCTATTGGTATCTACTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL548 Paratanytarsus sp. water mite diet isolate 548-BHL040517-GBD3679_13942-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTATGTATATTAATTCGAGCATAATTAGGACACCCTTGAATATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGAGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5487 Paratanytarsus sp. water mite diet isolate 5487-BHL032417-GBD4212_9681-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACGACCCCCATCTGTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL549 Paratanytarsus sp. water mite diet isolate 549-BHL040517-GBD13917_7776-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTCGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGATCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCCATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATTCCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCATATAAATAATATAAGTTTTTGATTACTTCCCCTATCTTTAACCCTTCTTCTATCAAAAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5490 Chironomidae sp. water mite diet isolate 5490-BHL032417-GBD14547_17401-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATAGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGATCCCTCTTATATTAGGAATCCCAGACATAGCTTTCCCCCCGTATAAATAATATAAGATTTTGGCTTTTACCCCCGTCATTAACATTACTTCTTTCTAGTTCAATTATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5491 Paratanytarsus sp. water mite diet isolate 5491-BHL032417-GBD26351_6560-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGTACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACACCCCGGAACTTTAATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCCTTTCCTCGAATAAATAAAATAAGATTTTGGCTTCTTCCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5496 Chironomidae sp. water mite diet isolate 5496-BHL032417-GBD21601_15062-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGAAATTGTTACTGCCCATGCTTTTATTATATTTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAAACATAGCTTTCCCACGTATAAATAATATAAGTTTTTGGCTTTTACCACCGTCATTAACTTTACTTCTTTCTAGTGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5497 Lebertia sp. water mite diet isolate 5497-BHL032417-GBD17938_28667-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTTGGAAGTGACCAAATTTACAATACAATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGGTTTGGGAACTGATTAGTTCCACTAAAAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAAAAATATAAAATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL550 Orthocladiinae sp. water mite diet isolate 550-BHL040517-GBD15909_25994-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGACTAGTGGGCACTTCTTTAATAATTTTAATTCGACTAGAATTAGGACACCCAGTCTAATTGATCGTAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTATCCTTGATATTATGAGCCCCTGATATAGCTTTTCCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTGCATTAACCTTACTTTTATCAAAATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5500 Chironomidae sp. water mite diet isolate 5500-BHL032417-GBD4188_12003-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTTGGCGCCTGATCTGGGCTAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGCCGCCCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTGCTTTCTAGTTCAATGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5502 Lebertia sp. water mite diet isolate 5502-BHL032417-GBD25204_6761-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACTCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTACTCATGCTTTCGTTATAATTTTTTTCATAATAATACCAATAATAATTGGAAGTTTTGGAAACTGATTAGTTCCACTAATAATCAGATCCCCAGATATAACCTTTCCACCAATAAATAAAAAAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5503 Oligochaeta sp. water mite diet isolate 5503-BHL032417-GBD12616_15432-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTAATTGGAGGTTTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTC---TTCTTCCTTCTAGTCCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.4% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL5508 Lebertia sp. water mite diet isolate 5508-BHL032417-GBD25074_11200-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAATCCTAATTCGACTTGAATTATGACAACCAGGCTCACTCCTAGGAAGTGATCAAATTTACAATACAATTGTTACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGGTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCCTTTCCCCGAATAAAAAAAAATAAGATTTTGACTTCTTCCCCCAACCTTAACTCTACTTATATCAAGTTCCATTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL551 Chironominae sp. water mite diet isolate 551-BHL040517-GBD12810_24423-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCATTTAGTATATTAATTCGAGCAAAACTTGGTCACCCTGTAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACATCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTCTCATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGTGCCCCTGATATAGCTTTTCCTCGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTAACTCTTCTTCGTTCTAGCGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5513 Oligochaeta sp. water mite diet isolate 5513-BHL032417-GBD2924_20456-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGAACTTTATATTTTATTTTTAGGAGTTTGAGCCGGATTAATTGGAATCGGCACTAGAATTTTAATTCGGCTTGACTTAGCTCAACCAGGATCATTCCTATGGAGAGATCAGTTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTTTAGTTATACCAGTATTTACTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATGGCCTTCCCACGACTTAACAATTTAAGATTTTGACTTCTACCACCTTCACCAATCCTACTGGTTTCTTCTGCTGCGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.9% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL5516 Chironomidae sp. water mite diet isolate 5516-BHL032417-GBD22634_8402-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGATCAGCATTAGGACGACCCGGAACTTTCATTGGTGACGATCTAATTTATAACGTAATTGTTACAGCCAATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGTCATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTATCTTTACTTCGTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5518 Lebertia sp. water mite diet isolate 5518-BHL032417-GBD16237_17749-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAATGACCAAATTTACATTACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGGTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAAAAATATAAGAATTTGACTTCTTCCTCCATCCTTAACTCTACTTCTAACAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL552 Cricotopus sp. water mite diet isolate 552-BHL040517-GBD25506_8264-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGACTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAACATAAGATTTTGACTATTACCCCCTTCTTTAACCCTATTACTATCAAAATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5520 Oligochaeta sp. water mite diet isolate 5520-BHL032417-GBD3873_21041-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGATCTGGAATAATTGGAACATAAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCATAGGAAGAGATCAACTATATAATACTCTTGTAACTGCTCATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATATAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL553 Chironominae sp. water mite diet isolate 553-BHL040517-GBD12356_11314-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KT115418, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL554 Chironominae sp. water mite diet isolate 554-BHL040517-GBD22934_13191-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5540 Paratanytarsus sp. water mite diet isolate 5540-BHL032417-GBD5485_9619-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCAGGAACATTTATTGGAGATGACCAAATTTTTAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGAAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATAAAGCTTTTCCTCGAATAAATAATATAAGATTTTGGCTTCTTCCCCCCTCTTTAACTCTTTTACTTTAAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5544 Lebertia sp. water mite diet isolate 5544-BHL032417-GBD15479_17526-Ldc34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTAACTTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATATTAAATGGAGGTTTTGGAAACTGATTAGTTCCACTAAAAATCAGAGCCCCAAATATAGCTTTTCCACGAATAAATAATAAAAGATTTTGACTACTTCCTCCATCCTTAACCCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL555 Orthocladiinae sp. water mite diet isolate 555-BHL040517-GBD15608_23905-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTGATCGGAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGTCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5558 Chironomus riparius water mite diet isolate 5558-BHL032417-GBD19073_14303-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACCTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAAATAATATAAGTTTCCGACTTTTACCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL556 Orthocladiinae sp. water mite diet isolate 556-BHL040517-GBD20475_27120-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTGATCGGAGACGACCAAATTTATAATGTAATTGTTACGACACATGCTTTTGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTATCCTTGATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5561 Amphichaeta raptisae water mite diet isolate 5561-BHL032417-GBD13604_21897-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL5563 Lebertia sp. water mite diet isolate 5563-BHL032417-GBD4891_23609-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGGAACTGATTAGTTCTACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5564 Orthocladiinae sp. water mite diet isolate 5564-BHL032417-GBD8249_10100-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGGGCCTGATCTGGGATAGTTGGAACTTCTTTAAGAATTCTTATTCGTGCGGAATTAGGACATGCTGGTTTCTTAATTGGAGACGACCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGACTAGTTCCCTTAATATTAGGAGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCTTTAACTCTTCTTTTATCAAGCTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR693741, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5565 Chironominae sp. water mite diet isolate 5565-BHL032417-GBD9030_27312-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTACTTTATTTTTGGAGCTTGATCCGGAATAGTAGGAACATCTTTAAGAATACTAATTCGAGCAGAATTAGGACATCCAGGAACATTGATTGGGGATGATCAAATTTACAATGTAATTGTCACAGCTCATGCTTTTATTATAATTTTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGACTTTTACCTTTAATACTTGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCATCTATTTCATTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR759090, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5567 Psectrocladius sp. water mite diet isolate 5567-BHL032417-GBD10107_11917-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATAAAAGTTTTTGATTACTTCCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5568 Psectrocladius sp. water mite diet isolate 5568-BHL032417-GBD8352_15801-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCTGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTACTTGTTATCACTCACGCCTTTGTAATAATTTTTTTTTATAGTAATACCAGTTTTAATTGGAGGATTTGGAAATTGATTAGTCCCATTAATATTAGGAGCACCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL557 Paratanytarsus sp. water mite diet isolate 557-BHL040517-GBD21226_16078-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGTAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAAGATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5570 Psectrocladius sp. water mite diet isolate 5570-BHL032417-GBD8379_22810-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCACCTGATATAGCATTCCCTCGAATAAATAATATAATTTTTAGATTACTTCCCCCGTAATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5571 Chironominae sp. water mite diet isolate 5571-BHL032417-GBD7383_7829-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTAAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR641103, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5572 Chironominae sp. water mite diet isolate 5572-BHL032417-GBD25966_9122-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTAGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTATAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5574 Chironomus sp. water mite diet isolate 5574-BHL032417-GBD11625_23203-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATACTTCATTTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGATCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGCTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5575 Psectrocladius sp. water mite diet isolate 5575-BHL032417-GBD2731_12876-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTATGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGTCACCCTGGTTCCTTAATTGGTGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAATAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5576 Chironomidae sp. water mite diet isolate 5576-BHL032417-GBD20968_10679-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5578 Paratanytarsus sp. water mite diet isolate 5578-BHL032417-GBD16900_26547-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCCAAATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCATCTTTAACTCTTTTACGATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5579 Psectrocladius sp. water mite diet isolate 5579-BHL032417-GBD11719_28340-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTTTATTTTATTTTTGAAGTCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTCACGTTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATAATCTATCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL558 Paratanytarsus sp. water mite diet isolate 558-BHL040517-GBD13144_20224-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTTAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCATTTCCACGTATAAATAATATAAGATTTTGATTACTTCCCCCATCTTTAACCCTACTTCTATCAAGAAGAGTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5580 Chironomus sp. water mite diet isolate 5580-BHL032417-GBD14462_2542-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGAGCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCGGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTAGAATGTGATAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTAGGAAACTGACTTGTCCCCCTAAAACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTAGCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5581 Chironomidae sp. water mite diet isolate 5581-BHL032417-GBD18700_9628-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGAACATTATACTTCATTTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACATATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGATCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTACAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGCGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR165695, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5582 Lebertia sp. water mite diet isolate 5582-BHL032417-GBD16093_18789-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAAATAATTGGAGCTCGATTAAGAACCCTATTTCGACATTAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGTCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCCCCATCCTTATCCCTACTTCTATCAAGTTCCTTTCCAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5584 Chironominae sp. water mite diet isolate 5584-BHL032417-GBD25312_6972-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAATTTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5585 Lebertia sp. water mite diet isolate 5585-BHL032417-GBD23145_9340-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAGGAATCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAATGACCAAATTTACAATACAAATGTAACTGCTCATGCTTTCGTTATAATTTTTTTTCAAAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCCCGAAAAAATAAAATAAGATTTTGACTTCTTCCCCCATCCTTAACCCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5587 Chironomus sp. water mite diet isolate 5587-BHL032417-GBD16634_10201-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATGGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.4% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5588 Cricotopus sp. water mite diet isolate 5588-BHL032417-GBD24149_17256-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTTATAGTAATATCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5589 Psectrocladius sp. water mite diet isolate 5589-BHL032417-GBD28549_16034-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTAGAGCCTAATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCGGTTTCCTTAATTGGAGATGATCAAATTTATACTGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTATGAGCCAACGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL559 Paratanytarsus sp. water mite diet isolate 559-BHL040517-GBD22345_12947-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATTTTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5590 Chironomus sp. water mite diet isolate 5590-BHL032417-GBD16240_12219-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTACATTAGGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATTAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCTTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTTGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5591 Chironomus sp. water mite diet isolate 5591-BHL032417-GBD26780_21712-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGTAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTATAATTGGAGGATTTGGAAACTGACTTGTCCCCCCTAATACTTGGTGCACCTGACATAGCTTTTCCTCGAAAAAATAATATAAATTTCTGACTTTTAGCCCCCTCTCTTACTCTTCTTCATTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5592 Lebertia sp. water mite diet isolate 5592-BHL032417-GBD17937_26700-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCC-AGGAAGTGACTAAATTTACAATACAATTGGAACTGCTCATGCTTTCGTTATAAATTTTTTTCATAGTAATACCAATAATCATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAACTTTTCCACGAATAAATAAAATAAGATTTTGGCTTCTTCCCCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5593 Chironomidae sp. water mite diet isolate 5593-BHL032417-GBD23090_25164-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACATTATATTTTATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGATCAAATCTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTACTTCCACCGTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR171593, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5594 Lebertia sp. water mite diet isolate 5594-BHL032417-GBD27454_19197-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGTATAATAGGAGCTAGATTAAGAACCCTAATTCGACGTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTTACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCCTTTCCACGAATAAAAAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTAACAAGGTCCTTTACATGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5596 Chironominae sp. water mite diet isolate 5596-BHL032417-GBD6582_5746-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTT-GGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTCATTCGAGCAGAACTTGGACGACCTGGTACTTTTTTTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5599 Chironomidae sp. water mite diet isolate 5599-BHL032417-GBD22026_8720-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGTATTAGGACGGCCAGGAACTTTTATTGGAGATGATCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCACGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTTGTTCATTTGTAGGAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR165695, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL560 Paratanytarsus sp. water mite diet isolate 560-BHL040517-GBD15755_13848-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTCGGAGCTTGATCTGGAATAATAAGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTTATAGTTATACCTGTTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTTCCCCATCTTTAACCGTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.8% identical to accession ID KR758568, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5600 Chironomidae sp. water mite diet isolate 5600-BHL032417-GBD17398_10288-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATACTTCATCTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTTTATTGGAGATGATCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTTATAGTTATACCAATTTTAATTAGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCCCCATCTTTAACTCTGCTTCTTTCTTGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR287035, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5601 Orthocladiinae sp. water mite diet isolate 5601-BHL032417-GBD26567_22511-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGGGCCTGATCTGGGATAGTTGGAACTTCTTTAAGAATTCTTATTCGTGCAGAATTAGGACATGCTGGTTCCTTAATTGGAGACGACCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAACTGGAGGGTTTGGAAACTGACTAGTTCCCTTAATATTAGGAGCACCAGATATGGCTTTCCCGCGAATAAATAATATAAGTTATTGATTACTTCCCCCCGCTTTAACTCTGCTATTAACAAGCTCAATTGTTGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR693741, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5602 Orthocladiinae sp. water mite diet isolate 5602-BHL032417-GBD25127_19405-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGGGCCTGATCTGGGATAGTTGGAACTTCTTTAAGAATTCTTATTCGTGCAAAATTAGGACATGCTGGTTCCTTAATTGGAGACGAACAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGACTAGTTCCCTTAACATTAGGAGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR693741, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5604 Phaenopsectra sp. water mite diet isolate 5604-BHL032417-GBD24975_21172-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTCATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCTTTCTCTATCTTTACTACTTGCTAGCTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5605 Lebertia sp. water mite diet isolate 5605-BHL032417-GBD19426_21144-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGTTTTTGGAGCATGATCCGGAATAATTGGAGCTTGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAATGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTTGTTATAATTTTTTTGCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAAAAATCAGAGCCCCAGATATAGCTTTTCCACGAAAAAATAATAAAAGATTTTGACTTCTTCCTCCATCCTTAACCCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5606 Chironomidae sp. water mite diet isolate 5606-BHL032417-GBD8815_14185-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAATATACTTATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGATCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATATTTTTTTTTTATAGTTATACCAATTTTAAATGGGGGTTTCGGAAATTGATTAGTACCTTTAAAGTTAGGAGCCCCTGGCATAGCCTTCCCGCGAATAAATAATATAAGAATTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTTTCTAGTTCAATTGTAAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR287035, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5607 Lebertia sp. water mite diet isolate 5607-BHL032417-GBD25196_8173-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAGTTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGCAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCTACGAATAAATAATATAAGATTTTGACTTCTGCCGCCATCCTTAACTCGACTACTAGCAAGTTCCTTTACAGGAAAATAGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5609 Chironomus sp. water mite diet isolate 5609-BHL032417-GBD7183_17343-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGAGCTTGATCCGGCATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTCACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCCCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTACTATCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL561 Chironominae sp. water mite diet isolate 561-BHL040517-GBD11761_8112-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAACATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR689936, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5612 Dicrotendipes sp. water mite diet isolate 5612-BHL032417-GBD23148_5377-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGGGCCTGATCTGGGATAGCTGGAACTTCTTTAAGAATTCTTATTCATGCAGAATTAGGACATGCTGGTTCCTTAATTGGAGACGACCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID KR521898, identified in GenBank as Dicrotendipes modestus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5615 Homo sapiens water mite diet isolate 5615-BHL032417-GBD14396_22367-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACACATCATAAAGATATTGGCACATTATAGTATTCGGTGCTTGAGCCAGAGTAATAGGAACTGACATAAATCTCTTAATATGAGCCAAACTGGGTCAACCAGGAGCCCTATTAGGCAATGATCAAATTTATGTCATTATAACTGCCCATGCATTTGTAATAATCTTTTAATGGATATGCCAATTAAAATAAGAGGACTTGGTAACTGATTAGCTCCCTAAATGACTGAGCCGAGATACAGCATTCTCTTATAAACAATATAAGCTTCTGACTTTTTTCACCATCGTTTTGACTTCTGCTTGCCCCTTTACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID G_011402, identified in GenBank as Homo sapiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5616 Chironomidae sp. water mite diet isolate 5616-BHL032417-GBD8686_7271-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGTCTTCTTCCTCCATCCTTAACCCTTCTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5617 Chironomidae sp. water mite diet isolate 5617-BHL032417-GBD21377_21441-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATATTATTTTTGGTGTTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGAGATGATCAAATCTATAATGTAATTGTAACTGTACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTAGCTTTAATGTTAGGAGCCCCTGACATATCCTTCCCGCGAATAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR287035, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL562 Paratanytarsus sp. water mite diet isolate 562-BHL040517-GBD24908_18174-Ldc65 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATCGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5627 Culex pipiens water mite diet isolate 5627-BHL032417-GBD28405_9790-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTAATTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTAACGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATCATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGATACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL563 Psectrocladius sp. water mite diet isolate 563-BHL040517-GBD9366_15651-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTAAAATGTAATTGTTATCGCTCACGCCTTTGTAATAATTTTTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5633 Orthocladius sp. water mite diet isolate 5633-BHL032417-GBD20405_21889-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGACATGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTACTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5638 Lebertia sp. water mite diet isolate 5638-BHL032417-GBD19309_13527-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGTCTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCATTCCTAGGAAGTGATCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAAAAATCAGAGCCCCAGATATAGCTTTTCCACCAATAAATAATATAAGAATTTGACTTCTTCCTCCATCTTTAACACTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5639 Chironominae sp. water mite diet isolate 5639-BHL032417-GBD18181_6829-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTACTTTATTTTTGGAGCTTGATCCGGAATAGTAGGAACATCTTTAAGAATACTAATTCGAGCAGAATTAGGACATCCAGGAACATTGATTGGGGATGATCAAATTTACGATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGACTTTTACCTTTAATACTTGGAGCTCCTGATATAGCCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR759090, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5641 Lebertia sp. water mite diet isolate 5641-BHL032417-GBD28716_19910-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAATAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCCTTTCCACGAAAAAATAAAATAAGAATTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGGTACATTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5642 Lebertia sp. water mite diet isolate 5642-BHL032417-GBD25418_19304-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCGTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAATCTTAATTCGACTTGAATTAGGACAACCAGGCTCACTTCTAGGAAGAGACCAAATTTACAATACAATTGTAACTGCTCCTGCTTTCGTTATAATTCTTTTCATAGTAATACCAATAATAATTGGAGGTTTTAGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5643 Lebertia sp. water mite diet isolate 5643-BHL032417-GBD8437_7994-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTTCTTTTGGAGCATGATCCGGAATAATTGGAGCTTGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGATGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATATTTTTTTTCATAGTAATACCAATAATAATTGGTGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCCGATATAGCTTTTCCACTAATAAAAAATATAAGATTTTGACTTCTTCCCCCATCCTTAACTCTTCTTCTATCAAGTTCCTTTACAGGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5644 Chironomus sp. water mite diet isolate 5644-BHL032417-GBD9366_2993-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCCTGATCTGGGATAGTTGGAACTTCTTTAAGAATTCTTATTCGTGCAGAATTAGGACATGCTGGTTCCTTAATTGGAGACGACCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTACATAATTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCGTCTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5645 Chironomus sp. water mite diet isolate 5645-BHL032417-GBD11575_24951-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCATCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCATCTCTAACCCTACTTCTTTCTAGTGCATCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5646 Orthocladiinae sp. water mite diet isolate 5646-BHL032417-GBD28666_11594-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGGGCCTGATCTGGGATAGTTGGAACTTCTTTAAGAATTCTTATTCGTGCAGAATTAGGACATGCTGGTTCCTTAATGGGACACGAGCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGACTAGTTCCCTTAATATTAGGAGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCTCTTTAACTCTTCTTTTATCAAGCACAGTTGTTGAAAATGAAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR693741, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL565 Dicrotendipes sp. water mite diet isolate 565-BHL040517-GBD15697_12973-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTTTTATGGTTATACCTATTCCAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGGTATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5651 Psectrocladius sp. water mite diet isolate 5651-BHL032417-GBD11138_28499-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGTACTTCTTTAAGAATTTTAATTCGCGCAGAACTCGTTCAAGCTGTTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTGTATAGTAATACATATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAAGATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5656 Lebertia sp. water mite diet isolate 5656-BHL032417-GBD25771_13497-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATACTTAATCTTAGGAGTATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGAAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5658 Lebertia sp. water mite diet isolate 5658-BHL032417-GBD27436_19190-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTCGATTAAGAACCCTAATTCGACGTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAAATGGAGGTTTTGGAAAATGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCCATTCCACGAATAAATAATATAAGATTTTGACTTATTCCTCCATACTTAACTCTACTTCTAACAAGGTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL566 Diptera sp. water mite diet isolate 566-BHL040517-GBD25477_6898-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGTAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGTTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACACTATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.0% identical to accession ID KR262681, identified in GenBank as Toxonevra carterosoma. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5665 Hydrachnidiae sp. water mite diet isolate 5665-BHL032417-GBD25287_15236-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTTGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGATCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.5% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5666 Chironomus sp. water mite diet isolate 5666-BHL032417-GBD4763_21535-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCAGGGACTTTCATTGGAGATGACTAAATTTATAATGTTGTAGTTAATGTACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAGCTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAAAAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5669 Orthocladiinae sp. water mite diet isolate 5669-BHL032417-GBD4277_19616-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGGGCCTGATCTGGGATAGTTGGAACTTCTTTAAGAATTTTTATTCGTGCAGAATTAGGACATCCTGGTTCCTTAATTGGAGACGACCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAACTGACTAGTTCCCTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCCTCTTTAACTCTTCTTTTATCAAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR693741, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5670 Lebertia sp. water mite diet isolate 5670-BHL032417-GBD13224_15499-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGTTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAGTTGTAACTGCTCATGCTTTCGTTATAATTTTTTTTCATAGTAATACCAATAATAATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTA	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5672 Chironomus sp. water mite diet isolate 5672-BHL032417-GBD18858_27244-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCCCTTAGAATACTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTTGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATAGGGACTTCCCCCGAAAAAATAATATAAGTTTTTGACTTCTCACCCCATCTTTAAACTCTTCTACTTTCTTGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.6% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL568 Chironomidae sp. water mite diet isolate 568-BHL040517-GBD15089_17410-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTAGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5683 Lebertia sp. water mite diet isolate 5683-BHL032417-GBD28686_17221-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTTGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTTGGAAGTCACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAAATTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCCTTTCCACGAATAAATAATAAAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGATACTTTACAGGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5685 Lebertia sp. water mite diet isolate 5685-BHL032417-GBD29654_15692-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTCGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGATCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAAATTTTTTCATAGTAATACCAATAATAATTGGAAGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAAAAATATAAAATTTTGACTTCTTCCCCCATCCTTAACTCTACTCCTATCAAGGTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5686 Lebertia sp. water mite diet isolate 5686-BHL032417-GBD6698_4914-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAAGAATACCAATAATAAATGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAAAAAAGAAAATAAGATTTTGACTTCTTCCCCCATCCTTAACCCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5688 Chironomidae sp. water mite diet isolate 5688-BHL032417-GBD19822_26178-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGAACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGGCCAGGAACTTT-ATTGGAGATGATCAAATCTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAGATTGATTATTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID KR165695, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5689 Chironominae sp. water mite diet isolate 5689-BHL032417-GBD9494_26126-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATACTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTATTTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATGTGTTATTACCACTAATATTAGGAGAAACTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATAACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL569 Paratanytarsus sp. water mite diet isolate 569-BHL040517-GBD27472_13211-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCTCCCCTCTCTTTAACTCTTTTACATTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5690 Chironominae sp. water mite diet isolate 5690-BHL032417-GBD6184_10476-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGTACTTCCCTAAGTATATTTATTCGAGCAGAATTAGGACTGCCAGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCTGACATAGCCTTCCCGCGAAAAAATAATATAAGATTTTGGCTTCTTCCACCGTCTCTTACTCCTCTTCTTTCCAATTCAATTGTTGAAAATGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR641103, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5696 Lebertia sp. water mite diet isolate 5696-BHL032417-GBD7050_13045-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGTTTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5697 Orthocladiinae sp. water mite diet isolate 5697-BHL032417-GBD28280_15652-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTT-GGGGCCTGATCTGGGATCGTTGGAACTTCTTTAAGAATTCTTATTCGTGCAGAATTAGGACATGCTGGTTCCTTAACTGGAGACGACCAAATTTATAATGTAATTGTTACTGCACACGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGACTAGTTCCCTTAATATTAGGGGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTATTACCCCCATC	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR693741, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5699 Oligochaeta sp. water mite diet isolate 5699-BHL032417-GBD20381_21991-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACATGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGTACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCA--AGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL570 Psectrocladius sp. water mite diet isolate 570-BHL040517-GBD1866_13779-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATATTATTTTTGGAGCCTGATCAGGCATAGTAGGTACTGCTTTAAGAATTTTAATTCGAGCAAAACTCGGTCACGCCGATTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5702 Orthocladiinae sp. water mite diet isolate 5702-BHL032417-GBD5638_6931-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGGGCCTGATCTGGGATAGTTGGAACTTCTTTAAGAATTCTTATTCGTGCAGAATTAGGACATGCTGGTTCCTTAATTGGAGACGACCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGACTAGTTCCCTTAATATTAGGAGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR682563, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5703 Chironomus sp. water mite diet isolate 5703-BHL032417-GBD27821_17994-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACGGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5706 Chironomus sp. water mite diet isolate 5706-BHL032417-GBD18874_27256-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATAATAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAAATTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGATTTGTCCCTTTAATATTAGGAGCTCCAGATAAGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAAACTCTACTACTATCTTGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5708 Psectrocladius sp. water mite diet isolate 5708-BHL032417-GBD19937_25010-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATCTTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCCAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCATTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTAGCTATTATCTAGCACGCGCGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL571 Dicrotendipes sp. water mite diet isolate 571-BHL040517-GBD19850_7270-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGACTAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTGATAGGAGATGATCAAATCTACATTGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATGGTTATACCCATTCTAATTGGAGGTTTCGGAAATTGATTAGTCCCTATAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5715 Lebertia sp. water mite diet isolate 5715-BHL032417-GBD20882_26471-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTAGGAGCATGAGCCGAAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCACGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTATTCCTCCATCCTTAACACTGCTACTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5716 Lebertia sp. water mite diet isolate 5716-BHL032417-GBD26817_12434-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTAGGAGCATGATCCGGAATAATTGGAGCTGGATTAAGAACACTAATTCGAATTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGGTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTATTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGCTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5718 Lebertia sp. water mite diet isolate 5718-BHL032417-GBD26430_8834-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTTGAGCTAGATTAAGAACCCTAATTCGCCTTGTATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGGTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACGCTACTGCTATCAAGTGCCTTTACAGGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5719 Lebertia sp. water mite diet isolate 5719-BHL032417-GBD4567_13823-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTCGGACAACCAGGCTCATTCCTAGGAAGTGACCAAATTTACAATACAATTGTTACTGCTCATGCATTCGTTATAATTTTTTTCATAGTAATTCCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAAAAAATAAAATAAGATTTTGACTTCTTCCCCCATCCTTAACCCTACTTCTAACAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL572 Chironomus riparius water mite diet isolate 572-BHL040517-GBD23029_6003-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGATTGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTGGGAAACTGACTTGTCCCCCTAA-ACTTGGAGCACCTGACATAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5722 Culex pipiens water mite diet isolate 5722-BHL032417-GBD11487_16621-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGGTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCGGAATTAAGTCAACCAGGTGTATTTATTGGAAATGGTCAAATTTATAATGTTATTGTAACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTAATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTTGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5726 Orthocladiinae sp. water mite diet isolate 5726-BHL032417-GBD18702_18464-Ldc25 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGGGCCTGATCTGGGATAGTTGGAACTTCTTTAAGAATTCTTATTCGTGCAGAATTAGGACATGCTGGTTCCTTAATTGGAGACGACCAAATTTATAATGTAATTGTTACTGCTCACGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGGTTTGGAAACTGACTGGTTCCCTTAATATTAGGAGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACGTCCCCCCTCTTTAACACATCATTAAGCAAGCGCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR693741, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5729 Chironomus riparius water mite diet isolate 5729-BHL032417-GBD26401_18634-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTTACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTATCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL573 Chironominae sp. water mite diet isolate 573-BHL040517-GBD16338_7204-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTATTTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5731 Chironomidae sp. water mite diet isolate 5731-BHL032417-GBD23284_20359-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGAGTAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5732 Chironomidae sp. water mite diet isolate 5732-BHL032417-GBD1971_12886-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAAAACTCGGTCACGCTGGGTCTTTAATCGGAGACGATCACATTTATGATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGTGAGCCCCCGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCACCCGTCATTAACTTTATTATTATCTAGCTTTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5733 Chironomidae sp. water mite diet isolate 5733-BHL032417-GBD12942_3722-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATACTTCATTTTTGGGGCTTGATCAGGAATAGTAGGCACTTCCTTAAGTATACTTATTCGAGCAGAGTTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTAACCGCACATGCTTTTATTATAATTTTTTTTTATAGTTATACCGATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGGGCCCCTGATATAGCCTTCGCGCGAATAAATAATATAAGATTTTGACTTCTCCCACCATCTCTTTCTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KJ209337, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5734 Chironomus sp. water mite diet isolate 5734-BHL032417-GBD8180_9216-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATCGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCATGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAAGTTTCGAAAATTGACTTGTCCCTTTAATATTAGGAACTCCAGATATGGCCTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTCCCCCTATCTTTAACACTTCTTCTTTCTAATTCATTTCGAGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5735 Chironomidae sp. water mite diet isolate 5735-BHL032417-GBD15626_10675-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAAAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTGTTTTAATTAGAGTGTTTGGAAATTGATTAGTTCCTTTAATATTGAGAGCCCCTGATATAGCATTCCCTCGCATAAATAATATAATTTTTTTATTCCTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAACAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5736 Chironomus sp. water mite diet isolate 5736-BHL032417-GBD18005_13723-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGTTATTGGAACTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAACACGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAATTTGACTTGTCCCTTTAATATTAGGAGCTCCTGATATGGTCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCTATCTTTAACTCTTCTTCTTTTCTAATGCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5737 Rheotanytarsus sp. water mite diet isolate 5737-BHL032417-GBD15308_2433-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGTGCATGATCAGAAATAATTGGAACTTCTTTAAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGAGATGACCAAATTTATAATATAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGACTTTTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCTCGAATAAATAACATAAGTTTCTGATTACTTCCTCCCTCTCTTTCTCTTCTTCTTTCAAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR271819, identified in GenBank as Rheotanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5739 Chironomus sp. water mite diet isolate 5739-BHL032417-GBD23927_14308-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACT-TTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.1% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL574 Diptera sp. water mite diet isolate 574-BHL040517-GBD26504_12281-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTCATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATAACAATTATAAATGGTGGATTCGGGAAACTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGATTTTAACTTCTTCCACCATCACTTACACTATTATTAGTAAAAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.3% identical to accession ID EU493679, identified in GenBank as Scaptomyza frustulifera. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5740 Chironomus sp. water mite diet isolate 5740-BHL032417-GBD17073_19742-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCGTCATTAACT-TTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5741 Chironomus crassicaudatus water mite diet isolate 5741-BHL032417-GBD14797_4453-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATGTATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCCTTAGAATATTAATGCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAATTTTAGAATGTAGTAGTTACAGCGCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTAGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCTATCTTTAACTCTTCTTCTTTCTAATTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.8% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5743 Chironominae sp. water mite diet isolate 5743-BHL032417-GBD22751_7065-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTCATTTTTGGGGCTTGATCAGGAAAAGTAGGCACTTCCTTAAGTATACTTATTCGAGCAGAGTTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTAACCGCACATGCTTTTATTATAATTTTTTTTTTATAGTTATACCGATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGGGCCCCTGATATAGCCTTCCCGCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACT-TTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR751654, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5744 Chironomidae sp. water mite diet isolate 5744-BHL032417-GBD11782_19081-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAAAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5745 Chironomidae sp. water mite diet isolate 5745-BHL032417-GBD13081_28942-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTATGGAGCCTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGTCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5746 Chironomidae sp. water mite diet isolate 5746-BHL032417-GBD8983_8771-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGAGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATACCCCCGAAAAAAAAATATAAAAGTTTGAATACTTCCCCCCGTCAGTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5747 Chironomus crassicaudatus water mite diet isolate 5747-BHL032417-GBD9065_5191-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTTGGTGCTTGATCAGGAATAGTAGGAACGTCCCTTAGAATATTATTTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATATTTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGATTTCTCCCTCTATCTTTAACTCTTCTTCTTTCTAATTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.1% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5748 Chironominae sp. water mite diet isolate 5748-BHL032417-GBD12759_25166-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAACGTAATTGTCACAGCACGCGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5749 Paratanytarsus sp. water mite diet isolate 5749-BHL032417-GBD25725_24558-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTACTTCCCCCATCTTTAACTCGTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL575 Dicrotendipes sp. water mite diet isolate 575-BHL040517-GBD17135_9204-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCAGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGGTATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5750 Amphichaeta raptisae water mite diet isolate 5750-BHL032417-GBD23010_18246-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCAACCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCATATGCATTTTTTAATAATTTTTTTCTTAGTAACACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL5751 Cricotopus sp. water mite diet isolate 5751-BHL032417-GBD3910_8748-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTATAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATAATAGAAGACCCAGATATAGCATTCCCTCTAATAAATAACATAAGATTTTGATAATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGGAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5752 Chironomus sp. water mite diet isolate 5752-BHL032417-GBD24963_25261-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTTCCTCGAATAAATAATACAAGTTTCTGACTTTTACCCCCTTCTCTAACCTTTCTTCTTTCTAGTGCTATCGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5753 Chironomidae sp. water mite diet isolate 5753-BHL032417-GBD23620_16233-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTTATGCTGGTTCTTTCATCGGAGACGATCAAATTTATAATGTACTTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCGCACTAGTTGAAAATGGAGTTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5755 Chironomidae sp. water mite diet isolate 5755-BHL032417-GBD27881_14235-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAAATCGAGCAAAACTCGGTCACGCTGGTTCGTTACTCGGAGACGAACAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATATTTTTTTTTAGAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGAGAGCCCCTGATATAGCATTCCCTCGAATAAATATTATAAGTTTTTCATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5756 Chironomidae sp. water mite diet isolate 5756-BHL032417-GBD5406_20807-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5757 Chironomidae sp. water mite diet isolate 5757-BHL032417-GBD11314_6191-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATGATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTATTTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACT-TTATTATTATCTAGCTCTCTAGTTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5758 Chironomidae sp. water mite diet isolate 5758-BHL032417-GBD23734_20672-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTCTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTACGAATTTTAATTCGAGCAAAACTCGGTCACTCTGGTTCTTTTCTCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCCCGCTTTTGTAATAATTTTTTTGATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGTGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTGATTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5759 Chironomidae sp. water mite diet isolate 5759-BHL032417-GBD18510_12933-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATTACGTAATTGTTATAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGGTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL576 Chironomus riparius water mite diet isolate 576-BHL040517-GBD14596_25957-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACTTGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAGATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5760 Chironominae sp. water mite diet isolate 5760-BHL032417-GBD9731_22939-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAAGTATAGTAGGTACTTCCTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTATTATAATTTTTTTTATGGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5761 Chironomidae sp. water mite diet isolate 5761-BHL032417-GBD7164_26046-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTATGTACTTCTTTAAGTATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTATAATCTGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTGATATTGGGAGCCCCTGATAAAGCATTCCCTCGACAAAATAATATAAGTTTTTGATTACTTCTCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5762 Chironomidae sp. water mite diet isolate 5762-BHL032417-GBD11682_6214-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCTGGTATAGTAGGTACTTCTTTAAGAATTTTTATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATATTTTTTTTTAATAGTGATACCTATTTTATTTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGAAGCCCCTGATATAGCATTCCCTCGAAAAAAAAATAAAAGTTTTTGATAACTT-CCCCGTCATTAACTTTATTATTATCTAGCTCTATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5763 Chironomidae sp. water mite diet isolate 5763-BHL032417-GBD3763_13319-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATTGGAGAAGATCAAATTTATAATGTAATTGTTACCGCTCGTGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAAGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAAAAAAAAAAATTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCCAGCTCTCTAGTTGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5764 Chironomidae sp. water mite diet isolate 5764-BHL032417-GBD15776_23144-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCACTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATAGTGGGAGCCCCTGATATAGCATTCCCCCCAATAAAAAAAATAAGTTTTTTATTACTTCCCCCCGTCATTAACTTTATTATTATCTAGCTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5765 Chironomus sp. water mite diet isolate 5765-BHL032417-GBD16199_7254-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCAGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACT-TTATTATTATCTAACTCTCTAGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5766 Chironominae sp. water mite diet isolate 5766-BHL032417-GBD7632_17911-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGGACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATATTATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5767 Chironomidae sp. water mite diet isolate 5767-BHL032417-GBD10165_14844-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTGGGAGCTCCAGATATGGCCTTCCCTAGAATAAATAATATAAGTTTTTGACTTCTTCCCCTATCTTTAACTCTTCTTCTTTCTAATTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.7% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5769 Chironomidae sp. water mite diet isolate 5769-BHL032417-GBD8327_19715-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAATAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGTTCACGCTTTTGTAATATTTTTTTTTATAGTGATACCTGTTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATTAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5770 Lebertia sp. water mite diet isolate 5770-BHL032417-GBD18774_15078-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAATTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5771 Chironominae sp. water mite diet isolate 5771-BHL032417-GBD11228_5551-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTCGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTAATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGTAGCCCCTCATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTTCCACCATCTCTTACTTTATTGCTTTCAAGAAGAAGAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5772 Chironomidae sp. water mite diet isolate 5772-BHL032417-GBD21006_3392-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATCTTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGTAGAACTCGGTTACGCTGGTTCTTTAATCGGAGACCATCAATTTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATATTTTTTTTATAGTGATACCTATTTTAATTGGAGTCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGAGTTTGATTATTACCCCGCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5777 Chironomidae sp. water mite diet isolate 5777-BHL032417-GBD10324_16140-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGAGATACCTATTTTAATTTGGAGGGTTTGGAAATTGATTTGTTCCTTTAATATTGAGAGCCCCTAAGATAGCATTCCCTCGCATAAATAATATAAGTTTTTGATTCCTTCCCCCGTCATTAACTTTATTATTATCCAGATCTCTAGTTGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5778 Chironomidae sp. water mite diet isolate 5778-BHL032417-GBD8103_16399-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTTATAGGGATCCCTTATTTAATTGGAGGGTTTGAAACTTGATTAGTTCCTTTAAAATTGGGAGCCCCTGAAATAGCATTCCCTCGAAAAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTACCTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5779 Chironomidae sp. water mite diet isolate 5779-BHL032417-GBD7269_5061-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAAAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATTGTGATACCTATTTTAATTAGAGTGTTTGGAAATTGATTAGTTCATTTAATATTGAGAGCAACTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTGATGTTTATCTAGCTCTCTAGTTGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL578 Psectrocladius sp. water mite diet isolate 578-BHL040517-GBD19448_21990-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACACCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGCTGTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCTTCATTAACCTTACTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5785 Chironomidae sp. water mite diet isolate 5785-BHL032417-GBD9260_16922-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTATTTCATTAAGTATAGTTATTCGAGCAAAGTTAGGACGGCCAGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTAACCGCACATACTTTTATTATAATTTTTTTTTATAGTTATACCGATTTTAATTGGAGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGGGCCCCTGATATAGCCTTCCCGCGAACAAATAATATAAGATTTTGACTTCTCCCACCGTCTCTTTCTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KJ208847, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5786 Chironomidae sp. water mite diet isolate 5786-BHL032417-GBD21258_7929-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGATTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTTATAGTGATTCCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAACAATCCCTCGAATAAAAAAAAAAAGGTTTTGAATACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL579 Psectrocladius sp. water mite diet isolate 579-BHL040517-GBD6230_8912-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCCTGATCAGGCATGGTAGGCACTTCTTTAAGAATTATAATTCGAGCAAAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGTCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5795 Insecta sp. water mite diet isolate 5795-BHL032417-GBD18391_7312-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATATTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTACAATGTAATAGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCTTCTCTTACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.6% identical to accession ID MF410860, identified in GenBank as Pterygota sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5796 Chironomidae sp. water mite diet isolate 5796-BHL032417-GBD12190_2993-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTTCTCCCACCGTCTCTTTCTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID KR725429, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5797 Chironomus sp. water mite diet isolate 5797-BHL032417-GBD17645_7543-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTATTTTTGTAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATCTTAATTGGAGGATTCGGAAACTGACTTGTTCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCTTCTCTTACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL580 Psectrocladius sp. water mite diet isolate 580-BHL040517-GBD27517_12646-Ldc66 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCCCGAATAAAAAAAATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCCAGCTCCCTAGGTGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5800 Chironomidae sp. water mite diet isolate 5800-BHL032417-GBD11653_21953-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACCCTGGTTCTTTTATCGGAGAAGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGTTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5804 Diptera sp. water mite diet isolate 5804-BHL032417-GBD16450_20832-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATGAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGTTGATCAAATTTATAATGTATTTGTTACCCCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACT-TTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.3% identical to accession ID KJ522842, identified in GenBank as Anopheles sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5807 Chironomidae sp. water mite diet isolate 5807-BHL032417-GBD13583_23438-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTGTATTTTATTTTTGGAGCCTGATCAGGTAGAGTAGGTATTTCTTTAAGAATTTTAATTCGAGCAGATCTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAACTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAAAAATATAAGTTATTGATTACGTCCCCCGTCATTAACATTATTAATATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5809 Chironomidae sp. water mite diet isolate 5809-BHL032417-GBD11216_6646-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGTATAATAGGTACTTCTTTAAGAATTTTAATTCGAGAAGAACTCGGTCACGCTGATTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAACTTCCCCTCAAAAAAAAAAAATAATTTTTTAATTCCTCCCCCCGCCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL581 Podocopida sp. water mite diet isolate 581-BHL072216-GBD4187_16966-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGGCCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTATCCTTATTAACAATTGGAATACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5812 Culex pipiens water mite diet isolate 5812-BHL032417-GBD28549_15485-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGGTCAAATTTATAATGTTATTGTAACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAGATTAATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTTGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACTCTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5814 Chironomidae sp. water mite diet isolate 5814-BHL032417-GBD27938_19774-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAGTTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAAACTATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGAGAGCCCCTGATATAGCATACCCTCGAAAAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCGAGCTCTCGAGTTGAAAATGGAGCTGAAACAG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL582 Chironomus riparius water mite diet isolate 582-BHL072216-GBD14492_13602-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5826 Oligochaeta sp. water mite diet isolate 5826-BHL032417-GBD27042_10017-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACCCTATACTTAATTCTAGGAGTTTGAGCCGGAATAATTGGAACCGGAACTAGTATATTAATTCGGATTTAATTAGCTCAACCAGGATCATTCCTAGGAAGAGATCAGCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATGGCCTTCCCACGACTAAACAATTTAAGATTTTGACTTCTACCACCTTCACTAATCCTACTGGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.1% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL5828 Chironomidae sp. water mite diet isolate 5828-BHL032417-GBD7006_24032-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCAAGCTGGTTCTTTAATCGGAGAAGATCAAATTTATAATGTAATTGTTACCGCTCACGCCTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTATTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCGTCATTAACTTTATTATTATCTAGCAGAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5829 Psectrocladius sp. water mite diet isolate 5829-BHL032417-GBD27976_9624-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTCGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGGAGCCCTGAATAAAGAATCCCCTCGAAAAAAAAAAATAA-TTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR761745, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5832 Chironomidae sp. water mite diet isolate 5832-BHL032417-GBD14261_19314-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATGGGGAGCCCCTAATATACCA-CCCCAAAAAAAAAAAAAAAAATTTTTTGGATACCCCCCCCCGCCATTAACTTTATTATTATCTAACTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.1% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5836 Chironomidae sp. water mite diet isolate 5836-BHL032417-GBD20982_21476-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGATCAAAACTAGGTCACGCTGGTTATTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCACTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCAAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5838 Chironominae sp. water mite diet isolate 5838-BHL032417-GBD10265_14149-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAACGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATGGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATCATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL584 Paratanytarsus sp. water mite diet isolate 584-BHL072216-GBD16299_16393-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5843 Limnophyes sp. water mite diet isolate 5843-BHL032417-GBD28021_13843-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTCGGAAATTGATTAGTACCTTTAATGTTAGAGGCCCCTGATATAGCCTTCCCGCGAATAAATAATATAAGATTTTGACTTCTCCCACCGTCTCTTTCTCTTCTTCTTTCTAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR957636, identified in GenBank as Limnophyes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5844 Chironomidae sp. water mite diet isolate 5844-BHL032417-GBD10494_10328-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACATTATTTTTGGGGATTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCAAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCAAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.7% identical to accession ID JF288072, identified in GenBank as Synorthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5845 Chironomidae sp. water mite diet isolate 5845-BHL032417-GBD24065_9766-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGCCACACTGGTTCTTTAATCGGAGATGATCAAATTTAAAATGTTATTGTTACCGCTCACGCTTTTGTTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAACCCCTGATATAGCATTCCCCCGAATAAATAATAAAAGTTTTTGATTACTACCCTCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5846 Chironomidae sp. water mite diet isolate 5846-BHL032417-GBD26261_14811-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACGTCCCCCGACATTAACATAATAATAAGCTAGCGCTCGAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL585 Chironominae sp. water mite diet isolate 585-BHL072216-GBD19344_2501-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTAATGGAGATGACCAATTTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTCTGACATTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5859 Chironomidae sp. water mite diet isolate 5859-BHL032417-GBD16566_12456-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGAGCCTGATCAAGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTCTAATCGGAGATGACCAAATTTATAACGTAATTGTAACCGCACATGCTTTTATTGTAATTTTTTTTATAGTTATACCGATTTTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGCTAGGGGCCCCTGATATAGCCTTCCCGCGAATAAATAATATAAGATTTTGACTTCTCCCACCGTCTCTTTCTCTTCTTCTTTCTAGTTCCATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.7% identical to accession ID KJ208847, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5865 Chironomidae sp. water mite diet isolate 5865-BHL032417-GBD15231_26293-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGTCACGCTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTATTTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCCCGAATAAATAATATAAGTTTTTGATTACTTCCCCCATCATTAACTTTATTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL587 Podocopida sp. water mite diet isolate 587-BHL072216-GBD14016_3854-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAGTTTTTGGTGGTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGGCCCTGATTGGTAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATGGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTATCCTTATTAACACTTGAAATACTTCCAGAAAATGGCGCTGGATCAG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5875 Chironominae sp. water mite diet isolate 5875-BHL032417-GBD21271_20828-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAACGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTATGGTTATGCCAATTTTAATTGGAGGTTTTGAAAATTGACTTGTCCCTTTAATACTAGGAGCTTCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCTATCTTTAACTCTTCTTCTTTCTAATTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL588 Chironomus sp. water mite diet isolate 588-BHL072216-GBD8684_22515-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5880 Chironomidae sp. water mite diet isolate 5880-BHL032417-GBD18254_7869-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGAAGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTGCCTTTAATATTGGGAGCCCCAGATATAGCATTCCCACGAATAAATAATATAAGATTTTAATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5882 Chironomidae sp. water mite diet isolate 5882-BHL032417-GBD12354_17260-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCAGAATTAGGTCACCCTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATGGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCTTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5887 Chironomidae sp. water mite diet isolate 5887-BHL032417-GBD14815_13377-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTATTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAAGCGGAGCCGATCATATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCATGATATAGCATTCCCTCGAATAAAAAAAATAAGTTATTGATTACGTCCCCCGTCATTAACATTATTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5890 Chironominae sp. water mite diet isolate 5890-BHL032417-GBD21567_26289-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGAACTTTTATTGGTGATGACCAAATTTACAACGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATGGTTTTGCCAATTTTAATTGGAGGATTCGGAAACTAACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGAGTTTTACCCCCTTCTCTTACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KR287664, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5892 Chironomidae sp. water mite diet isolate 5892-BHL032417-GBD11572_9672-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGTATAATAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGCCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGACCCCCTGATAAAGCACCCCCACAAAAAAAAAATAAAATTTTTTAATCACCCCCCCCGCCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.2% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5896 Chironomidae sp. water mite diet isolate 5896-BHL032417-GBD24892_7243-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTAATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGTCAAGCTGGTTCTTTAATCGGAGAAGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL590 Chironominae sp. water mite diet isolate 590-BHL072216-GBD3742_16255-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACTTATTATTTGCTGTTTTAGCTGGTATTGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCATCCCCCTTTATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5904 Psectrocladius sp. water mite diet isolate 5904-BHL032417-GBD25225_22985-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTAAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGTAGGGTTGGGAAATTGATTAGTTCCTTTAATATTGGGAGGCCCTGATATAGCATTCCCTCGAATAAACAATATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTACAATTAGCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5905 Chironomus sp. water mite diet isolate 5905-BHL032417-GBD13437_12390-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATTTATTTTTTGGAGCCTGATCAGGTATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGCCCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTGTAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGATTAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5911 Chironomus sp. water mite diet isolate 5911-BHL032417-GBD4737_10559-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTACACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAAAATTAGGACTACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTTCCTCGAATAAATAATACAAGATTCTGACTTTTACCCCCTTCTCTTACTCTTCTTCTATCTAGATCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5912 Chironomidae sp. water mite diet isolate 5912-BHL032417-GBD5331_13995-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTGTATTTTATTTTTGGAGCCTGATACGGTATAGTATGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACACTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATGCCCTCGAAGAAAAAAAAAAAGTTATTGATTACGTCCCCCGTCATTAACTTTATTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5914 Chironomidae sp. water mite diet isolate 5914-BHL032417-GBD14015_6906-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAATTCGGTAACGCTGGTTATTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCGTCATTAACTTTATTATTATCTAGCTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5917 Chironomidae sp. water mite diet isolate 5917-BHL032417-GBD15547_22559-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGGACCCCTGGAAAAACCTTTCCCCCAAAAAAAAATAAAAATTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5919 Chironomus sp. water mite diet isolate 5919-BHL032417-GBD5827_11847-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTATATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGTAGAATTAGGACGACCAGGAACTTTCCTTGGAGATGACCAAATTTATAATGTAGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTAACTTGTCCCCTTAATACTTGGAGCACCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTTTTTCCCCCTTCTCTTACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5922 Chironominae sp. water mite diet isolate 5922-BHL032417-GBD23368_6309-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGGACTTCTTTAAGTATGCTAATTCGAGCAGACCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAACATAATTGGTACAGCACACGCGTTTATTATAATTTTTTTTATGGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAAAAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTAATTTCAAATTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5925 Chironomidae sp. water mite diet isolate 5925-BHL032417-GBD14057_6508-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTAATCAGGTATAGTCGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTCGATTACTTCCCCCGTCATTAACCTTATTATTATCAAGCACACTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5927 Chironomidae sp. water mite diet isolate 5927-BHL032417-GBD24915_17413-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTAGGACATGCTGGTTCTTTAATCGGAAATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATCATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTGCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCACACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL593 Podocopida sp. water mite diet isolate 593-BHL072216-GBD5522_7434-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGGTATGATAGGAACAGCCTTAAGAGTACTTATTCGAGCTGAGTTCGGGCAACCTGGGACACTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAACTGGAAGACTAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5934 Chironomidae sp. water mite diet isolate 5934-BHL032417-GBD6158_9644-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGTAGAATTCGGTCACGCTGGTTCTTTATTCGGAAACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACCTTATTATTATCTAGCGCACTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5936 Chironomidae sp. water mite diet isolate 5936-BHL032417-GBD14620_28684-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGTAGAACTCGGACAAGCTGGATCTTTCATCGGAGACGATCAACTTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCTCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5937 Psectrocladius sp. water mite diet isolate 5937-BHL032417-GBD26127_15286-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGCACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTAGAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAAAAATATAAGTAATTGATTACTACCCCCGTCATTAACATGAGAATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL595 Podocopida sp. water mite diet isolate 595-BHL072216-GBD24121_19679-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGGCCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAAACGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAAATAAAGCATTTCCCCGAAAAAATAAAATAAGATTTTGATTACTTCCCCCCATCCTTAACCTTATTAACAACTGGAACACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5970 Chironomidae sp. water mite diet isolate 5970-BHL032417-GBD25217_7115-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGCTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCACTCACGCTTTTGTAATAATTTTTTTTATAGTTATACCGATATTAATTGGGGGTTTCGGAAATTGATTAGTACCTTTAATGTTAGGGGCCCCTGATATAGCATTCCCTCGAGTAAATAATATAAGTTTTTGATTACTT-CCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5977 Chironomidae sp. water mite diet isolate 5977-BHL032417-GBD2520_11095-Ldc26 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATAAGAATTTTGGAGACTGATAAGGTATAGTAGGTACTTCATGAAGAATTTTAATTCGAGAAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTAGTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCCTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL598 Podocopida sp. water mite diet isolate 598-BHL072216-GBD18513_24306-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTTATTTTTGGTGCTTGATCTGCTATGCTAGGAACATCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGTCCCTGATTGGGAATGATCAAATTTATAACACAATTGTTACTGCCCATGCTTTTATTATAATTTTTTTTATGGTAATACCAATTATAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCCCCAGATATAGCGTTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCATTAACCTTATTAACAACTGGAACACTAACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5989 Amphichaeta raptisae water mite diet isolate 5989-BHL032417-GBD23876_20421-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAAAGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAAAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL599 Chironomidae sp. water mite diet isolate 599-BHL072216-GBD16016_18178-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGATCCGGAACTTTCATTGGTGACGAACAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTACCCCAGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5990 Lebertia sp. water mite diet isolate 5990-BHL032417-GBD24621_20919-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAACTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAGCTGATTAGTTCCACTAATAATAAGAGCCCCAGATATAGCATTTCCACGAATAAATAAAATAAGATTTTGACTTCTTCCTCCCTCCTTCCTTAACTCTACTTCTATCAAGATCCATTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5991 Chironomus sp. water mite diet isolate 5991-BHL032417-GBD8814_18215-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATGCTCATTCGAGGAGAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACCGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGATGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5993 Lebertia sp. water mite diet isolate 5993-BHL032417-GBD24082_24892-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAATTTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAATCTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL5995 Chironominae sp. water mite diet isolate 5995-BHL032417-GBD19444_7696-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGTATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGAAATAGCATTTCCTCGAATAAAAAATATAAGAGTCTGATTACTTACCCCTTCTTTATCCCTTCTACTTTCTAGTTCAATTGTAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL5997 Chironomidae sp. water mite diet isolate 5997-BHL032417-GBD21286_11917-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCTTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR647156, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL600 Chironominae sp. water mite diet isolate 600-BHL072216-GBD17876_8632-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTTTAATAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTCTCACAGCACACGCTGTTATTATAATTTTTTTTTATAGATATGCCAATTTTAAATGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTGTCCCTCGAATAAATAATATAAGTTTTAGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6000 Chironominae sp. water mite diet isolate 6000-BHL032417-GBD19092_6779-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATAGTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAAAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTATTATTATAATTTTTTTCATAGTTATACCCATTTTAAATTGGAGGATTTGGAAATTGATTGGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCACCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6001 Lebertia sp. water mite diet isolate 6001-BHL032417-GBD27000_18851-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACATCCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6003 Chironominae sp. water mite diet isolate 6003-BHL032417-GBD24768_15075-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTCTATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAACATAAGATTCTGATTACTTCCCCCTTCTTTAACCCTTCTTCTATCTAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6004 Chironominae sp. water mite diet isolate 6004-BHL032417-GBD16933_29051-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTCACGATCAAATTTATAATGTTATCGTAACAGCTCATGCTTTTATTATAATTTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTCGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCTCCCTTCTTTATCTCTACTTCTATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6005 Chironomidae sp. water mite diet isolate 6005-BHL032417-GBD7433_26097-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATGCTTATTCGAGGAGAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.8% identical to accession ID GU944724, identified in GenBank as Chironomus circumdatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6006 Chironominae sp. water mite diet isolate 6006-BHL032417-GBD4436_18842-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGAGTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6007 Chironominae sp. water mite diet isolate 6007-BHL032417-GBD17726_3832-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAAAATTCTAATTCGAGCAAAATTAGGACATCCTGGAACTTTTATTGGTGACGACCTAATTTATAATGTTATTGTAGCAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACCTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6008 Chironominae sp. water mite diet isolate 6008-BHL032417-GBD21376_22441-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTTATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACACTACTTCTTTCTAGTTCTATTGTAGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6009 Chironominae sp. water mite diet isolate 6009-BHL032417-GBD23879_5839-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGACTAGTTGGAACTTCTTTAAGAATTCTAATTAGAGCAGAATTAGGACATCCTGGAACTTTTAATGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTCTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAAAAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6010 Chironominae sp. water mite diet isolate 6010-BHL032417-GBD13101_22779-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCCGGAATAGTAGGAACTTCTTTAAGAATTCTAATTCGAGCGGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAACTTGACTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6011 Chironominae sp. water mite diet isolate 6011-BHL032417-GBD24253_6469-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGATTTCTAATTCGAGCAAAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAACTCATGCTTTTATTATAATTTTTTTACATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGGTATAGCATTTCCTCGAATAAAAAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6013 Chironominae sp. water mite diet isolate 6013-BHL032417-GBD23564_21753-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTTTTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTTATTGTTGACGACCAAATTTATAATGTTATTGTAACAGCTAATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTAGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATAAAAGATTCTGATTACTTCCCCCTTCTTTATCTCTACTTCTTTCTAGATCTATTGTAGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6014 Chironomidae sp. water mite diet isolate 6014-BHL032417-GBD27432_11390-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTCCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAGATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCATCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6015 Chironominae sp. water mite diet isolate 6015-BHL032417-GBD18120_8447-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGTTCAGGAATAGTTGGAACTTCTTTAAAAATTCTATTTCGAGCGGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAATACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6017 Chironominae sp. water mite diet isolate 6017-BHL032417-GBD21619_18619-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTTTATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAATAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCATTATCTCTACTTCTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6018 Chironominae sp. water mite diet isolate 6018-BHL032417-GBD15788_15520-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAATTTTTATTGGTGACGACCAAATTTATAACGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTTCATAGTTATACCCATTTTAATTAGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGGATAAATAATATAAGATTCTGATTACTTCCCCCTTTTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6019 Chironominae sp. water mite diet isolate 6019-BHL032417-GBD18847_23230-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGTACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGTACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACGGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTACGACTATCTAATTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6020 Chironomus sp. water mite diet isolate 6020-BHL032417-GBD19236_17843-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATCTAAAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTCATAATTATACCAGTTTTAAATGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6021 Chironomus sp. water mite diet isolate 6021-BHL032417-GBD22307_26783-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAAAATAGGACGACCCAGAACTTTCATTGGAGATGACCAATTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATATTTTTTTTCACAGTTATAACAGTTTTAAATGGAGATGTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTATAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6022 Chironominae sp. water mite diet isolate 6022-BHL032417-GBD24688_16292-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGTATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGACGACCACATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAGTAAATAATATAAGATTCTGACTACTTCCCCCTTCTTTATCTCTTCTACTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6023 Chironominae sp. water mite diet isolate 6023-BHL032417-GBD25755_16626-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCAATTTAATTGTAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATCCTGATTACTTCCCCCTTCTATAACTCTACTTCTTTCTAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6024 Chironomus sp. water mite diet isolate 6024-BHL032417-GBD18999_27666-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGGGCTTGATCCGGAATTCTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAGTTTTAAATGTAGGATTCGGAAACTGACTTTTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6025 Chironominae sp. water mite diet isolate 6025-BHL032417-GBD12429_23743-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTATTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTATTATATTAGGAACACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTATTTCCCCCTTCTTTATCTCTTCTTCTTTCTGGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6026 Chironominae sp. water mite diet isolate 6026-BHL032417-GBD15078_27145-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGATCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGTATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCACTGCTTCATTCTAGTTCTCTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6027 Chironominae sp. water mite diet isolate 6027-BHL032417-GBD23732_6702-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAAATTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCAACAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTGATCTCGTCGTCGGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6028 Paratanytarsus sp. water mite diet isolate 6028-BHL032417-GBD18982_22671-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTGTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6029 Chironominae sp. water mite diet isolate 6029-BHL032417-GBD17428_2569-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGGATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGTAACTTTAATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTTCTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGACCAG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6030 Chironominae sp. water mite diet isolate 6030-BHL032417-GBD27157_14012-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACACTTTATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTAATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCTGCTTTATCTCTTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6031 Chironominae sp. water mite diet isolate 6031-BHL032417-GBD6164_21474-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTATTGGAGCCTGATAAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCTTTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTACTTCTTTCTAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6032 Chironominae sp. water mite diet isolate 6032-BHL032417-GBD5500_16876-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGCTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATGGTATAAGTTTCTGACTTTTACCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6033 Chironominae sp. water mite diet isolate 6033-BHL032417-GBD25346_13336-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAAATGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCACGAATAAAAAAAATAAGATTCTGATCACTTCCCCCTTCATTAACTCTTCTTCTTTCCTAGTACTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6035 Chironominae sp. water mite diet isolate 6035-BHL032417-GBD19996_16049-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTCGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCGTTATCTCTTCTTCTAGCTAGTGCTATAGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6037 Chironominae sp. water mite diet isolate 6037-BHL032417-GBD18537_23459-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTGTATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTGGGACATCCTGGAACTTTTATTGGTGACGAACAAATTTATAATGTTATTGTAACAGCTCATGTTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTACTACTATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6038 Chironomus sp. water mite diet isolate 6038-BHL032417-GBD11896_13275-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCATTGAGAATGCTTATTCGAGCAGAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAAACTAACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGAATTTTACCCCCCACTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6040 Lebertia sp. water mite diet isolate 6040-BHL032417-GBD15729_20447-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGAATAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGGAAACTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAGGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6041 Chironominae sp. water mite diet isolate 6041-BHL032417-GBD14440_6000-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATGCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCGCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTCGTTCTATTGTAGAAAATGGCGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6042 Chironominae sp. water mite diet isolate 6042-BHL032417-GBD2124_13534-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAAAATTCGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGGTATACCCATTTTAATTGGAGGATTTGGAAATTGATTATTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCCTCTTTCTAGTCCCATTGTAGAAAAAGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6043 Chironominae sp. water mite diet isolate 6043-BHL032417-GBD23144_13579-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTTTATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGATCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTACTTTAACACATCATCAAGCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6044 Chironominae sp. water mite diet isolate 6044-BHL032417-GBD29168_12442-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGATATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTTCTCTTATATTAGGAGCACCAGATATAGCATTTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTACTTTATCTCTGCTACTTTCTAATACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6045 Hydrachnidiae sp. water mite diet isolate 6045-BHL032417-GBD13982_10107-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCTAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6046 Chironominae sp. water mite diet isolate 6046-BHL032417-GBD28963_13953-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAAGATAAGATTCTGATTACTTCCCCCGTCGTTAACTCTTCTTCTTTCGAGGTCGATTATAGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6048 Chironominae sp. water mite diet isolate 6048-BHL032417-GBD12113_21932-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTTATCAGGAATAGTTGGAACTTCTTTAAGAATTCTTATTCGAGCAGAATTAGGACATCCTGGAACTTCTATTGGTGACTACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAAATGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6050 Chironominae sp. water mite diet isolate 6050-BHL032417-GBD24509_20765-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGACTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATACAGCATTTCCTCGAATAAATAATTTAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTAGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6051 Lebertia sp. water mite diet isolate 6051-BHL032417-GBD20698_18107-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCCTGATCAGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAATTTTACAATACAATTGTAACTACTCATGCTTTCGTTATAATTTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGTCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6052 Chironominae sp. water mite diet isolate 6052-BHL032417-GBD15483_2843-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATGATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATGAGGACATCCTGTAACTTTTATTGGTTACGACCTAAATTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6054 Chironominae sp. water mite diet isolate 6054-BHL032417-GBD17974_9869-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACACTTTATCTTATTTTCGGAGCTCGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTCCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6056 Chironominae sp. water mite diet isolate 6056-BHL032417-GBD29448_17324-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAAAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGTTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAATTTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTTTCCTCGAATAAATAATATAAGATTCTGATGACTTCCCCCTTCTTTATCTCATCTGCTTTCTAGTTCTATTATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6057 Chironominae sp. water mite diet isolate 6057-BHL032417-GBD23577_8305-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTGATTCGATCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCTCTTCTTTAGCTCTTCTTGTTTCTAATTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6059 Chironomidae sp. water mite diet isolate 6059-BHL032417-GBD15626_8745-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCATTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTATATCTCTTCTTCTT-TCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6061 Chironominae sp. water mite diet isolate 6061-BHL032417-GBD18482_26938-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATATTTGGAACTTCTTTAAGTATTTTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGTACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCATCTTTGACTCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6063 Chironominae sp. water mite diet isolate 6063-BHL032417-GBD29047_17660-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCATGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGGTAAAGACCAAATTTATAATGTTATTGTAACAGCTCGTGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6064 Chironomus sp. water mite diet isolate 6064-BHL032417-GBD28021_13883-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGAGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTCTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAAAAAATAGTATAAGGTTCTGACTTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6065 Chironominae sp. water mite diet isolate 6065-BHL032417-GBD4094_12049-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGTAACCTTTATTGGTGACTACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATAGAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCCTTATCTCTTCTTCTTTTCTAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6066 Chironominae sp. water mite diet isolate 6066-BHL032417-GBD23303_8214-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGATTTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAAATTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGGGATTGATTTGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACATCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6067 Chironominae sp. water mite diet isolate 6067-BHL032417-GBD24145_9969-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGATTTCTAATTCGAGTAGAATTAGGACATCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATATTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCACGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACCCTTCTTCTTTCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6070 Chironominae sp. water mite diet isolate 6070-BHL032417-GBD3768_19162-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATAGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTACCACCTTCTTTAACTCTACTTCTTTCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6071 Chironominae sp. water mite diet isolate 6071-BHL032417-GBD6934_18842-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAAAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCCATTTTAATTGGAGGATTTTGGAAATTGATTAGTTCCTCTTATATTAAGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCCTCTTCTTTCTAGTTCCATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6072 Chironominae sp. water mite diet isolate 6072-BHL032417-GBD5175_17412-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGTATTCTAATTCGAGCTGAATTAGGTCATCCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAACATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6073 Chironominae sp. water mite diet isolate 6073-BHL032417-GBD29581_16808-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATAAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGTAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATGCCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACGGGAGGACTTGCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6074 Chironominae sp. water mite diet isolate 6074-BHL032417-GBD23906_23677-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAAATCTAACTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACATCCCCCTTCTTTATCGCTACTACTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6076 Chironominae sp. water mite diet isolate 6076-BHL032417-GBD2219_14264-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGTAGAATTAGGACATCCCGGAACTTTTATTGGTGACGACCAAATTTAAAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTACTCCTTTCTAGATCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6077 Chironominae sp. water mite diet isolate 6077-BHL032417-GBD27058_17760-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTGTATTTTATTTTTGGAGCCTTATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGTTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCATCTTCTTTCTAGTTCTTTTGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6079 Chironominae sp. water mite diet isolate 6079-BHL032417-GBD20056_4709-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACGTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGTACTTTTATTGGTGACGACCAAAATTATAATGTTATTGTGACAGCTCATACTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL608 Chironominae sp. water mite diet isolate 608-BHL072216-GBD22494_12710-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACATTATTTTTGGGGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGATAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCCTCGAATAAATAATACAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTATTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6080 Chironominae sp. water mite diet isolate 6080-BHL032417-GBD12451_23475-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTCGGACATCCTGGAACTTTTATTGGTGACGACGAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTTATATTAGGAGCACCAGATACAGCATTTCCTCGAATAAATAATATAAGAGTCTGATTACTTCCCGCTTCCTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6081 Chironominae sp. water mite diet isolate 6081-BHL032417-GBD24411_6870-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAACTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTCATTGGAAGATTTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCATCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTACGTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6082 Chironominae sp. water mite diet isolate 6082-BHL032417-GBD27142_18147-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGAAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTCACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGATTACTTCTCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6084 Chironomus sp. water mite diet isolate 6084-BHL032417-GBD2715_20264-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAAATGACCAACTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCTCTCTCTTACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6085 Chironominae sp. water mite diet isolate 6085-BHL032417-GBD3979_8285-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGTTTGATCAGGAATAGTTGGAATTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGCCATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTAGTGTAACAGCTCTTGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6086 Chironominae sp. water mite diet isolate 6086-BHL032417-GBD28852_15998-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATCCTGGAACCTTTATTGGTGACGAACAAATTTATAATGTTATTGTAACAACTCATGCTTTTATTATAAATTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTTGGAAATTGATTAGTTCCTCTGATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTACTTCTATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6089 Chironominae sp. water mite diet isolate 6089-BHL032417-GBD17976_25291-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTAAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGTACTTTTATTGGTGACGGCCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTTGGAAATTGATTAGTTCTTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAGTATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6090 Chironominae sp. water mite diet isolate 6090-BHL032417-GBD19518_26726-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGAAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGTACTTTTATTGGTAACGAACAAATTTATAATGTTATTGTAACAGCTCATGCTTCTATTATAATTTTTTTTCATAGGTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6091 Chironominae sp. water mite diet isolate 6091-BHL032417-GBD21887_16124-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCACGAATAAATAATATAAGATTCTGATTACTACCCCCATCTTTAACTCTTTTTCTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6092 Chironominae sp. water mite diet isolate 6092-BHL032417-GBD21383_16561-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTCCTAATTCTATTGTCGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6095 Chironominae sp. water mite diet isolate 6095-BHL032417-GBD10508_22708-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGTATTCTTATTCGGGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGAACAAATTTATGATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6096 Chironominae sp. water mite diet isolate 6096-BHL032417-GBD13517_25154-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACCTCCTGGATCTTTTATTGGTGACGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCAATTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCGCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6097 Chironominae sp. water mite diet isolate 6097-BHL032417-GBD9348_13193-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCCGGAATAGTGGGAACTTCTTTAAGAATGCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGAAGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATAATAGGAGCACCAGATATAGCATTTTCCTCGAATAAATAATATAAGATTCTGATTACTACCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6098 Chironominae sp. water mite diet isolate 6098-BHL032417-GBD25848_13258-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATATTTTTTTTCATAGTTATACCCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACGTCCCCCTTCTTTAGCACTACTTCTATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6100 Chironominae sp. water mite diet isolate 6100-BHL032417-GBD25243_5731-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGGATATTTGGAACTTCTTTAAGTATTCTAATTCGAGCAAAATTAGGACATCCTGGAATTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCCCGAATAAATAATATAAGATTCTGACTACTTCCCCCGTCTTTATCTCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6101 Chironominae sp. water mite diet isolate 6101-BHL032417-GBD19845_22766-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCCGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCAAAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCACGAATAAATAATATAAGATTCTGATTACTACCCCCATCTTTAACTCTACTACTTTCTAATTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6102 Phaenopsectra sp. water mite diet isolate 6102-BHL032417-GBD7348_15223-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGTGCCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATATTTACATCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6105 Chironominae sp. water mite diet isolate 6105-BHL032417-GBD7872_22335-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATACTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTTTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCATCTTATACTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAGCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6106 Chironominae sp. water mite diet isolate 6106-BHL032417-GBD21457_14570-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGATGGCCAAAATTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATGTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTCCTAGTTCTATTGCAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6107 Chironominae sp. water mite diet isolate 6107-BHL032417-GBD14575_16977-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTTGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACATCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAGTAATATAAGATTCTGATTACTTCCCCCCTTCTTTATCTCTTATTCCTTCTAATTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6110 Lebertia sp. water mite diet isolate 6110-BHL032417-GBD18691_18060-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCTTAATTCGACTTGAATTAGGACAACCAGACTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCTAGATATAGCTTTTCCACGAATAAATAATATAAGAATTTGACTTCCTACCCCATCCTTAACTCTACTTCTATCAAGATCCTGTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6112 Chironomus sp. water mite diet isolate 6112-BHL032417-GBD11148_23881-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGTATTGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTGGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAGACTGAATTGTCCCCCTTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6114 Chironominae sp. water mite diet isolate 6114-BHL032417-GBD18064_23985-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGAAGATCAAATTTATATTGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGAGTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6115 Chironominae sp. water mite diet isolate 6115-BHL032417-GBD8748_24358-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGATTTCTAATTCGAGCAGAATTAGGGCATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATCGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTGCTTTAGCTCTACTTCTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6117 Chironominae sp. water mite diet isolate 6117-BHL032417-GBD8512_8546-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAAATCTAATTCGAGCAGAATTAGGACATCCTGGAGCTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAACTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGACTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTCCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCCCTTCTTCTTTCTAGTTCTACTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6118 Chironomidae sp. water mite diet isolate 6118-BHL032417-GBD20663_27673-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTCTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTAACATTTATCAAGAGCAAGAGTAGAAAGTGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6119 Chironominae sp. water mite diet isolate 6119-BHL032417-GBD17609_14914-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6121 Chironominae sp. water mite diet isolate 6121-BHL032417-GBD7717_14393-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATCGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCATCAGATATAGCATTTCCTCGAATAAAAAAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTTTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6130 Chironominae sp. water mite diet isolate 6130-BHL032417-GBD13444_2748-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTTGAACTTTTATTGGTGACGACCAAACTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTACTCTTATATTAGGAGCACAAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTCCTATCGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6131 Chironominae sp. water mite diet isolate 6131-BHL032417-GBD18006_11375-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACCTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTATTTCGAGCAGAATTAGGACATCCTGTAACTTTTATTGGTGACGACGAAATTTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATGTGGAAATTGATTAGTTCCTCTTATATTAAGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6132 Chironominae sp. water mite diet isolate 6132-BHL032417-GBD14541_1862-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACTAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCATTAACACTACTACTATCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6135 Chironomus sp. water mite diet isolate 6135-BHL032417-GBD6570_10543-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAATAATGCTTATTTGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATATTGTAGTTACTGCACATGCCTTTATTATAAATTTTTTTCATAGTTATACCAGTTTTAATTTGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6136 Chironominae sp. water mite diet isolate 6136-BHL032417-GBD10291_12962-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGATCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAATTTTATAATGTTATTGTAACAACTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTTGGAAATTGATTAGGTCTTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6138 Orthocladius sp. water mite diet isolate 6138-BHL032417-GBD24119_18714-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAGTTAGGACATGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTCTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6139 Chironominae sp. water mite diet isolate 6139-BHL032417-GBD3647_20143-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGGGCCTGATCAGGAATAGTCGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACACCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTATCTAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6140 Chironominae sp. water mite diet isolate 6140-BHL032417-GBD15034_3156-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGGACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCACTTTAATTGGAGGATCTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTATTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6142 Chironominae sp. water mite diet isolate 6142-BHL032417-GBD12214_24620-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATACTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTAATGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCGTCATTATCTCTACTTCTATCTAGCTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6145 Chironominae sp. water mite diet isolate 6145-BHL032417-GBD5013_13823-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTTGGAGCCTGATCAGGATTAGTTGGAACTCCTTTAAGATTTCTATTTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAATTTTATAATGTTATTGTAACAGCTCATGCTTTTATTATATTTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCTTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCTCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6146 Chironominae sp. water mite diet isolate 6146-BHL032417-GBD6863_24471-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGTAACTTCTCTAAGAATCTTAATCCTAACGGAATTAGGTCATTCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCACCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6148 Chironominae sp. water mite diet isolate 6148-BHL032417-GBD22928_18442-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTTTATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAGCTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCAATTTTAATTGGAGGATTTGGAAATTGATAAGTTCATCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCTCTTCTTTATCTCTTCTTCTATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6149 Chironominae sp. water mite diet isolate 6149-BHL032417-GBD28767_17124-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTATTCTAATTCGAGCAGAATTAAGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTATTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATGATATAAGATTCTGATTACTTCCCCCTTCATTATCTCTTCTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6150 Chironominae sp. water mite diet isolate 6150-BHL032417-GBD23652_12510-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGTATTCTAATTCGTGCAGAATTAGGTCACCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCAATTTTAATTGGAGGATTTGGAGATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCCATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6152 Chironomidae sp. water mite diet isolate 6152-BHL032417-GBD17552_21124-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTCCTTTAATCGGAGACGAGCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCGTCATTAACTTTATTATTATCTAGCACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6153 Chironominae sp. water mite diet isolate 6153-BHL032417-GBD3585_19127-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATGCTTATTTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAACTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAACATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6154 Chironominae sp. water mite diet isolate 6154-BHL032417-GBD14642_26793-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGAAACTTCTTTAAGAATTCTAGTTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAATTATACCCATTTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCATCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTCCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6155 Chironominae sp. water mite diet isolate 6155-BHL032417-GBD22204_7274-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGATCTTTTATTGGTGACGAACAAATTTATAATGTTATTGTAACAGGTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTCCCTCGAATAAATAATATAAGGTTCTGATTACTTCCCCCGTCATTATCTCTACTACTATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6157 Chironominae sp. water mite diet isolate 6157-BHL032417-GBD20493_5487-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAGCTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCACTTCCTCGAATAAATAATATAAGATTCTAACTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6159 Chironomidae sp. water mite diet isolate 6159-BHL032417-GBD7120_17285-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAATAATTCTAATTCGAGCAGAATTAGGACATGCGTGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGTTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL616 Podocopida sp. water mite diet isolate 616-BHL072216-GBD29362_17948-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGAGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTACTTATTCGAGCTGATCTCGGACAAACTGGGTCCCTGATTGGGAATGATCAAATTTATAACACAATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTATCCTTATTAAAAAGTGGAAGACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6161 Chironominae sp. water mite diet isolate 6161-BHL032417-GBD9933_18272-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTTGGTACTTCTTTAAGTATTCTAATTCGAGCAGAATTTGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCATCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGTTTACTTCCCCCTTCTTTAACTCTTCCTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6164 Chironominae sp. water mite diet isolate 6164-BHL032417-GBD23359_10922-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGACATCCTGGAACTTTCATTGGTGACGTCCAAATTTATAATTTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTGATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTATTTCCCCCTTCTTTATCTCTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6166 Culex pipiens water mite diet isolate 6166-BHL032417-GBD8054_15386-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAAGGTTATTGTAACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTAAATGTTAGGAGCTCCTGATATGGCCTTTCCTCGAATAAATAATATAAGTTCTTGAATACTATCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6167 Chironominae sp. water mite diet isolate 6167-BHL032417-GBD15050_7985-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCGGGAATAATTGGCACTTCCTTAAGTATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCATTAACCCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6168 Chironominae sp. water mite diet isolate 6168-BHL032417-GBD13410_13434-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTAAATTGGAGGATTTGGAAATTGATCAGTTCCTCTTATATTAGGAGCACTAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGAATACTTCCCCCTTCTCTATCTCTTCTTCTTTCTAGTTCCATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6172 Chironominae sp. water mite diet isolate 6172-BHL032417-GBD24754_21721-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTAATCAGGAATAGTTGAAACTTCTTTAAGAATTCTAATTCGAGCAAAATTAGGACATCCTGGAACTTTAATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTATTAGGAGGATTTGGAAATTGATTAGTTCATCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6176 Chironominae sp. water mite diet isolate 6176-BHL032417-GBD17418_13717-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCAAGCAGAATTAGGACACCCTGGAACTTTTATAGGTGACGTCCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCAGATTACTTCCCCCTTCTTTATCTCTTCTTCATTCTAGTTCTATTATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6177 Chironominae sp. water mite diet isolate 6177-BHL032417-GBD22271_25957-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGAAATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCCTGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTAGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCATCTACATAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6179 Chironominae sp. water mite diet isolate 6179-BHL032417-GBD20283_9924-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACACTTTATTTTATTTTCGGAGCTTGAACAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAAAATTAGGACATGCAGGCTCGTTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL618 Podocopida sp. water mite diet isolate 618-BHL072216-GBD25362_24573-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTGTACCTAATTTTTGGGGCTTGATCTGCTATGCTAGGAGCAGCCTTAAGAGTAATTATTCGAGCTGATCTCGGGCAACCGGGGGCCATGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGACACCAGATATAGCGTTTCCTCGAATAAATAATAAAAGATTTTGATTACTTCCCCCATCCTTATCCTTATTAACAACTGGAACACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6182 Chironominae sp. water mite diet isolate 6182-BHL032417-GBD25719_6468-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTATTTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGCATAAATAATATAAGATTCTGATTACTTCCCCATGCTTTATAACTACTTCTTTCTAATTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6183 Chironominae sp. water mite diet isolate 6183-BHL032417-GBD15129_25726-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTTGGAGCCTGCTCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACATTTATTGGTGACGACCAAATTTATAATGTTATCGTAACAGCTCATGCTTTTATTATAATTTTTTCCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCATCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTAATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6186 Chironominae sp. water mite diet isolate 6186-BHL032417-GBD23889_15090-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATATTAATTGGAGGATTTGGAAATTAATTAGTTCCTCTTATATTAGGAGCACCAGATATAACATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTACTACTTTCTAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6188 Chironominae sp. water mite diet isolate 6188-BHL032417-GBD7583_26429-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACCTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTTGGAACTTCTTTAAGACTTCTACTTCGAGCAGCATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6189 Chironomidae sp. water mite diet isolate 6189-BHL032417-GBD26571_18320-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATTCAGGCTCATTAATGGGAGACGATCAAATTTATAATGTAATTGTTACGACTCATGCTTTTGTAATAATTTTTTTTTTTAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAAAAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL619 Podocopida sp. water mite diet isolate 619-BHL072216-GBD19547_4183-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACATCCTTAAGAGTAATTATTCGAGCTGAGTTCGGTCAACCTGGGTCCTTGATTGGGAATGATCAAATTTATAACACAATTGTTACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTATAATGGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCATTAACCTTATTAACAACTGAAACACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6190 Chironominae sp. water mite diet isolate 6190-BHL032417-GBD24487_7443-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATACTTTTATTATAATTTTTTTCATAATTATACCCAATTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTATGAGAACCAGATATAGCATTTCCTCGAATAAAAAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6197 Chironominae sp. water mite diet isolate 6197-BHL032417-GBD23438_14450-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATTTTTTATTTTTGGAGCCTGATCAGGAATAATTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAACTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTTGGAAATTGATTAGATCCTCTTATATTATAAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6198 Chironomidae sp. water mite diet isolate 6198-BHL032417-GBD15009_4423-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTTGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTAACAGCTCATGCCTTCGTTATAATTTTTTTCATAGTAATACCGATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTAATTCTATCAAGTTCCTTTACCGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.1% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6199 Chironominae sp. water mite diet isolate 6199-BHL032417-GBD14451_3028-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCGTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAATTTGATTAGTTCCTTTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAACAATATAAGATTCTGATTACTTCCCCCTTCATTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6200 Lebertia sp. water mite diet isolate 6200-BHL032417-GBD19892_25372-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGTATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTTCACTAATAATCAGAGCCCCAGATATAGCCTTTCCACGAAAAAATAATATAAGATTTTGACTTCTTCCCCCATCCTTAACCCTACTTCTAACAAGTCCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6202 Chironomidae sp. water mite diet isolate 6202-BHL032417-GBD3246_9737-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCATTAAGAATTTTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTGCCACGAATAAATAAAATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.8% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6204 Chironomus sp. water mite diet isolate 6204-BHL032417-GBD7661_25131-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACCTCATTGAGAATGCTTATTCGAGCAGGAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATATCAGTTTTAAATGTAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACAATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTATTACCCCCCTCTCTTACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL621 Chironominae sp. water mite diet isolate 621-BHL072216-GBD25696_10829-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTAGATACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTCATTATAATTTTTTTTTATAGTTATGCCAATTTTATTTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTACTTTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6212 Chironominae sp. water mite diet isolate 6212-BHL032417-GBD3263_20195-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGACTTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTGATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTGCTTCCCCCTTCTTTATCTCTACTACTTTCTAGTTCTTTTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6213 Chironominae sp. water mite diet isolate 6213-BHL032417-GBD28829_18967-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTTGGTGCCTGCTCAGGATTAGTTGGAACTTCTTTAAGATTTCTAATTCGATCTGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTACTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6214 Drosophila sp. water mite diet isolate 6214-BHL032417-GBD21248_4014-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTCGAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.6% identical to accession ID AY750090, identified in GenBank as Drosophila lacertosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6215 Chironominae sp. water mite diet isolate 6215-BHL032417-GBD24450_20542-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAAAATTAGGACATGCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTAATGTAACAGATCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6216 Chironomidae sp. water mite diet isolate 6216-BHL032417-GBD26022_8718-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGAAGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATGATCTAACTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6218 Chironominae sp. water mite diet isolate 6218-BHL032417-GBD10241_10031-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATCTTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAAATTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTATTTGGAGGATTTGGAAATTGATTAGTTCCTCTAATTTTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL622 Podocopida sp. water mite diet isolate 622-BHL072216-GBD5381_19337-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTTATTTTTGGTGCTTGATCTGCTATGCTAGGAACATCCTTAAGAGTAATTATTCGAGCTAAGCTCGGGCAACCTGGGGCCCTTATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTTATGGTAATACCAATTATAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATAATAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGAATTCTTCCCCCATCCTTAACCTTATTAACAACTGGAATACTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6220 Chironominae sp. water mite diet isolate 6220-BHL032417-GBD18049_11381-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACATTTTATTTTATTTTTGGAGTCTGATCAGGAATAGTTGGCACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACCTTTATTGGTGATGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCTTCTTTATCTCTTCTTCTATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6223 Chironominae sp. water mite diet isolate 6223-BHL032417-GBD27166_17436-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATCGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATTTAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCCTCTTCTTGCTAATTCTATTGTAGAAAATGGAGCTGAAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6224 Chironominae sp. water mite diet isolate 6224-BHL032417-GBD21433_27559-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATAGTTTATTTTTTGGAGCTTGATCAGGAATAGTTGGCACTTATTTAATAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACTACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTTTTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6226 Chironominae sp. water mite diet isolate 6226-BHL032417-GBD14243_4760-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAAGTAGGACATCCTTTAACTTTTATTGGGTACGTCCAAATTTATAATGTTATTGTAACATCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACAAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6227 Chironomus sp. water mite diet isolate 6227-BHL032417-GBD27109_15681-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTAATTGGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTAACTGCACATGCTTTTATTATATTTTTTTTCATAGTTATACCAATTTTAGTTGGAGGACTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCTTCTCTTACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6228 Chironominae sp. water mite diet isolate 6228-BHL032417-GBD14174_23016-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGAACAAGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATAGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAACAAATAATATAAGATGCTGATTACTACCCCCTTCTCTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6230 Chironomus sp. water mite diet isolate 6230-BHL032417-GBD5019_17247-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATGCTTATTCGAGCAAAATTATGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATGGCTTTTCCTCGAATAAATAGTATAAGATTCTGACTTTTATCCCCCTCTCTTACTCTACTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6231 Chironominae sp. water mite diet isolate 6231-BHL032417-GBD18257_26818-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAAGTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGATGACAAAATTTATAATGTTATTGTAACAACTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGGGGATTTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTTCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6235 Chironominae sp. water mite diet isolate 6235-BHL032417-GBD17671_4084-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAGTAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCACATGCTTTTATTATAATTTTTTTCACAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTTAGATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATAAAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6241 Chironominae sp. water mite diet isolate 6241-BHL032417-GBD15361_5849-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAAAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGAAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTCGAAACTG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6242 Chironominae sp. water mite diet isolate 6242-BHL032417-GBD26807_9684-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTTGGTGACGTCTAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTATTATATTAGTAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCGTCTTCGTTCTAGTTCTATTGTAGAAAATGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6243 Chironominae sp. water mite diet isolate 6243-BHL032417-GBD14531_17560-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTAAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAACACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTGCTGCCCCCTTCTTTAACTCTACTCCTATCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6246 Chironomidae sp. water mite diet isolate 6246-BHL032417-GBD6579_23459-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTATTTTTTGAAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGCATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCATTTTTAAATGGAGGATTCGGAAACTGACTTGTCCTCCTAATACTGGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCCGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6248 Chironominae sp. water mite diet isolate 6248-BHL032417-GBD25491_18981-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAAGAGTGTATTTTATTTTTGGAGTCTGATCAGGAATAGTTGGAACTTCTTTTAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAATAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGAATCTGATTACTTCCCCCTTCTTTATATCGTCTTCTTTCTAGTTCTATTGTAGAAAATCGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL625 Chironominae sp. water mite diet isolate 625-BHL072216-GBD22395_6774-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTTGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGCTACTGCACATGCTTTTTTTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACCTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCCTCGAATAAATAATACAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6251 Chironominae sp. water mite diet isolate 6251-BHL032417-GBD28814_14556-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTTGGAGCCTGATCAGGCATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGACTTAGGACATCCTGGAACTTTTATTGGTGACGTCCAACTTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCATCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6253 Chironominae sp. water mite diet isolate 6253-BHL032417-GBD26595_12174-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACCTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTACACCCATTTAAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTATATCTCTTCGTCTTTCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6255 Chironominae sp. water mite diet isolate 6255-BHL032417-GBD14075_23617-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTATTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCACATTCTTTAACTCTACCACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6259 Chironominae sp. water mite diet isolate 6259-BHL032417-GBD21296_10015-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGGACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGTAGAATTAGGACATCCTGGCTCTTTTATTGGTGACGACCATATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCCCTTCTTCTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL626 Chironominae sp. water mite diet isolate 626-BHL072216-GBD4411_15847-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGCTATAGTAGATACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGTGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTCATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCTCCCTTCATTAACTCTTTTACTTTCAAATTCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6261 Chironominae sp. water mite diet isolate 6261-BHL032417-GBD11018_15063-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTATTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGAATTGGAAATTGATTAGTTCCTCTTATATTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAATTCTCTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6262 Chironominae sp. water mite diet isolate 6262-BHL032417-GBD26163_13792-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTTGGAGCCTGATCGGGATTAGTTGGAACTTCTTTAGGATTTCTATTTCGAGCAGATTTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6264 Chironominae sp. water mite diet isolate 6264-BHL032417-GBD3451_13504-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCGGGAATAGTTTGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGAACAAAATTATAATGTTATTGTAACAGATCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATACTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAATTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6267 Chironominae sp. water mite diet isolate 6267-BHL032417-GBD17488_27803-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTTATATTAGGAGCACCAGATATAGCATTCCCCCCAATAAATAATCTTAGATTCTGAATACTTCCCCCTTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6268 Chironomus sp. water mite diet isolate 6268-BHL032417-GBD18858_11680-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTTATTGAGAATGCTTATTCGACCAGAAATAGGACGACCCGGAATTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTATCATAGTTATACCAGTTTTAAATGGAGAATTCGGAAACTGACTTGTCCCCCTAATACTTGGAACACTTGACATGGCTTTTCCTCGAATAAATAGTATAAATTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6270 Chironomus sp. water mite diet isolate 6270-BHL032417-GBD18058_28507-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGTTCCGGATTTGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGATATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCGTTCTAGTTCTATTGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6272 Chironominae sp. water mite diet isolate 6272-BHL032417-GBD24353_25449-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGATCTTTATATTTTATTTTCGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGTATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTTATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACCCTTCTTCTATCAAGAACATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6274 Chironominae sp. water mite diet isolate 6274-BHL032417-GBD8735_24103-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATACTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGACGATTTGGAAATTGATAAGTTCCTCTTATATTATGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCACTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6279 Chironominae sp. water mite diet isolate 6279-BHL032417-GBD6442_20935-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTCTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTACTTCCTATAATATTAGGAGCTCCAGATATAGCATTTCCTCGAATAAATAACATAAGATTCTGATTACTTCCCCCTTCTTTAACCCTTCTTCTATCTAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6287 Neoptera sp. water mite diet isolate 6287-BHL032417-GBD3351_10388-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTTCATTATATTTTATTTTTGGAGCTTGTTCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTGCTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGGTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID MF458986, identified in GenBank as Patrobus longicornis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6288 Chironominae sp. water mite diet isolate 6288-BHL032417-GBD25136_12935-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCACGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTAACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTAATATAATTTTTTTCATAATTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTTCCCCGTCTTTATCTCATCTTCTTTCTAGTTCTATGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6289 Chironominae sp. water mite diet isolate 6289-BHL032417-GBD19534_24380-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTAATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATACTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCCGATTACTTCCCCCTTCTTTATCCCTACTACCATCTAGTACTATTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6290 Chironominae sp. water mite diet isolate 6290-BHL032417-GBD9956_26262-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCATGTATAGTTGGTACTTCTTTAAGTATTCTAATTCGAGCAGAATTAGGACATCCTGGTACTTTTATTGGTAATGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTACTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6291 Chironominae sp. water mite diet isolate 6291-BHL032417-GBD25663_16655-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGTCCAAATTTATAAGGTTATTGTAACAGCTCATGCTTTTCTTATAATTTTTTTCATAGTTATACCCATTTTAATAGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6297 Cricotopus sp. water mite diet isolate 6297-BHL032417-GBD28164_18373-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGAAGCATGATCAGGAATAGTAGGAACATCTCTAAGAATTTTAATCCGGGCCGAATTAGGACATGCCGGATCATTAATTGGTGACGATCAAATTTACAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAACTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGTTCCTGATGTAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCTCTTACATTACTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG448919, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6305 Lebertia sp. water mite diet isolate 6305-BHL032417-GBD24821_14215-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTAACAAGATCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.1% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6309 Chironominae sp. water mite diet isolate 6309-BHL032417-GBD2424_18882-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTTGGAGCCTGATCAGGAATAGTTGGAAATTCTTTAAGAATTTTATTTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAATTTTATACTGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTATCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL631 Podocopida sp. water mite diet isolate 631-BHL072216-GBD26632_17339-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGTCTTAAGAGTATTTATTCGAGCTGAGCTCGGGTAACCTGGGGCACTGTTTGGGAATGATCAAATTTATAAAACAATTGTGACTGCCCATGTATTTATTATAATTTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGACACCAGATATAGCGCTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTATCCTGATTAACAAGTGGAATACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6310 Chironominae sp. water mite diet isolate 6310-BHL032417-GBD27413_16939-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGCTCAGGAATAGTTGCAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCTTGTAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAAGATAAGATTCTGATTACTTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6312 Chironominae sp. water mite diet isolate 6312-BHL032417-GBD12786_13610-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACATTTATTGGTGACGAACAAATTTATAATATTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACCCTTCTACTTTCTAATGCTGTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6315 Chironominae sp. water mite diet isolate 6315-BHL032417-GBD20551_27638-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTTGGAGCCTGATCAGGATTAGTTGGAACTTTTTTTAAGAATTCTATTTCGCGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACATCCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTT-AATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6323 Chironominae sp. water mite diet isolate 6323-BHL032417-GBD13406_12024-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCCAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACACGGCTGCGCTCCAGTTCGATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL633 Podocopida sp. water mite diet isolate 633-BHL072216-GBD20053_17290-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTCATTTTTGGTGCTTGATCTGCTATGCTAGGAACTGCCTTAAGTGTAATTATTCGAGCTGAGCTCGGACAACCTGGGACCCTGATTGGTAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTATGGTAATACCAATTTTAATCGGAGGGTTTGGAAATTGATTAGTTCCTTTAATACTAGGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCATCCTTAACCTTATTAACAACTGGAATACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6332 Chironominae sp. water mite diet isolate 6332-BHL032417-GBD5965_23092-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTATGACATCCTGGATCTTTTATTGGTGACGAACAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTATAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCATTATCCCTTCTTCTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6340 Chironominae sp. water mite diet isolate 6340-BHL032417-GBD9330_6807-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACATTATATTTTATTTTTGGAGCCTGATCAGGATTAGTTGTTACTTCTTTAAGAATTCTAATTCGAGCAGCTTTAGGCCATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTGCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6343 Chironominae sp. water mite diet isolate 6343-BHL032417-GBD17284_13414-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACACCCTGGAACTTTTATTGGTGACGAACAAATTTATAATGTTATTGTAACCGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCGTCTTTAACTCTTCTTCTATCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6344 Chironominae sp. water mite diet isolate 6344-BHL032417-GBD15882_4408-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTTGGAGCATGAGCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATGCGAGCAGAATTAGGACATCCGTGAACTTTTATTGGTGACGTCCAAATTTAAAATGTTAATGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6350 Chironominae sp. water mite diet isolate 6350-BHL032417-GBD26574_11550-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGCACTTCTTTAAGAATTCTAATTCGAGTAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTTATATTAGGGGCACCAGATATAGCATTTCCGCGAATAAATAATATAAGATTCTAATTACTACCCCCTTCATTATCCCTACTTCTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6356 Chironominae sp. water mite diet isolate 6356-BHL032417-GBD28608_18085-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTTGGCGCCTGATCAGGAATAGTTGGAACTTCTTTAAGATTTCTAATTCGAGCAGACTTAAGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATGACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6358 Chironomus sp. water mite diet isolate 6358-BHL032417-GBD9200_9707-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGTTCCGGAATTGTGGGAACTTCATTGAGAATGCTTATTCGAGCATAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6366 Chironominae sp. water mite diet isolate 6366-BHL032417-GBD15215_15588-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGATCAAAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCTGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCACCTTCTTTATCTCTACTTCTTTCTAGTACTAAAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6370 Chironominae sp. water mite diet isolate 6370-BHL032417-GBD11839_2994-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGAGACGACCAACTTTATAATGTTCTTGTTACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCCTTTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACCCTTCTTCTTTCTAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6374 Chironominae sp. water mite diet isolate 6374-BHL032417-GBD17276_27099-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCCATAGTTATATCCATATTAATTGGAGGATTTGGAAATCGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCGTTATCCCTACTACTTTCTAATTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6377 Chironomidae sp. water mite diet isolate 6377-BHL032417-GBD22619_25146-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGATTGAGGTCATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGATCCTCTTATATTAGGAGCACCAGAAATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR647156, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6385 Chironominae sp. water mite diet isolate 6385-BHL032417-GBD25706_8305-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGTATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTTATATTAGGAGCGCCAGATATAGCATTTCCTCGAATAAATAATATAAGAGTCTGATTACTTCCCCCATCTTTATCTCTTCTTCTTTCTAGTACTAGTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6388 Chironominae sp. water mite diet isolate 6388-BHL032417-GBD28618_12475-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGAGCCTGATCAGGCATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTAATGGTGATGACCAAATTTATAATGTTATTGTAACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCGTCTTCTTTCTAGTTCTAGTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL639 Podocopida sp. water mite diet isolate 639-BHL072216-GBD10766_17241-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGTGCTTGATCTGCTATGCTAGGAACATCCTTAAGAGTAATTATTCGAGCTGAGTTCGGGCAACCTGGGGCCATGATTGGGAATGATCAAATTTATAACACGATTGTTACTGCCCATGCATTTATTATAATTTTTTTCTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTAACCTTATTAACAATAGGAATACTAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6391 Chironomidae sp. water mite diet isolate 6391-BHL032417-GBD25594_20794-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGCGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATCATATTTTTTTT-ATAGTTATATCCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR647156, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6402 Chironominae sp. water mite diet isolate 6402-BHL032417-GBD25556_18077-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGTCCTTGATCAGGAATAGTTGGAACTTCTTTTAGAATTTTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCTCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6403 Lebertia sp. water mite diet isolate 6403-BHL032417-GBD20867_27423-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCAGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCATGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGGTTTGGAAACTGATTAGTTCCACTAATAATCAGAACCCCAGATATAACCTTTCCACGAATAAATAAAATAAGAATTTGACTTCTTCCTCCACCCTTAACTCTACTTCTATCAAGTTCCATTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6405 Chironominae sp. water mite diet isolate 6405-BHL032417-GBD14538_25667-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTTTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATATTATTGTAACAGCTAATGCTTTTATTATAATTTTTTTTTATAGTAATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGAATACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTGTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6407 Chironominae sp. water mite diet isolate 6407-BHL032417-GBD20244_2366-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATATTTGGAACTTCTTTAAGAATGCTAATTCGAGCAAAATTAGGACAACCCTGGAACTTTTATTGGTGACGACTAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATGTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6421 Lebertia sp. water mite diet isolate 6421-BHL032417-GBD12766_28774-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAATAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTTACCAAATATACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAATAATACCAATAATAATTGGAGGTTTTGGAAAATGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAAAATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTATAACAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6424 Chironominae sp. water mite diet isolate 6424-BHL032417-GBD16117_5033-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACAGTATAGTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATGCGAGCAGAATTAGTACATCCTGGAACGTTTATTGGGGACGACCAAATTTATAATGATATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGCGCTGGACCAG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6426 Chironominae sp. water mite diet isolate 6426-BHL032417-GBD14627_18847-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAACTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGCATAAATAATATAAGATTCTGATAACTTCCACCTTCTATAAAACTGCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6431 Chironominae sp. water mite diet isolate 6431-BHL032417-GBD23843_4281-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACATTATAATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACATTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTACTTACTAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6439 Chironominae sp. water mite diet isolate 6439-BHL032417-GBD24473_12540-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAGCATTATATTTTATTTTTGGAGCCTGATCAAGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGATATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTGCTAATACGATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6448 Chironominae sp. water mite diet isolate 6448-BHL032417-GBD23177_26814-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAATATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAAGTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATACAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTATAAAATCGCGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL645 Chironominae sp. water mite diet isolate 645-BHL072216-GBD22349_15036-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTCTCACAACACACGCTTTTATTATAATTTTTTTTATAGATATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTGTCCCTCGAATAAATAATATAAGTTTTAGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6453 Chironomus sp. water mite diet isolate 6453-BHL032417-GBD17052_9073-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATGCGTATTCGAGCAGAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAAATGGAGAATTCGGAAACTGACTTGTCCCCCTAATACTCGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTTTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6456 Lebertia sp. water mite diet isolate 6456-BHL032417-GBD6586_5784-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGATGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGGTTTGGAAACTGATTAGTTCCACTAATAATCAGAGTCCCAGATAAAGCTTTTCCACGAATAAATAATATAAGAATTTGACTTCCTCCTCCATCCTTAACCCTACTTCTATCAAGTTCCATTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6459 Chironomus sp. water mite diet isolate 6459-BHL032417-GBD8703_7961-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTATCATAGTTATACCAATTTTAAATGGAGAATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTTGAATAAATAGTATAAGTTTCTGACTTTAACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6460 Chironominae sp. water mite diet isolate 6460-BHL032417-GBD8801_3285-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTATTATATTTTTTTTCATAGTTATACCCATTTTATTTGGAGGATTTGGAAATTGATTAGTTCTTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTGTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6466 Chironomidae sp. water mite diet isolate 6466-BHL032417-GBD25711_11075-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCCTTATATTCTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGAAATTAGGTCATCCTGGTACATTTATTGATGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAAATGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6468 Chironominae sp. water mite diet isolate 6468-BHL032417-GBD19570_3663-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGCAGCACCAGTTATAGCTTTTCCCCGAATAAATAATATAAGATTCTGATTCCTTCCCCCTTCTTTATCTCTTCTTCTTCCTAGTTCTAATGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6472 Lebertia sp. water mite diet isolate 6472-BHL032417-GBD5434_20015-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTAAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGTTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGATCCCCAGATATAGCCTTTCCACCAATAAAAAATAAAAGATTTTGACTTCTTCCTCCATCCATAACTCTACTTCTAACAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6473 Chironominae sp. water mite diet isolate 6473-BHL032417-GBD18717_23552-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAATTTTATAATATTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACGTCCCCCTTCTTTAGCACTACATCTTGCTAGTGCTATAGTAGAAAATGGAACTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6474 Chironominae sp. water mite diet isolate 6474-BHL032417-GBD4457_18769-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATGCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATCTAGCATTTCCTCGAATAAATAATATAAGATTCTGATCACTTCCCCCTCCTTTATATCTTCTTCTTTCCAGTTCTATTGTAGAAAATGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6476 Chironominae sp. water mite diet isolate 6476-BHL032417-GBD27202_20924-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCCGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGATGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6480 Chironominae sp. water mite diet isolate 6480-BHL032417-GBD8892_26750-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAAAAGTATAGTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTATTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGAGTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTCGTTCTATTGTATAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6482 Chironominae sp. water mite diet isolate 6482-BHL032417-GBD26835_8724-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAACCTGATAAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATACTGTAACTTTTATTGTTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTCTTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTACTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6486 Lebertia sp. water mite diet isolate 6486-BHL032417-GBD15502_7690-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTACTTTGCTTTTGGAGCTTGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCATTCCTAGGAAGTGACCAAATTTTCAATACAATTGTAACTGCTCAGGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAAATGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGTCCCAGATATAGCTATTCCACGAATAAAAAATATAAGATTTTGAATTCTTCCTCCATCCTTAAGTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL649 Podocopida sp. water mite diet isolate 649-BHL072216-GBD15646_5314-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGAGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATGATTCGAGCTGAGCTCGGGCAACCTGGGGCCCTGATTGTTAATGATCAAATTTATAACACAATTGTGACTGCCCATGCAGTTATTATAATTTTTTTTATGGTAATACCAATTTAAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCCCCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTATCCTTATTAACACTTGGAATACTTCCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6498 Chironominae sp. water mite diet isolate 6498-BHL032417-GBD11637_4626-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTAATTTTGGAGCCTGATAAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACGTCCCCCTTCTTCATCTCTTCTTCTTTCTAGTTCTAGAGTATAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6505 Chironominae sp. water mite diet isolate 6505-BHL032417-GBD15690_26753-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATAGTTTATTTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGAATTAGGAAATCAAGGAAATTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAGTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGATCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAACAATATAAGATTCTGATTACTTCCCCCATCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6508 Chironominae sp. water mite diet isolate 6508-BHL032417-GBD13425_28589-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGTATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGGGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTACTTTATCTCTTCTTCTTTCTAGTTCTATAGAATAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6509 Lebertia sp. water mite diet isolate 6509-BHL032417-GBD2689_16480-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTACTTTTGGAGCATGATCCGGAATAATTGGATCTATATTGAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTACTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAAATGGATGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCACCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGAATTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6510 Chironominae sp. water mite diet isolate 6510-BHL032417-GBD28050_21252-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGTACATTATATTTTATTTTTGGAGCCTGATCAGGAACAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTAGAACTTTTATTTGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTTTATAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6519 Lebertia sp. water mite diet isolate 6519-BHL032417-GBD29262_14826-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGTTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTTTTTATAATTTTTTTCATAGTAATATCAATAATAATTGGAGGGTTTGGAAACTGAATAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAAAAAATAATATAAAATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGGTCCTTTACAAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6523 Chironomus sp. water mite diet isolate 6523-BHL032417-GBD27878_21626-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTAATTGAGAATGCTTATTCGCGCAGAAATAGGACGACCCGTAACTTTCATTGGAGATGACCAAATTTATAAAGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTTGGAAACTTACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACGGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL653 Chironominae sp. water mite diet isolate 653-BHL072216-GBD24988_23876-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGTAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTT-ATTATTATTTTTTTTATAGTTATGCCAATTTCAATTGGAGGTTTTGAAAATTGACTTATTCCTTTAATGTTAGGGGCCCCAGATATGGCTTCCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6539 Chironominae sp. water mite diet isolate 6539-BHL032417-GBD20423_2729-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCAGATCAGGAATAGTTGGAACTTCTTTAGGAATTCTAATTCGAGTAAAATTAGGTCATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTAATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGAGTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6544 Lebertia sp. water mite diet isolate 6544-BHL032417-GBD8181_19222-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCATTATAATTTTTTTCATAGTAATACCAATATTAATTGGAGGTTTTGGAAACTGATTAGTTCCCCTAATAATCAGAGCCCCAGATATATCTTTTCCACGAATAAATAATACAACATTTTGACTTCTTGCCCCATCCATAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6546 Chironominae sp. water mite diet isolate 6546-BHL032417-GBD7204_25562-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTTGGAGCCTGATCAGGATTATTTGGAACTTCTTTAAGATTTCTAATTCGAGCTGAATTAGGACATCCTGGAACTTTTATTGTTGACGACCAAATTTTTAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCCCTACTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6547 Chironomus sp. water mite diet isolate 6547-BHL032417-GBD27653_22325-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAGCTTCATTGAGAATGCTTATTCGAGCAGAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTCTTTTCAAAGTTATCCCAGTTTTAAATGGAGGATTCGGAAACTGACTTGTCCCACTAATACTAGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6548 Chironomus sp. water mite diet isolate 6548-BHL032417-GBD14124_14039-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAAATAGGACGACCCGGAACTTTCGTTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACGTGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCCTCTCGTACGCTGCTTCGTTCTAGTTCTTTCGTAGAAAATGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6556 Chironominae sp. water mite diet isolate 6556-BHL032417-GBD26503_22132-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTCTATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTTTAATTCGAGCAGCATTCGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTCTAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGAATTGGAAATTGATTAGTTCCTCTTATTTTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6557 Chironominae sp. water mite diet isolate 6557-BHL032417-GBD8326_3685-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAACTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTCTTATTATAATTTTTTTCATAGTTATACCCATATTAATTGGAGGATTTGGAAATTGATTACTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATGATATAAGATTCTGATTATTTCCCCCTTCTTTATCTCTTCTTCTTTCTAATTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6559 Chironominae sp. water mite diet isolate 6559-BHL032417-GBD18641_23832-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGCGCCTGCTCAGGACTAGTTGGAACTTCTTTATGAATTCTAATTCGAACAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTATCAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTACGATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6564 Chironominae sp. water mite diet isolate 6564-BHL032417-GBD4699_19526-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTTGGAGCCTGCTCAGGAATAGTTGGAACTTCTTTAAGATTTCTAATTCGCGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACAAAATTTATAATGTTATTGTAACAGATAATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6568 Chironominae sp. water mite diet isolate 6568-BHL032417-GBD20309_27638-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTTTATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATGCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTAATTGGTGACGATCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTTTATAGGTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATTTTAGGAGCCCCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6569 Chironominae sp. water mite diet isolate 6569-BHL032417-GBD25514_10561-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGAACAAATTTATAATGTTATTGTAACAGCTCATCCTTTTATTATAATTTTTTTTCATAGTTATACACATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTCCCTCGAATAAATAATATAAGATTCGGATTACTTCCCCCTTCGTTAGCTCGACTTCTTTCTAATGCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6571 Chironominae sp. water mite diet isolate 6571-BHL032417-GBD14587_14155-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACAGTATAATTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGCATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTAATTGGTGATGACCAAATTTTTAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGACATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6573 Chironomidae sp. water mite diet isolate 6573-BHL032417-GBD28379_10875-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTTCATTATATTCTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGTAATTAGGTCATCCTGGAACATTTATTGATGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCCTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAAACCGACTTGTCCCCCTAATACTTGGAGCACTTGACATGGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID GU565708, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6576 Chironominae sp. water mite diet isolate 6576-BHL032417-GBD17534_3159-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATAGTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGAAAGCCTGTAACTTTTATTGGTGACGACCAAATTTATATTGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTGATATTAGGAGCACCAGATATAGTATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGACCAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6585 Chironominae sp. water mite diet isolate 6585-BHL032417-GBD3120_18146-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTGTATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAAGTTCTTTAAGAATTCTAACTCGAGCAGAAGTAGGACATGCTGGAACTTTTATTGGTGACGACCAAATTTGTAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTATAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6590 Lebertia sp. water mite diet isolate 6590-BHL032417-GBD6765_8103-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTACTTTGTTTTCGGAGCATGATCCGGAATAATTGGAGCTAGATTAAAAATCCTAATTCGACTTGAATTAGGACAACCGGGCACACTCCTAGGAAGTGACCAAATTTATAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCCTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCCAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6591 Chironominae sp. water mite diet isolate 6591-BHL032417-GBD9673_24103-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACATCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAAAAATATAAAATTCTGATTTCTTCCCCCCTCTTTATCTCTTCTTCTTTCCAGATCCAATGTAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6593 Lebertia sp. water mite diet isolate 6593-BHL032417-GBD27890_21912-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTTGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTTACCCCTAGGAAGTGACCAAATTTACAATACAATTGTAATTGCTCATGTTTTTGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAAAAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTTTCAAGGTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6596 Lebertia sp. water mite diet isolate 6596-BHL032417-GBD7364_25079-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCTACTTTAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCAACGAATAAATAATATAAGATTTTGCCTTATTCCTCCATACTTAACTATACTACTAACAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6598 Chironominae sp. water mite diet isolate 6598-BHL032417-GBD27775_12681-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTT-GGAGCCTGGTCAGGAATTGTTGGAACTTCTTTTAGGATTCTCATTCGAGCAAGATTTGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6599 Lebertia sp. water mite diet isolate 6599-BHL032417-GBD25918_24253-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTATACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTCGATTAAGAACCCTCATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTGTTGTAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGTTATAGCTTTTCCACGAATAAATAAAATAAGATTTTGACTTCTTCCCCCATCCTTAACTCTACTTCTATCAAGGTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6602 Chironominae sp. water mite diet isolate 6602-BHL032417-GBD27401_7999-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTTAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTAACGACCAAATTTATAATGTTATTGTAACAACTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAACAATATAAGATTCTGACTACTTCCCCCTTCTTTATCTCTACTAATTTCTAGTGCTACTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR287988, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6607 Chironomus sp. water mite diet isolate 6607-BHL032417-GBD5796_12329-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCATTGAGAATGTTTATTCGAGCAGAAATAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATGATAATTTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTGGTAAACTGACTTTTCCCCCTAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6618 Chironominae sp. water mite diet isolate 6618-BHL032417-GBD2319_11477-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTGGGACATCCTGGAACTTTTAGTGGTGACGACTAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6622 Chironomus sp. water mite diet isolate 6622-BHL032417-GBD14232_8919-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATAGTTTATTTTTGGGGCTTGATCCGGAATTGTGGGAACTTCCTTGAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACTTGACGTAGCTTTTCCTCGAATAAATAGTATAAGTTTCTGACTTTTATCCCCCTCTCTTACCCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6625 Lebertia sp. water mite diet isolate 6625-BHL032417-GBD27191_16237-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTAACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTTGTTATAATTTTTTTCATAGTAATACCAATAATAAATGGAGGGTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAAAATAAGATTTTGACTTCTTACTCCATCCTTAACTCTACTTTTATCAAGGTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6626 Chironomidae sp. water mite diet isolate 6626-BHL032417-GBD29026_18232-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGTGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCAATTTTAATTGGAGGATTTGGAAAGTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACACTTCATCTTTCTAGTTCCATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR647156, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6627 Chironominae sp. water mite diet isolate 6627-BHL032417-GBD28421_15723-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTTGGTGACAACCAATTTTATAATGTTTTGGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGACTACTTCCCCTTTCTTTATCTCTTTTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6631 Chironominae sp. water mite diet isolate 6631-BHL032417-GBD8978_15181-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATACTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTTATTGGTGACGACCAAATTTATAATGATATTGTAACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGTACCAGATAAAGCATTTCCTCGGATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6637 Chironominae sp. water mite diet isolate 6637-BHL032417-GBD13446_7704-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACATTATATTTTATTTTTGGAGTCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTAGTGACGACCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATATTAAGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTGCTATTGTAGAGAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6649 Lebertia sp. water mite diet isolate 6649-BHL032417-GBD19613_13182-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGTTTTTGGAGCATGATCCGGAATAATTGGAGCTAGTTTAAGAATCCTAATTCGACCTGAATTAGGACAACCAGGCTCACTCCTTGGAAGTGACCAAATTTATAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAAAAATAATTGGAGGGTTTGGTAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACCCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6655 Lebertia sp. water mite diet isolate 6655-BHL032417-GBD24555_19498-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGATCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAAAAAATGGAGTTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGACCCAGATATAGCTTTTCCCCGAATAAAGAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTAACAAGTTACTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6657 Chironominae sp. water mite diet isolate 6657-BHL032417-GBD19290_22656-Ldc27 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACTTTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGTATAATTAGGACAACCTGGAACTTTTATTGGTAACGACCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCATATTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTTAACTCTTCTTCTTTCTAGTGCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6661 Chironomus sp. water mite diet isolate 6661-BHL032417-GBD10667_19220-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCGGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTTGTTGTTACTGCACATGCTTATATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCCTCTTTCTAGTTTTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6663 Chironomidae sp. water mite diet isolate 6663-BHL032417-GBD20676_16042-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6664 Amphichaeta raptisae water mite diet isolate 6664-BHL032417-GBD21429_24320-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTAAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACACGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAGTTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL6665 Chironomus sp. water mite diet isolate 6665-BHL032417-GBD19977_10563-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGAGTTATAATGTTGTAGTTACTGCACATGCTTATATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6666 Chironomus sp. water mite diet isolate 6666-BHL032417-GBD25508_9875-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAAGTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTATATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCCTCTTTCTAGTTTTTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6667 Paratanytarsus sp. water mite diet isolate 6667-BHL032417-GBD18419_17943-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTCATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGTTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTATCAAGTATAAAAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6668 Culex sp. water mite diet isolate 6668-BHL032417-GBD14984_14866-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTAATTAGTTCCTTTAATGTTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6669 Paratanytarsus sp. water mite diet isolate 6669-BHL032417-GBD14662_18968-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTCGTAGTTACTGCACATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTTGACTTCTTCCCCCCTCTTTAACTCCTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6671 Chironomus sp. water mite diet isolate 6671-BHL032417-GBD21060_27266-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGATGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTATCCCCATAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCGCTTACTCTTCAACTTTCTAGTTTTTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6672 Culex sp. water mite diet isolate 6672-BHL032417-GBD9260_5244-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6673 Paratanytarsus sp. water mite diet isolate 6673-BHL032417-GBD18745_2802-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTCGGTGCTTGAGCAGGAATAGTGGGAACTTCCCTAATAATATTAATCCGAGCTGAACTAGGACATCCCGGAACTTTAATTGGAGATGACCAAATTTATAATGTAATTGTTACAACTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAAAAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6674 Culex pipiens water mite diet isolate 6674-BHL032417-GBD27325_21400-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGACAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGCTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAATTGTATCTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGTTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCAATCCTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTCAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6675 Chironomidae sp. water mite diet isolate 6675-BHL032417-GBD29295_14311-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTTGGTGCCTGCTCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTTTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACCTCTTGCTAGTTGTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.5% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6676 Paratanytarsus sp. water mite diet isolate 6676-BHL032417-GBD10073_23837-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCGTTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAAAATATTAATTCGAGCTGAACCAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTGTACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGACTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATGAGATTTTAACTACTTCCACCCTCTTTAACTCTTTTACGTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6677 Paratanytarsus sp. water mite diet isolate 6677-BHL032417-GBD21741_20410-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGAAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGTCCCAGATATAGCTTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTGTTACTTTCAAGTAGAATCGTGGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6678 Culex pipiens water mite diet isolate 6678-BHL032417-GBD7150_19701-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGCTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6679 Chironomus sp. water mite diet isolate 6679-BHL032417-GBD27061_17483-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTTGGTGCCTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTACATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAACAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCCTCTTTCTAGTTTTTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6680 Psectrocladius sp. water mite diet isolate 6680-BHL032417-GBD22165_11498-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTTATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR776852, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6681 Culex sp. water mite diet isolate 6681-BHL032417-GBD3459_20397-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6682 Chironominae sp. water mite diet isolate 6682-BHL032417-GBD26859_14500-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATATTAATCCGAACGGCATTAGGTCATCCTGGAACATTTATTGGTGATGACCATATTTATAATGTAATTGTTACTACTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGATATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6683 Paratanytarsus sp. water mite diet isolate 6683-BHL032417-GBD18496_5700-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCTTAACCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGACCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6684 Paratanytarsus sp. water mite diet isolate 6684-BHL032417-GBD8068_24902-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCCTCTTTCTAGTTTTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6686 Paratanytarsus sp. water mite diet isolate 6686-BHL032417-GBD11381_28380-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGCACTTTTATTGGAGATGACCAATTTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGTCCCAGATATAGCGTTTCCTCGAACAAATAAAATAAGATTTTGACTTCTTCCCCCCAGCTTTAACTCTTTTACTAGCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6688 Parachironomus sp. water mite diet isolate 6688-BHL032417-GBD21443_10102-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAGTGTAATTGTAACGGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATATGGAAATTGATTAGTTCCTCTTATATTAGTGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTGCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6690 Culex pipiens water mite diet isolate 6690-BHL032417-GBD18021_8215-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTTGGGGCTCGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTAAAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGGAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTATTGAATACTACCTTCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6691 Chironomidae sp. water mite diet isolate 6691-BHL032417-GBD6998_21584-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACTCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCCCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCATGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6692 Paratanytarsus sp. water mite diet isolate 6692-BHL032417-GBD7271_16918-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAAATTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTATTGCCTTTAATATTAGGTGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTATTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6693 Chironominae sp. water mite diet isolate 6693-BHL032417-GBD20195_4249-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCGTTATCTCTTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6694 Diptera sp. water mite diet isolate 6694-BHL032417-GBD18628_19641-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTTGGGGCTTTAGCTGGATTAGTTGGAACTTCTTTAAGTTTTCTATTTCGAGCAGAATTAAGACAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGGTTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.0% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6696 Chironomus riparius water mite diet isolate 6696-BHL032417-GBD11626_20349-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTAACCGCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6697 Paratanytarsus sp. water mite diet isolate 6697-BHL032417-GBD4380_8204-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGTTCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAACTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCACCCTCTTTAACTCTATTACAATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6699 Paratanytarsus sp. water mite diet isolate 6699-BHL032417-GBD7912_21154-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCGGGAATAGTAGGAACTTCCCTAAGATTATTAATTCGAGCCAAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTATTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTAAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCGCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGGACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6700 Paratanytarsus sp. water mite diet isolate 6700-BHL032417-GBD3064_13028-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATAGTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATTTTAATTCGAGCTGAACTAGGACATGCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTACAATAGTTGAAAATGAAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6705 Culex pipiens water mite diet isolate 6705-BHL032417-GBD14149_4377-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGGCAACAAATCATAAAGATATTGGAGCTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6706 Chironomus riparius water mite diet isolate 6706-BHL032417-GBD9275_25113-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATTCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGTACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCCTCTATCTAGTTCTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6707 Paratanytarsus sp. water mite diet isolate 6707-BHL032417-GBD19635_28379-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGTATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTAGAGGTAACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCGATTACGTTCAAGTAGAATAGTGGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6709 Phaenopsectra sp. water mite diet isolate 6709-BHL032417-GBD20194_21758-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCAAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL671 Podocopida sp. water mite diet isolate 671-BHL072216-GBD14255_29014-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACTGCCTTAAGAGTACTTATTCGAGCTGAGCTCGGGCAACCTGGGGCATTGATTGGGAATGATCAAATTTATAACACAATTGTGAATGCCCATGCTTTTATTATAAATTTTTTTATGGTAATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTACCCCCATCCTTAACCTCACTAACAACTGGAATACTCGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6710 Orthocladiinae sp. water mite diet isolate 6710-BHL032417-GBD26273_17904-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR282799, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6711 Chironomidae sp. water mite diet isolate 6711-BHL032417-GBD20429_15944-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAATAATATTATTTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTAAAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTACTTTAATTGGAGGATTTGGGAAATGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCCTCTTTCTAGTTTTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID KR282105, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6714 Diptera sp. water mite diet isolate 6714-BHL032417-GBD20946_19296-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATTTTCGGAGCTTGATCAGGAATATTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATATTTTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTGTCAAGTAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.9% identical to accession ID EU493571, identified in GenBank as Chymomyza procnemis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6715 Chironominae sp. water mite diet isolate 6715-BHL032417-GBD13023_12829-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6718 Cricotopus sp. water mite diet isolate 6718-BHL032417-GBD23031_5293-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAGTGTAATTGGTACTGCTCATGCTTTTGTAATAATTTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6720 Paratanytarsus sp. water mite diet isolate 6720-BHL032417-GBD23037_10559-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTCGGAGCCTGATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGACACCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAGTAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6721 Chironomus sp. water mite diet isolate 6721-BHL032417-GBD20406_20222-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGATTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTATATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAAAACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACATTTACCCCCCTCTCTTACTCTTCCTCTTACTAGTTTTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6723 Chironomus sp. water mite diet isolate 6723-BHL032417-GBD13359_24320-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTATATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGAAGCACCTGACATAGCTTTTCCCCCAAAAAATAATAAAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCCTCTTACTAATTTTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6724 Paratanytarsus sp. water mite diet isolate 6724-BHL032417-GBD19899_19737-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTACCTAAGAATATTAATTCGAGCTGAACTAGGATATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTATTTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCCAGATATAGCTTTTCCTCGAATAAATAATATAGGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6726 Paratanytarsus sp. water mite diet isolate 6726-BHL032417-GBD18276_8061-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAAATTATAATGCAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATATTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCATCCCCCCTCTTTAACTCGTTTACGTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6728 Paratanytarsus sp. water mite diet isolate 6728-BHL032417-GBD2926_20825-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCTTAAGAATATTAATTCGAGCTGAACTAGGGCATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCTTAGTTATACCTTTTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6731 Chironomus riparius water mite diet isolate 6731-BHL032417-GBD24541_8827-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGAACCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGAATTCGGAAACTGACTTATCCCCCTGATACTTGAAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTTCTCTTACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6735 Paratanytarsus sp. water mite diet isolate 6735-BHL032417-GBD18432_22024-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCTTTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTTAGAATTTTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATACAGCATTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCTCCTCTTTAACACTATTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6736 Cryptochironomus sp. water mite diet isolate 6736-BHL032417-GBD8578_7392-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTCATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6738 Chironomus sp. water mite diet isolate 6738-BHL032417-GBD5059_9092-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATAGTTTATTTTTAGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAGATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTACCACTATCTAGTTATTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6741 Chironomus sp. water mite diet isolate 6741-BHL032417-GBD24343_24292-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGGCTTGTTCCGGAATAGTGGGAACTTCATTAAGATTGCTTATTCGAGCAGATTTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTGTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACCTCTTTCTAGTTGTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6744 Culex pipiens water mite diet isolate 6744-BHL032417-GBD3979_13569-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAGGTCAACCAGGTGTATTTATTTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTCATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTGCCTTTAATGTTAGGAGCTCCAGATATGGCTTTTCCTCGAATAAATAATATAAGATTTTGAATACTACCTCCCTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6746 Chironomus sp. water mite diet isolate 6746-BHL032417-GBD18278_23835-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGCGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTATATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCCGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCGCTAACTCATCCTCTTTCTAGTTGTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6749 Orthocladius sp. water mite diet isolate 6749-BHL032417-GBD20426_9187-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAATTAGGATATTCGGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTAGTTATAATTTTTTTTACGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6752 Culex pipiens water mite diet isolate 6752-BHL032417-GBD22920_9716-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGAAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACAACCTTCCTACAATGAAACTACGACTGTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6754 Chironomus sp. water mite diet isolate 6754-BHL032417-GBD26958_11971-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGCTCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGATTATATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGCCATAGCCTTTCCCCGAATAAATAATATAAATTTCTGACTTTTACCCCCCTCTCTTACTCTTCCTCTTTCTAGTTTCTTTGGTGGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6755 Chironomus sp. water mite diet isolate 6755-BHL032417-GBD13945_21318-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAGTACTTGGAGCACCTGACATAGCTTTTCCCCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTGCTCTTCCTCTTTTCTAGTTTAATGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6758 Paratanytarsus sp. water mite diet isolate 6758-BHL032417-GBD17277_3311-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCGTTATATTTCATTTTCGGGGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCTGAACTTTTATTGGATATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6764 Paratanytarsus sp. water mite diet isolate 6764-BHL032417-GBD23881_9428-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTTAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGAAATAGCTTTCCCCCGAAAAAAAAAAAAAAGA-TTTGACTTCTACCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6767 Chironomidae sp. water mite diet isolate 6767-BHL032417-GBD9874_27581-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAAGTAGGACATCCCGGTACTTTTATTGGAGATGACAAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCCTCTTTCTAGTTTTTTTGGGAGAAAATGCAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6773 Chironomus sp. water mite diet isolate 6773-BHL032417-GBD23750_12580-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTATATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTTGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGGTTCTGACTTTTACCCCCCCGCTCTTACACGGCCTCGTTCTAGGTTATTGGTAGAAAATGGAGCAGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6774 Culex pipiens water mite diet isolate 6774-BHL032417-GBD1993_15649-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAGGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTAATTAGTTCCTTTAATGTTAGGAGACCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTATCAAGTACTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6777 Paratanytarsus sp. water mite diet isolate 6777-BHL032417-GBD5119_14582-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGAGCTGAACTCGGACATCCTGGATCTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTTCCTTTAATATTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6778 Paratanytarsus sp. water mite diet isolate 6778-BHL032417-GBD18093_6607-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGCACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAACGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGTAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTACTTCCCTCCTCATTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6779 Culex sp. water mite diet isolate 6779-BHL032417-GBD20221_8962-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTATGTCAACCAGGTTTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGAATACTACCACCTTCACTGACCCTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6780 Chironomus sp. water mite diet isolate 6780-BHL032417-GBD20375_22821-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCAGAACTTTCATTGGAGATGACCAGATTTATAATGTAGTAGTTACTGCACATGCTTATATTATAATTTTTTTCATAGTTATACCAATTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAAAAAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTACCACATTCTAGTATTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6781 Chironomus sp. water mite diet isolate 6781-BHL032417-GBD13485_5609-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGGATTAGGACGACCCGTAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTATATTATAATTTTTTTCATAGTTATACCAATTTTAATGGGAGGATTAGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGTCATAGCTTTTTCTCGAATAAATAATATAAGTTTCTGACTTTTCCCCCCCCTCTCTTACTCTTCCTCTTTCTAGTTTTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6783 Chironomidae sp. water mite diet isolate 6783-BHL032417-GBD7593_12691-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATAAAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6795 Culex sp. water mite diet isolate 6795-BHL032417-GBD13730_3795-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGAGCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGTAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTATATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGGATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACCCTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6812 Paratanytarsus sp. water mite diet isolate 6812-BHL032417-GBD5739_16059-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTATTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGGAATTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTATCAAGTACAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6813 Chironomus sp. water mite diet isolate 6813-BHL032417-GBD20124_27862-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTATATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTGGGAAACTGACTTTTCCCCCTAATATTTGGAGCACCTGACATAGCTTTTCCTCGAACAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTTCCTCTTTCTAATTGTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6832 Chironomus riparius water mite diet isolate 6832-BHL032417-GBD14681_8187-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCAGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTATATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAGATAATGTAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTGTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6833 Culex pipiens water mite diet isolate 6833-BHL032417-GBD21633_11079-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACATTCTATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTATGTTTAGTAATTCGAGCAGAATTAAGTCAACAAAGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATAACAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6834 Culex sp. water mite diet isolate 6834-BHL032417-GBD25344_23617-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTACATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAATTTCTTTAAGTTTCCTTATTCGAGCAGAATTAAGCCAACCAGGTGTATTTATTGGAAATAATCAAATTTATAATGTTATTGTAACTGTTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGACTTTCCCCGAATAAAAAATATAAGTTTTTGAATACTACCTCCTTCATTTGACACTACTACTTTCAAGTAGTTTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6838 Paratanytarsus sp. water mite diet isolate 6838-BHL032417-GBD8748_18306-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTGATTATTCTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAATAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCATTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTGTGACCTCTTCCCCCCTCTTTAACACTTTAACATTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6843 Chironomus sp. water mite diet isolate 6843-BHL032417-GBD25113_25066-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCCGGCATAGTGGGAACTTCATTAAGTATGTTTATTCGAGTAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTGGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACCTCTTTCTAGTTTTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6846 Chironomus sp. water mite diet isolate 6846-BHL032417-GBD9565_8805-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATATTGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGTAGGATTCGGAAATTGACTTGTCCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTTCCACTATCTAGTTTTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL685 Podocopida sp. water mite diet isolate 685-BHL072216-GBD16385_4322-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTAATTTTTGGTGCTTGATCTGCTATGCTAGGAACAGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGGCCCTGATTGTTAATGATCAAATTTATAACACAATTGTGACGGCCCAGGCATTTATTATAATTTTTTTATGGTAATACCAATTCTAATGGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGGGCACAAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTATCCTTATTAACACTTGAAATCCTTCCAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6853 Paratanytarsus sp. water mite diet isolate 6853-BHL032417-GBD17312_6144-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGAGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGTAGATGACCATATTTATAATGTAATTGTTACAGCTCAGGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCAAGATATAGCCTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6862 Culex pipiens water mite diet isolate 6862-BHL032417-GBD29001_13262-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGCTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATCTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACAACAAGCAAGTAGTTTAGTATAAAATGGAGCTGG	Using NCBI BLASTN in June 2018, this sequence was 97.7% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6864 Paratanytarsus sp. water mite diet isolate 6864-BHL032417-GBD24693_21322-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTATATTATAATTTTTTTCCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6867 Paratanytarsus sp. water mite diet isolate 6867-BHL032417-GBD12600_27258-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCTTTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAAATCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGGCTTTAATATTAGGAGCCCCAGAAATAGCCTCTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6871 Paratanytarsus sp. water mite diet isolate 6871-BHL032417-GBD20532_26713-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATAGTTCATTTTCGGTGCATGATCAGGAATAGTGGGAACTTACCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGTAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAATAGAATAGTGGTAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6876 Lebertia sp. water mite diet isolate 6876-BHL032417-GBD5957_8706-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTAAATTAAGACAACCAGGCTCACACCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6882 Paratanytarsus sp. water mite diet isolate 6882-BHL032417-GBD29372_14069-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTTATTTTACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTACTTCGAGCTGAACTAGGACATCCTGGAACTTTTCTTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCACTTCAACACATTAACAAGCAAGTAGAATAGTGGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6885 Paratanytarsus sp. water mite diet isolate 6885-BHL032417-GBD2661_17307-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATACTTCATTTTCGGGGCCTGATCAGGAATAGTGGGAACTTCCCTGAGAATGTTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAGTTGTTACAGCTCATGCATTTATTATAATTTTTTTTAATAGTTATACCTATTTTAATTGGAGGTTTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR282105, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6886 Culex pipiens water mite diet isolate 6886-BHL032417-GBD20113_22628-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGGATAGTTGGAACTTCTTTAAGTTTACTAAATCGAGCAGAATTAAGACAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGATCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATTATAATTGGAGGATTTGGAAATTAATTAGTTCCTTTAATTTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6888 Chironomus sp. water mite diet isolate 6888-BHL032417-GBD23427_25919-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATCATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAGCTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAAGATTCGGAAACTGACTTGTCCCCCTAATACATGGAGCACCTGACATAGCTTTTCCACGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTTCCTCTTTCTAGTTTTTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6896 Paratanytarsus sp. water mite diet isolate 6896-BHL032417-GBD11896_9275-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTTTACTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATTTTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCACTAACTCTATTACTAGTAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6898 Paratanytarsus sp. water mite diet isolate 6898-BHL032417-GBD9497_9596-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTTATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCTCTAAGAATATTAATTCGATCTGAACTAGGACATACTGGATCTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATGGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCCTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCGTCATTAACTCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6901 Chironomus sp. water mite diet isolate 6901-BHL032417-GBD25147_23414-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTCATACATTATTTTTGGGGCTTGAGCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGCTACTGCACATGCTTATATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCCCGAACAAATAATATAAGTTTCTGACTGTTTACCCCCCTCTCTTACCCTACCTCTTTCTAGTTTTTTGGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6905 Paratanytarsus sp. water mite diet isolate 6905-BHL032417-GBD10974_17869-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATCCTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGTACTGATTATTGCCTTTAATATTATGAGCCCCAGATATAGCCTTTCCTCGAATAAATAATATAAGAGTTTGACTTCTTCCCCCCTCTTTAACTCTTTGACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR754001, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6913 Paratanytarsus sp. water mite diet isolate 6913-BHL032417-GBD23628_20876-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGGGCCTGATCCGGAATAGTAGGAACTTCCTTAAGAATATTTATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTGTGACTTTTTCCCCCCTCTTTAACTCATTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6918 Chironomidae sp. water mite diet isolate 6918-BHL032417-GBD29098_18767-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGATTTCTCTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCTTTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGACATTAACTTAACTTCTTTCTAGTTCAATTATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6922 Culex pipiens water mite diet isolate 6922-BHL032417-GBD26528_19853-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGATGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCATTTAATGTTAGGAGCGCCAGATATGGCCGTTCCTCGAATAAATAATATAAGATTTTGAATACTACCTCCTTCATTGACCCTACTACGATCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6931 Paratanytarsus sp. water mite diet isolate 6931-BHL032417-GBD15036_6010-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCGGATAAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCTTAACTTTTATTGGAGATGACCAAATTTAGAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATGGGAGGATTTGGGAACTGATTATGGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6932 Psectrocladius sp. water mite diet isolate 6932-BHL032417-GBD8745_7362-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTCATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTGTTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGAGATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6934 Paratanytarsus sp. water mite diet isolate 6934-BHL032417-GBD15882_28780-Ldc28 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGATTTTATTTCATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACGTCCCCCCTCTTTAACACATTAACAATCAAGTAGAAGAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6937 Cryptochironomus sp. water mite diet isolate 6937-BHL032417-GBD4072_8764-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6938 Lebertia sp. water mite diet isolate 6938-BHL032417-GBD10167_19935-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAGTTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCATTAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6939 Chironominae sp. water mite diet isolate 6939-BHL032417-GBD14972_15671-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCATTAATATTAGGAGCCCCAGATACGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATCACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6940 Chironominae sp. water mite diet isolate 6940-BHL032417-GBD25755_23289-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTACTCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCATATTTATAATGGATTTGTTACTGCTCATGCTTTTCTTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATAGGTTATTACCACTAATAGTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6941 Chironomidae sp. water mite diet isolate 6941-BHL032417-GBD9918_2786-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTGTATTCGGAGCCTGATCAGGTATAGTAGGTACTTCCCTTAGTATTCTAGCACGAGCTGAATTAGGACATCCCGGGGCATTAATTGGAGACGATCAAAATTATAACGTAATCGTTACAGCTCATGCCTTTGTAATAATTTTCTTTATAGTAATACCTATTTTAATTGGTGGATTTTGGAAATTGATTAGAACCACTAATATTAGGTGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGCTTTTGATTATTACCCCCATCTTTAACATTACTATTAGCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR291645, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6942 Chironominae sp. water mite diet isolate 6942-BHL032417-GBD2861_18609-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATAAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGACAGGAATTAGGTCATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATTTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAAAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6943 Chironomus sp. water mite diet isolate 6943-BHL032417-GBD17357_27473-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAACTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6944 Chironominae sp. water mite diet isolate 6944-BHL032417-GBD7967_11630-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCGTCCTGGAACATTTATTGGTGGTGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTATTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGATCCCCTGATATGGTTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTATTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6945 Cryptochironomus sp. water mite diet isolate 6945-BHL032417-GBD13965_23840-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAAGGGCTATTAGGAACCTCTTTAAGTTTATTATTTCGAGCAGAATTAGGACAACCAGGTACTTTTATTGGAGACAACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCACCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGTCTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAAATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6946 Chironomus riparius water mite diet isolate 6946-BHL032417-GBD19979_23797-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCCTAGTTATACCAATTTTAATTTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTAACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6947 Chironomus sp. water mite diet isolate 6947-BHL032417-GBD17199_11821-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTGGAGCTGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAA-TTTTTTCATAGTTATACCAATTTTAATTGGAGGAATCGGAAAACTGACTTGTCCCCCTAATACTTGGAGCATCTGACATAGCGTTTCCTCGAATAAAAAATATAAGTTTCTGACTTTTACCCCCCCCTCTCTTACTCTTCTTCTTTCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6948 Chironomus riparius water mite diet isolate 6948-BHL032417-GBD19265_7903-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGATCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6949 Chironominae sp. water mite diet isolate 6949-BHL032417-GBD17988_4257-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCGTCCTGGAACATGTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAAAAATATAAGATTTTGATTATTCCCACCATCTCTTACTTTATTACTTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6950 Chironominae sp. water mite diet isolate 6950-BHL032417-GBD20276_9317-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACATTATTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGATTATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAGTTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAGTACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCATTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6951 Chironominae sp. water mite diet isolate 6951-BHL032417-GBD14819_10574-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAATATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6953 Cryptochironomus sp. water mite diet isolate 6953-BHL032417-GBD13896_9651-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCCTTTATTATAATTTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAAAATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6954 Drosophila sp. water mite diet isolate 6954-BHL032417-GBD17873_2532-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAACAAATCATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACTACCCAGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTATCCCCATCTCTTACTTTATTTCTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.3% identical to accession ID AY750090, identified in GenBank as Drosophila lacertosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6955 Cryptochironomus sp. water mite diet isolate 6955-BHL032417-GBD24887_7018-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGAAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6956 Chironominae sp. water mite diet isolate 6956-BHL032417-GBD15504_10402-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6957 Chironomidae sp. water mite diet isolate 6957-BHL032417-GBD6757_23757-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGACACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCCTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAACTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCAAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6958 Chironomus riparius water mite diet isolate 6958-BHL032417-GBD7826_18343-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTCGTTCGAGCAGAATTAGGACGACCCGGGACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTTCTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAGTTGGAGGATTCGGAAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6959 Cryptochironomus sp. water mite diet isolate 6959-BHL032417-GBD5119_21962-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6960 Chironomus riparius water mite diet isolate 6960-BHL032417-GBD9024_15996-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCATATTTATAATGTTGTAGTTACTACACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCTCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCAAAAAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6961 Chironomus riparius water mite diet isolate 6961-BHL032417-GBD22579_13823-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGGCTTGATCGGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGTATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACGCCCCTCTCTTACACTACTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6962 Chironomus sp. water mite diet isolate 6962-BHL032417-GBD13516_14735-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6963 Chironomus riparius water mite diet isolate 6963-BHL032417-GBD2415_12176-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATGAGGACGACCCGGAACTATCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCCTAGTTATACCAATTTTAATTGGAGGATTCGGAACCTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6964 Parachironomus sp. water mite diet isolate 6964-BHL032417-GBD1908_13896-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCTTTAAGAATACTTATTCGAGCTGAATTAGGACGACCCGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTAACGGCACATGCTTTTATTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGGGCTCCAGACATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTTTGACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR777748, identified in GenBank as Parachironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6965 Chironominae sp. water mite diet isolate 6965-BHL032417-GBD14923_26401-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTGTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGACATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTTATTGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGGTTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6966 Chironominae sp. water mite diet isolate 6966-BHL032417-GBD4363_16633-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGAAATTAGGTCATCCTGGAACATTTGTTGGTGATGACCAAATTTATAATGTAATTGATACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGGAGAATAGTAGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6967 Chironomus sp. water mite diet isolate 6967-BHL032417-GBD28478_17395-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTACTTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTTTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6968 Chironomus riparius water mite diet isolate 6968-BHL032417-GBD28335_15320-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATCTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAAGTTTAATTGGAAGGATTCGGAAACTGACTTGGCCCCCTGATACTTGGAGCACCTGACATAGTTTTTCCTCGAATAAATAATATAAGTTTCTTACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6970 Chironomus riparius water mite diet isolate 6970-BHL032417-GBD18868_17793-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGCACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTGCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACTCCCCTCACTTACTCTACTTCTATCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6971 Cryptochironomus sp. water mite diet isolate 6971-BHL032417-GBD3144_12761-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTTGGAGCTTGATCAGGGATATTAGGAACTTCATTAAGTATATTAATTCGAGCAGAATTAGGGCGACCCGGAACCTTTATTTGGAGACGACCAATTTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTCGGAAATTGATTATTACCTCTAATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTAACTCTTCGTCTTTCAAAATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6973 Chironomus sp. water mite diet isolate 6973-BHL032417-GBD5605_21587-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATATTGTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6974 Chironomidae sp. water mite diet isolate 6974-BHL032417-GBD11917_10798-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTACTTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6975 Chironomus sp. water mite diet isolate 6975-BHL032417-GBD23178_21844-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATTCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGCTGACCAAATTTATAATGTTGTGGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGTGGTTTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCCCTTACTCTTCGTCTTTCTAGTTCTTTCGTAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6976 Chironominae sp. water mite diet isolate 6976-BHL032417-GBD9639_26997-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGATCTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGTTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAAAAAATAATATAAGATTTTGATTATTACCACCATCACTTACTTTACTATTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6978 Chironomus riparius water mite diet isolate 6978-BHL032417-GBD22152_5752-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGAACGACCCGGAACTTCCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCACTTACTCTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6979 Chironomus riparius water mite diet isolate 6979-BHL032417-GBD21800_4989-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGGATTAGTGGGAATTTCATTAAGATTGCTTATTCGAGCGGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCACTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL698 Lebertia sp. water mite diet isolate 698-BHL072216-GBD15090_28178-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCCCTAATACTCAGAGCCCCAGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGACTTCTTCCCCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6980 Chironominae sp. water mite diet isolate 6980-BHL032417-GBD28031_20388-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGCATATTAATCCGAACGGAATTAGGTCATCCTGGTACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAAAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6981 Chironomus riparius water mite diet isolate 6981-BHL032417-GBD8090_24483-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTGGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCACGAATAAATAATATAAGATTCTGACTATTACTCCCCTCTCTTACTCTTCTTCTTTCCAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6982 Amphichaeta raptisae water mite diet isolate 6982-BHL032417-GBD12806_19321-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAACACCAGTTTTTAATGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL6983 Chironomus sp. water mite diet isolate 6983-BHL032417-GBD9025_3757-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATATTTTATTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATACTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAGTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6984 Chironomus riparius water mite diet isolate 6984-BHL032417-GBD3006_20282-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATATTAATTGGAGGATTTGGAAACTGACTCGTCCCCCTAATACATGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACGTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6985 Chironomus riparius water mite diet isolate 6985-BHL032417-GBD22229_4223-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTACACATTATTTTTGGGTCTTGATCCGGAATAGTGGGCACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTACCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6986 Chironomus riparius water mite diet isolate 6986-BHL032417-GBD13003_26238-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAATTTTAAATGGAGGATTCGGAAACTGACTTGTCACCCTGATACTTGGAGCCCCTGACATAGCTTTTCCTCGAATAAATAATAAAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGATCCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6987 Chironominae sp. water mite diet isolate 6987-BHL032417-GBD15173_22323-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTTTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTCCCACGAATAAAAAATAAAAGATTTTGAATATTACCACCATCTCTTACCTTATTACTTACAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6989 Penicillium citrinum water mite diet isolate 6989-BHL032417-GBD5435_7295-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TAAAGATATTGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTAATAGATACAGCCTTTTCTGTGTTAATAAGATTAGAATTATCAGGACCAGGTGTACAATATATATCAGATAACCAATTATATAATAGTATAATTACAGCACACGCTATAATGATGATTTTCTTTATGGTTATGCCAGCATTAATAGGTGGTTTTGGTAATTTCTTATTACCATTATTAGTAGGAGGTCCAGATATGGCATTTCCTAGATTAAATAATATAAGTTTCTGATTATTAGTTCCAAGTTTATTTTTATTTATATTCTCAGCAACTATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID EF180189, identified in GenBank as Penicillium citrinum. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL699 Chironominae sp. water mite diet isolate 699-BHL072216-GBD5248_10558-Arr95 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGATAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGAATTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCCTCTAATAAATAATACAAGTTTGTGACTTCTTCCCCCTCCATTAACTCTTTTACTTTCAAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6990 Chironominae sp. water mite diet isolate 6990-BHL032417-GBD11382_18315-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAACATAAGATTTTGATTACTACAACCATCTCTTACCTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6991 Chironominae sp. water mite diet isolate 6991-BHL032417-GBD9254_12354-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATCCGACCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGTTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACCTTATTGCTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6992 Chironominae sp. water mite diet isolate 6992-BHL032417-GBD22695_9332-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6994 Paratanytarsus sp. water mite diet isolate 6994-BHL032417-GBD18070_18307-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTATTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTAAACCTATTTTAATTGGAAGATTTGGGAACTGATCATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6995 Chironominae sp. water mite diet isolate 6995-BHL032417-GBD7657_23185-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTTTTAGAATATTAATCCGAATGGAATTAGGTCATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6996 Chironomus riparius water mite diet isolate 6996-BHL032417-GBD16061_17901-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTATGACGGCCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTACACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6997 Chironomus riparius water mite diet isolate 6997-BHL032417-GBD8885_26937-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGACTGCTTATTCGAGCAGACTTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTAATGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTATCTAGCTCTTTCGTAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL6998 Chironominae sp. water mite diet isolate 6998-BHL032417-GBD3286_19515-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAATATTTATTGGTGATGATCAAATTTATAATGAAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCTCTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL6999 Chironominae sp. water mite diet isolate 6999-BHL032417-GBD24015_7637-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTATTTAAGAATTTTAATCCGAACGGAATTCGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTTAATTGGAGGATTTGGAAATTGTTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7000 Chironominae sp. water mite diet isolate 7000-BHL032417-GBD18182_19636-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATCTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGATTATTATTCAGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGGTATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7001 Chironominae sp. water mite diet isolate 7001-BHL032417-GBD5557_9119-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGAACAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAACTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7002 Chironominae sp. water mite diet isolate 7002-BHL032417-GBD4782_16352-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGGACTTCTCTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATCGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCCCTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTTCTTTCAAGAAGAATAGTAGGAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7003 Oligochaeta sp. water mite diet isolate 7003-BHL032417-GBD16644_6689-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTCGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTTCCCACGACTAAACAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL7004 Chironominae sp. water mite diet isolate 7004-BHL032417-GBD7213_8039-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTGTATTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7005 Cricotopus sp. water mite diet isolate 7005-BHL032417-GBD3085_14084-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGACCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATAAAGCATTCCCTCGAATAAATATCATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7006 Chironomidae sp. water mite diet isolate 7006-BHL032417-GBD27629_20601-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTGATAGTAATACCTATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTGACTCCCCTCTCTTACTCTTCTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.6% identical to accession ID KR173465, identified in GenBank as Tanytarsus recurvatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7007 Chironominae sp. water mite diet isolate 7007-BHL032417-GBD14391_16496-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGAACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTTTATGAATTCTAATTCGAGCAGAATTCGGACATCCTGGAACTTTTATTGGTGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATAGATATACCCATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTCTTATATTAGGAGCACCAGATATAGCATTTCCTCGAATAAATAATATAAGATTCTGATTACTTCCCCCTTCTTCATCTATTCTTCTTTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281121, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7008 Chironomus riparius water mite diet isolate 7008-BHL032417-GBD24368_19823-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTTGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCGTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTAGTCCCCCTGATACTTGGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7009 Chironominae sp. water mite diet isolate 7009-BHL032417-GBD23877_9382-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGAAATACCTATTTTAATTGGAGGATTGGGAAAATGGGTTATTACCACTAATATTAGGAGCCCCTAGTATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL701 Chironomus maturus water mite diet isolate 701-BHL072216-GBD6823_5584-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTCTTAGTATGCTTATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTAACTACCCACGCATTTATTATATTTTTTTTTTTCATAGTTATACCAATTCTAATTGGTGGTTTTGGTAATTGACTTGTACCCTTAATATTAGGAGCCCCAGATATGGCTTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTTACTCTTTTACTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR665396, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7010 Chironomus riparius water mite diet isolate 7010-BHL032417-GBD11675_24478-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGCTGTAGTTACTGCACAAGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTATTTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTACTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7011 Phaenopsectra sp. water mite diet isolate 7011-BHL032417-GBD21529_9584-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAATACCTCTAATATTAGAAGCCCCTGATATAGCATTTCTTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTGCTTCTTTCGAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7012 Chironominae sp. water mite diet isolate 7012-BHL032417-GBD19272_9755-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTAGTTATTACCACTAATATTAGGAGACCCTGATATGGCTAATCCACGAATAAATAATATAAGATTTTGATAATTACCACCATCTCTTACTTTATTACCATCAAGAAGAATAGTAGAAAATGGAGTTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7013 Chironominae sp. water mite diet isolate 7013-BHL032417-GBD14804_4422-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAAACCGAACGGAATTAGGTCATCCTGGAACATTTATTGGGTATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGTCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGACTAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7014 Chironominae sp. water mite diet isolate 7014-BHL032417-GBD8659_17537-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTACTTTAAGAATATTAATCCGAACGGGATTAGGTCATCATGGAACATTTATTGGTGATGACCAAATTTATAATTTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGATGGTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7015 Chironominae sp. water mite diet isolate 7015-BHL032417-GBD27234_18000-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTCGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAATTGGTTTTTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7016 Chironomus riparius water mite diet isolate 7016-BHL032417-GBD14730_22226-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTATGAATGCTTATTCGAGCAGAATTAGGTCGACCCGGAACTTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATACTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCTCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTGCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7019 Chironominae sp. water mite diet isolate 7019-BHL032417-GBD11641_7193-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGACCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTGTAATTTTTTTTAATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTGACTTTATTAATTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7021 Chironomidae sp. water mite diet isolate 7021-BHL032417-GBD26032_9351-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATCGGAGGATTTGGAAACTGATTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTGTTATCTAGATCAATTGTGGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7023 Chironomus sp. water mite diet isolate 7023-BHL032417-GBD18916_17371-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACTCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACTCCCCTCTCTTACTCTACTACTTTCTAGTACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7024 Chironomus riparius water mite diet isolate 7024-BHL032417-GBD26481_16573-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAAATTGACGTGTTCCCCTAATACTTGGAGTACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7026 Chironominae sp. water mite diet isolate 7026-BHL032417-GBD27927_10442-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTTAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCATTAATATTAGGAGCCCCTGATATGGCATTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCTTCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7027 Chironominae sp. water mite diet isolate 7027-BHL032417-GBD20177_14485-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGCATTGTAGGAACTTCTTTATGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATCTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAAATGGTTATTACCACTAATATTAGGAGCCCATGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7028 Chironominae sp. water mite diet isolate 7028-BHL032417-GBD6852_6706-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGTCCAAATTTATAATGTAATTGTTACTGCTAGTGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGTAGGGTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATAGAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7029 Chironomus riparius water mite diet isolate 7029-BHL032417-GBD15888_7223-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACCTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGCCTTGTCCCACTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATATGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTTTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL703 Polyphemus sp. water mite diet isolate 703-BHL072216-GBD7477_11233-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAAGAATACTCATTCGTGCTGAATTAGGACAAGCAGGAAGATTAATTGGTGATGATCGAATTTATAACGTAATTGTAACTGCCCATGCTTTTGTTATAATTTTTTTTATAGTGATGCCTATTATAATTGGGGGGTTTGGTAATTGACTTGTTCCTCTAATGTTAGGAGCTCCTGATATGGCTCTTCCTCGGTTAAATAATTTAAGTTTCTGATTCCTTCCTCCTGCTTTAACTCTTCTCTTAGTTGGGGGGGGCTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID GQ406859, identified in GenBank as Polyphemus pediculus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7030 Chironomus riparius water mite diet isolate 7030-BHL032417-GBD12748_14333-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGGCTTGTTCCGGAATAGTGGGAACTTCATTAAGAATGCTTTTTTGAGCAGAATTAGGACGACCAGGAATTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7032 Chironominae sp. water mite diet isolate 7032-BHL032417-GBD5422_24312-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGCACTTCTTTAAGAATTTTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTAATACCACTAATATTAGGAGCCCCCTGATATGACTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTAACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7033 Chironominae sp. water mite diet isolate 7033-BHL032417-GBD11918_18614-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGCACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCATGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTTTTACTTTACTACTGTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7034 Chironominae sp. water mite diet isolate 7034-BHL032417-GBD13420_5384-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAGTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATACTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7035 Chironominae sp. water mite diet isolate 7035-BHL032417-GBD29119_17393-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGAAACATTTATAGGTGATGAACAAAATTATAATGTAATTGTTAGTGATCATGCTTTTATTATAAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7036 Chironominae sp. water mite diet isolate 7036-BHL032417-GBD19372_28422-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTTGGAATTTCTTTAAGAATACTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGACGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATCCCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7037 Chironominae sp. water mite diet isolate 7037-BHL032417-GBD25794_23413-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTGTAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATATAGTAATGCCTTTTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATTTCTAACTTCATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7039 Chironominae sp. water mite diet isolate 7039-BHL032417-GBD15861_3332-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTTTAACATTTATTGGTTATGACCATATTTATAATGTAATTGTTACTGCTCATGCTTTTACTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGGATAGTAGCAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7040 Chironomus riparius water mite diet isolate 7040-BHL032417-GBD17462_27709-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACTAAATTTATAATGTTATAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGATATACCAATTTTAATTGGAGGATTCGGAAACTGAGTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7041 Chironomus riparius water mite diet isolate 7041-BHL032417-GBD5440_14662-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGGACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTTTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7042 Chironominae sp. water mite diet isolate 7042-BHL032417-GBD16668_4903-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATGGGTGATAACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTACAATTTTTTTTAATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGTTTATTACCCCCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7043 Chironominae sp. water mite diet isolate 7043-BHL032417-GBD27162_22964-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCCGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAAGATTTGGAAATTGGTTAGTACCACTAATATTAGGAGCCCCTAATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGAATATTATAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7044 Chironomus riparius water mite diet isolate 7044-BHL032417-GBD25624_21543-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCACTAAGAATGCTTAATGGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATATTTTTTTTCATAGTTATACCAATTTTAACTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGTCATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7045 Orthocladius sp. water mite diet isolate 7045-BHL032417-GBD24111_18698-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGTACTTCATTAAGAATTTTAATTCGAGCTGAGTTAGGACATGCTGGTTCTTTGATTGGAGACGACCAAATTTATAATGTTATTGTAACAGCTCATGCTTTTGTTATAATTTTTTTTTTATGGTTATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTACCTTTAATGTTAGGAGCCCCAGATATAGCTCTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCATTAACTTTATTATTGTCTAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR756349, identified in GenBank as Orthocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7046 Chironomus riparius water mite diet isolate 7046-BHL032417-GBD13611_20516-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTATGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATAACCAAATTTATAATGTCGTAGTTACTGCATATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7047 Chironomus riparius water mite diet isolate 7047-BHL032417-GBD11604_15477-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAAGTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTAGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCATTTTCCTCGAATAAATAATATAAGTTTCCGACTTTAATCCCCCTCTCTTACTCTTCTTCCATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7048 Chironomus riparius water mite diet isolate 7048-BHL032417-GBD16595_28792-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGTTTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACTCCCCTCTCTTACTCAGCTACTTTCTAGTACTTTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL705 Podocopida sp. water mite diet isolate 705-BHL072216-GBD14772_24749-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATCTTATTTTTGGTGCTTGATCTGCTATGCTAGGAACTGCCTTAAGAGTAATTATTCGAGCTGAGCTCGGGCAACCTGGGGCCCTGATTGGGAATGATCAAATTTATAACACAATTGTGACTGCCCATGCATTTATTATAATTTTTTTTTATGGTAATACCAATTATAATCGGAGGGTTTGGAAATTGATTAGTACCTTTAATACTAGGAGCACCAGATATAGCGTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCCCCATCCTTATCCTTATTAACAATTGGAATACTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID HM397651, identified in GenBank as Podocopida sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7050 Chironominae sp. water mite diet isolate 7050-BHL032417-GBD18231_6323-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGTTTATTACCATATTTATAATGTAATTGATACTTCTCATGCTTTTATTATAATTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCATGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7051 Chironominae sp. water mite diet isolate 7051-BHL032417-GBD26628_15613-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGCATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGAACAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGACCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCGCCTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGCGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7052 Chironominae sp. water mite diet isolate 7052-BHL032417-GBD21469_5667-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGAAATTAGGTAATCCTGGAACATTTATTGGTGATGACCAAATTTATATTGTAATTGTTACTGTTCATGCTTTTATTATAATTTTTTTTCTAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGTGCCCCTGATATGGCTTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7053 Chironominae sp. water mite diet isolate 7053-BHL032417-GBD6002_8967-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATACTAGAACATTTATTGGTAATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGATGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATTGCTGTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAACTGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7056 Lebertia sp. water mite diet isolate 7056-BHL032417-GBD5857_23866-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTAGATTAAGAACCCTAATTCGATTCGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGTCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTCGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL706 Chironomus riparius water mite diet isolate 706-BHL072216-GBD15888_25317-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGGCTTGATCCGTAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAAGTTTTCCTCGAATAAATATTATAAGTTTCTGACTTTTACCCCCATCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7060 Chironominae sp. water mite diet isolate 7060-BHL032417-GBD16008_27710-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTAATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTTAGAATATTAATCCGAACTGAATTAGGTCATCCTGGAACATTTATTGGTAATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTTATAGTAATACCTATTTTAATTGGAGTATTAGTAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7061 Chironominae sp. water mite diet isolate 7061-BHL032417-GBD9184_23043-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTGGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAATGGAATTATTTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTGGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7066 Chironominae sp. water mite diet isolate 7066-BHL032417-GBD7087_15101-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGATATAGTAGGAACTTCTTTAAGAATATTAATCCAAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGAAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCATTTACACGAATAAATAATATAAGATTTTGATAATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7067 Chironominae sp. water mite diet isolate 7067-BHL032417-GBD11371_20038-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTTGGAACTTCTTTAAGAATTTTAATCCGAACGGAATTAGGTCATCCTGGCACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTGTTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTCATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7068 Chironominae sp. water mite diet isolate 7068-BHL032417-GBD18391_23232-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGTAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTAAATTGGAGGGTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGACTTTTCCACGAAAAAATAATATAAGATTTTGATTATTACCACCAACTCTAACTATATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL707 Chironomus riparius water mite diet isolate 707-BHL072216-GBD18781_11138-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTATGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATATTTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGTAAACTGACTTGTCACCCTAATACTTGGAGCACCTGACATAGCTTTTCCACGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7070 Chironomus riparius water mite diet isolate 7070-BHL032417-GBD22443_23047-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGAAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTAACTCTACTACTCTCTAGTGCATTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7073 Chironominae sp. water mite diet isolate 7073-BHL032417-GBD21946_20027-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTATTTTTGGAGCTTGTTCAGGTATAGAAGGAACTTCTTTAAGATTATTATTCCGAACGGAATTAGGTCATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7074 Chironominae sp. water mite diet isolate 7074-BHL032417-GBD18529_3262-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTTGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTCATTGTTACTGCTCATGATTTTATTATAAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATCGATTATTACCACTAATATTAGGAGCCCCTGACATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7075 Chironominae sp. water mite diet isolate 7075-BHL032417-GBD18643_4164-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGGAGCTTGACCAGGTATAGTAGGAACTCCTTTAAGAATATTAATCCGACCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAATTTTATAATGTAATTGTTAATGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7076 Chironomus riparius water mite diet isolate 7076-BHL032417-GBD21838_11156-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACATCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCACTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACCTTTACCCCCCTCCCATACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7078 Chironomus sp. water mite diet isolate 7078-BHL032417-GBD17134_12883-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCTTAATATTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCCTCTCTTACCCTACTTCTTTCTAGTTCATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7079 Chironomus riparius water mite diet isolate 7079-BHL032417-GBD10903_4420-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACAAAGCTTTTCCCCCAATAAATAATATAAGTTTCTGATTTTTTACCCCCTTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL708 Polyphemus sp. water mite diet isolate 708-BHL072216-GBD20910_27131-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAAGAATTCTCATTCGTGCTGAATTAGGACAAGCAGGAAGATTAATTGGTGATGATCAAATTTATAACGTAATTGTAACTGCCCATGCTTTTGTTATAATTTTTTTTATAGTGATGCCTATTATTATTGGGGGGGTTTGGTAATTGACTTGTTCCTCTAATGTTAGGAGCTCCTGATATGGCTTTTCCTCGGTTAAATAATATAAGCTTCTGGTTCCTTCCTCCTGCTTTAACTCTTCTCTTAGTTGGGGGGGCTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID GQ406859, identified in GenBank as Polyphemus pediculus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7081 Chironominae sp. water mite diet isolate 7081-BHL032417-GBD27835_9832-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTATGAATATTAATCCGAACGGAATTAGGTCGTCCTGGAACATTTATTGGTGATGACCAAATATATAATGTAATTGTTACTGCTCATGCTTTTATTATATTTTTTTTTTATGGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7082 Chironomus riparius water mite diet isolate 7082-BHL032417-GBD17255_2235-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTAATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCCTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGGAACCTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCACGAATAAATAATATAAGTTTCCGACTTTTTCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7084 Chironominae sp. water mite diet isolate 7084-BHL032417-GBD11404_16547-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCCGGTATCGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATCAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTAATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTTATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATGACCACCATCTCTTACTTTATTACTAGCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7085 Chironomidae sp. water mite diet isolate 7085-BHL032417-GBD11577_21821-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAAAAATATAAGTTTTTGGC-TTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7086 Chironomus sp. water mite diet isolate 7086-BHL032417-GBD4414_11237-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTTGAGCAGAATTAGGATGACCCGGAACTTTCATTGGAGATGAACAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATCCCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAAAATAAGTTTCCGACTTTTACCCCCCTCTCTTACCCTTCTTCTTTCTAGTACGTTCGGAGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7087 Chironomus riparius water mite diet isolate 7087-BHL032417-GBD25109_19770-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGAAGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCCATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTAACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTTACCCCCCACTCTAACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7088 Chironominae sp. water mite diet isolate 7088-BHL032417-GBD13562_14636-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAATTGAGTTAGGCCATCCTGGAACATTTATTGGTGATGACCAAATTTATAACGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7089 Chironominae sp. water mite diet isolate 7089-BHL032417-GBD11746_6293-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAAGAACTTCTTTAAGAATTTTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATACTGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTATTTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCCTTTCCACGAATAAATAATATAAGATTTTGAATATTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7090 Chironominae sp. water mite diet isolate 7090-BHL032417-GBD19403_23436-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGAGTTTGATTATTACCACCAACTCCTACTTAATCACTTTCAAGAAGAAGAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7091 Chironomus sp. water mite diet isolate 7091-BHL032417-GBD25364_8047-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACAACCCGGAACTCTCATTGGAGATGACCAAATTTATAATGGTGTAGTTACTGCACGTGCTTTTATTATATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTGCCCTCTCTTACTCTTCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7092 Chironominae sp. water mite diet isolate 7092-BHL032417-GBD21192_17465-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTACAGTAAGACCTATTTTAATTGGAGGAGTTGGAAATTGGTTATTACCACCAATATTAGGAGTCCCTGATATGGCTTGTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7095 Chironominae sp. water mite diet isolate 7095-BHL032417-GBD26907_11410-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGTTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCTTTAATATTAGGAGCCCCTGATATGGCTGTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTTATTACTATCAAGAAGAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7099 Chironomus riparius water mite diet isolate 7099-BHL032417-GBD24659_15649-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACCTGCTTTTATTATAATTTTTTTTCATAGTTATACCATTTTTAATTGGAGAATTCAGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGATTAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7102 Chironominae sp. water mite diet isolate 7102-BHL032417-GBD5570_24245-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGAGCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGACATCCTGGAACTTTTATTGGTGATGACCAAAGTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCATTTCCACGAATAAATAATATAAGATTTTGATTATTCCCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7103 Chironomus riparius water mite diet isolate 7103-BHL032417-GBD14082_14723-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGACCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGGTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTGATACTTGGATCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGCTTCTGACTTTTACCCCCCTCTCTGACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7104 Lebertia sp. water mite diet isolate 7104-BHL032417-GBD4548_8412-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGTATGATCCGGAATAGTTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAAATTTTTTCATAGTTATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAAAAATCAGAGCCCCAGATATAGCTTTTCCCCGAATAAAAAATATAAGATTTTGAATTCTTCCTCCATCCTTAACTCTACTCCTAACAAGTTACTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7105 Chironominae sp. water mite diet isolate 7105-BHL032417-GBD26710_6734-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCCTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTACTACCTCTAATATTAGGAGCCCCTGATATGGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTCTCAAGAAGAATAGTAGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7106 Chironominae sp. water mite diet isolate 7106-BHL032417-GBD27259_21641-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATATTAATCCGAACAGAATTAGGACATCATGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGATCATGCTTTTATTATAATTTTTTTTTTATAGTAATGCCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCATCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7107 Chironominae sp. water mite diet isolate 7107-BHL032417-GBD24745_25712-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTACGTATCTTTATCCGAACGGAATTAGGTCAACCTGGAACATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTTCCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7108 Chironominae sp. water mite diet isolate 7108-BHL032417-GBD20723_5187-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATGTTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAAATATTATTCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCCCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGTAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTATTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7109 Chironomus sp. water mite diet isolate 7109-BHL032417-GBD27463_19125-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGTAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTAACTGCACATGCTTTTACTATAATTTT-TTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTACTACTTTCTAGATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7111 Cryptochironomus sp. water mite diet isolate 7111-BHL032417-GBD25417_19755-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGAAACTTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTCACAGCTCATGCTTTTATTATAATTTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTTGGAAATTGATAAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTATTACCCCCATCCTTAACTCTTCTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7113 Chironomus sp. water mite diet isolate 7113-BHL032417-GBD14613_16629-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCTAGCAGAATTAGGACGACCCGAACCTTTCATTGGAGATGACAAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCTCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTTCTAGTTATTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7116 Chironominae sp. water mite diet isolate 7116-BHL032417-GBD4915_21933-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTGTTTAAGAATATTAATTCGAATGGAATTAGGTCATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTACTTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTATTTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7117 Chironomus riparius water mite diet isolate 7117-BHL032417-GBD7688_9248-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGGACTTTCATTGGATATGACCAAATTTACAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCATTTTTAATTGGAGGTTTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7118 Cryptochironomus sp. water mite diet isolate 7118-BHL032417-GBD17037_28070-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATATTGTAATTGTAACAGCTCATGCCTTTATTATAATTTTTTTCATAGTTATACCATTTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATAATGGTAGCCCCAGATATAGCCTTTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7120 Chironominae sp. water mite diet isolate 7120-BHL032417-GBD14348_8071-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTATTCCGAACGGAATTAGGTCATCCTGTAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGTAGGGTTTGGAAATTGGTTATTACCACTAATATTAGGAGTACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTACTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7121 Chironomus sp. water mite diet isolate 7121-BHL032417-GBD23046_4490-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGTTGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAA-TTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCACGAATAAATAATATAAGATTCTGACTATTACCCCCCTCTCTTACCCTACTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7123 Chironominae sp. water mite diet isolate 7123-BHL032417-GBD12551_4432-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCAACCTGGAACATTTCTTGGTGATGACCAAATTTATAATATAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7124 Chironomus riparius water mite diet isolate 7124-BHL032417-GBD11888_26799-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGGAATAGTGGTAACTTCATTAAGATTGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTGCTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGAATTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCTAATAAATAGTATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7128 Chironominae sp. water mite diet isolate 7128-BHL032417-GBD22618_14770-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGTCCAAATTTACAATGTAATTGCTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTTCTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7129 Lebertia sp. water mite diet isolate 7129-BHL032417-GBD18249_15966-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAGTTGGAGCTAGATTAAGAACTCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAATGACCAAATTTACAATACAATTGTAACTGCTCACGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGGTTTGAAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATAAAGCTTTTCCACGAATAAAAAAAATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTTCTTCTAACAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7130 Chironominae sp. water mite diet isolate 7130-BHL032417-GBD29347_18001-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATATTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTGTAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATAATGAGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTGCAAGAAGAATAGTATAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7131 Chironominae sp. water mite diet isolate 7131-BHL032417-GBD16407_15925-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTCGGAGCTTGATCAGGTATAGTAGGGACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTCCCACTAATATTAGGTGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACTATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7137 Chironomus riparius water mite diet isolate 7137-BHL032417-GBD18298_28250-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTGTTTTTGGGGCTTGATCCGGAATAGTCGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCATGATACTTGGAGCACCTGACATAGCTTGTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTTTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACGGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7138 Chironomus riparius water mite diet isolate 7138-BHL032417-GBD18160_5591-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTGATTCGAGCAAAATTAGGACGACCCTGAACTCTCATTGGAGATGACCAAATTTATAATGGTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCCTCTTTCTCGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7139 Chironominae sp. water mite diet isolate 7139-BHL032417-GBD3237_15497-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAGCTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGAGATGACCAAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCTCCTGGTGTGGCTGTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL714 Chironomidae sp. water mite diet isolate 714-BHL072216-GBD8173_13681-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGAACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTCTTAGTATGCTTATTCGAGCAAAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTAACTACCCACGCATTTATTATATTTTTTTTTCATAGTGATGCCTATTATAATTGGGGGGTTTGGTAATTGACTTGTTCCTCTAATGTTAGGAGCTCCTGACATGGCTTTTCCTCGGTTAAATAATTTAAGTTTCTGATTCCTTCCTCCTGCTTTAACTCTT	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID DQ648208, identified in GenBank as Chironomus whitseli. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7143 Chironominae sp. water mite diet isolate 7143-BHL032417-GBD24837_25680-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTATGAACTTCTTTAAGAATATTAATCCTAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATAACTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTGTTCCACGAATAAATAATATAAGATTTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7144 Chironominae sp. water mite diet isolate 7144-BHL032417-GBD13135_19128-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAATAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTCTAATTGGAGGAGTTGGAAATTGGTTATTACCACTAATGTTAGGAGCCCCTGATATGGTTCTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTCTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7145 Chironominae sp. water mite diet isolate 7145-BHL032417-GBD27248_22828-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATCTATAATGTAGTTGTTACTGCACATGCTTTTAGTATAATTTTTTTAATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATAACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7146 Chironominae sp. water mite diet isolate 7146-BHL032417-GBD21870_27006-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTTGGAGCTTGATCCGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAACGTAATTGTTACTGTTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTTCCACTAATATTGGGAGCCCCTGATATGGCTTTTCCACGAACAAATAATATAAGATTTTGATTATTACCACCATTCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7147 Chironominae sp. water mite diet isolate 7147-BHL032417-GBD6348_16260-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGAAATTAGGTCATCCTGGAACATTTATTGGTGGTGACCAAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCATTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACCATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7149 Chironominae sp. water mite diet isolate 7149-BHL032417-GBD23500_11519-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCCTGATCAGGTATAATAGGAACTTCTTTAAGCATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGAACAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCACCTGGTATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCAGCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL715 Polyphemus sp. water mite diet isolate 715-BHL072216-GBD2776_17702-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAAGAATTCTCATTCGTGCTGAATTAGGACAAGCAGGAAGATTAATTGGTGATGATCAAATTTATAACGTAATTGTAACTGCCCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTATAATTGGGGGGTTTGGTAATTGACTTGTTCCTCTAATGTTAGGAGCTCCTGATATGGCTTTTCCTCGGTTAAATAATATAAGTTTCTGATTCCTTCCTCCTGCTTTAACACTACTACTAGCTGGGGGGGCTGCTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID GQ406884, identified in GenBank as Polyphemus pediculus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7151 Chironominae sp. water mite diet isolate 7151-BHL032417-GBD21164_7650-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTCTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGTAAATTGTTTATTACCACTAATATTAGGAGCCCCTGAGATGGCTTTTCCACGAATAAATAATTTAAGATTTTGATTATTACCACCATCTCTTACTTAATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7153 Chironominae sp. water mite diet isolate 7153-BHL032417-GBD12061_17580-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTTGGAACTTCTTTAAGAATTTTAATCCGAACTGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTTTAATGTAATTGTTACTGCTCATGCTTTTATTATCATTTTTTTTCATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7154 Chironomus sp. water mite diet isolate 7154-BHL032417-GBD12716_16333-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATATTTTATTTTTGGAGCTTGATCCGAAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCAGATGCTTTTATTATAATTTT-TTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCTTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7156 Chironomus sp. water mite diet isolate 7156-BHL032417-GBD8482_20668-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACCTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGTATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTGTCCCAATTTTAATTGGAGGATGCGGAAACTGACTTGTCCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAATTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTTCTAGTTCTTTCGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7157 Chironominae sp. water mite diet isolate 7157-BHL032417-GBD18756_12539-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATTTTAATCCGAGCGGAATTAGGTCATCCTGGTTCATTTATTGGTGATGAACAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATCGATTATTACCACTAATATTAGGAGCCCCTGATATAGCATTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7159 Chironominae sp. water mite diet isolate 7159-BHL032417-GBD20368_20506-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTTCTTCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGAATTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTAATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7160 Chironomus riparius water mite diet isolate 7160-BHL032417-GBD7504_4344-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTCTTTCATATTTATACCAACTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGATTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTACTTTAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7161 Chironominae sp. water mite diet isolate 7161-BHL032417-GBD18109_26682-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGACAACCAGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCTCTAATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7164 Chironominae sp. water mite diet isolate 7164-BHL032417-GBD14921_5001-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGGAGCTTGAGCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTTCAACATTTATTGGTGATGACCAAATTTAGAATGTAATTGTTACTTCTCATGCTTTTTTTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7166 Chironominae sp. water mite diet isolate 7166-BHL032417-GBD18521_6008-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGCACTTCTTTAAGAATTTTAATCCGACTGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATATTGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGACCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACTGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7167 Chironomidae sp. water mite diet isolate 7167-BHL032417-GBD20303_18085-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATTAGAGCCCCAGATATAGCTTATCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTACCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7171 Chironominae sp. water mite diet isolate 7171-BHL032417-GBD2247_11966-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTTTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGAACAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATCATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCACTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTGTTACTTTCAAGAATAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7172 Chironominae sp. water mite diet isolate 7172-BHL032417-GBD10117_2974-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATACTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAGCTGAATTAGGTCATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTCTTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR769900, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7174 Chironominae sp. water mite diet isolate 7174-BHL032417-GBD15389_18369-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGACCGGAATTAGGTCATCCTGGTACATTTATTGGTAATGACCAAATTTATAATGTAATTGTTACTGCTAATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGTACCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAGGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7175 Chironominae sp. water mite diet isolate 7175-BHL032417-GBD13799_28969-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGACATTGGTTATTACCACTAATATTAGGAGCCTCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCATCTCTTACATTATAACAATCAAGAAGAATAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7176 Chironomus sp. water mite diet isolate 7176-BHL032417-GBD10781_23077-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTTTCCCCTTAATACTTGGAGTACCTGACATAGCTTTTCCTCGAATAAATAACATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTATCTAGTAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7178 Lebertia sp. water mite diet isolate 7178-BHL032417-GBD8037_7229-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCTTGATCAGGTATAGTTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAATTTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACCCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7179 Chironominae sp. water mite diet isolate 7179-BHL032417-GBD7195_24098-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGAGCTTGATCAGATATAGTAGGAACTTCTTTAAGATTATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGAATATTACCACCATCTCTGACTTTATTACTTTCAAAGAGAATAGTAGAAAATGGAGCTGGGACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7180 Chironominae sp. water mite diet isolate 7180-BHL032417-GBD15649_6069-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTTGAACATTTATAGTTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTCTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTGCTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7182 Chironomus sp. water mite diet isolate 7182-BHL032417-GBD17745_6853-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCACTGGAGACGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCATCTCTTACCCTTCTTCTTTCTAGTACATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7191 Chironomus sp. water mite diet isolate 7191-BHL032417-GBD14612_24009-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATATTTTATTTTTGGAGCTTGATCAGGGCTATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTT-TTCATAGTTATACCAATTTTTATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGAATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7192 Chironomus sp. water mite diet isolate 7192-BHL032417-GBD20672_12258-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGAGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATGCTTATTCGAGCAGAATTATGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTCGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGGTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7194 Neoptera sp. water mite diet isolate 7194-BHL032417-GBD15839_6067-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGATCATTATAATTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTATATCAAGTTCCTTTACTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID MF458986, identified in GenBank as Patrobus longicornis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7196 Chironominae sp. water mite diet isolate 7196-BHL032417-GBD17523_16098-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATCATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGATATTGGTTATTACCACTATTATTAGGATCCCCTGATATGGCTTTTCCACAAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7197 Chironominae sp. water mite diet isolate 7197-BHL032417-GBD14416_3032-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTTGAACATTTATTGGGTATGACCATATTTATAATGTAATTGTTACTTCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAGTAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACCGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7202 Chironominae sp. water mite diet isolate 7202-BHL032417-GBD5914_9651-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTTGGAGCTTGCTCAGGGATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAGCATTTATTGGTGATGACCAAATTTATAACGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTATCATCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7204 Chironomus sp. water mite diet isolate 7204-BHL032417-GBD19515_13580-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAA-TTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCACGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCATACTCTACTTCTTTCAAGTACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7205 Chironominae sp. water mite diet isolate 7205-BHL032417-GBD29222_16745-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCTGAACGGAATTAGGTCATCCTGGAACATTTTTTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTCTCAAGAAGAAATATTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7206 Chironominae sp. water mite diet isolate 7206-BHL032417-GBD8203_19565-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTATGAATATTAATCCTAACGGTATTAGGTCATCCTGAAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTATGAGTCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7208 Chironomus riparius water mite diet isolate 7208-BHL032417-GBD15622_13909-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGTGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGATACTGCACATGCTTTTATTATAATTTTTTTCATAGTGATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTACCCCTAATACTTGGAGCACCTGACATAGCTTTTCCGCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7210 Chironomus riparius water mite diet isolate 7210-BHL032417-GBD21211_6589-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAAGACGACCCGGAACTTTCATTGGTGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAAATGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAACACCTGACAAAGCTTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7212 Chironominae sp. water mite diet isolate 7212-BHL032417-GBD10076_26142-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTATGTACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCGTGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACAACTAATATTATGAGCCCCTGATATGGCTTTTCCACGAAAAAACAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTAATTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7213 Chironomus sp. water mite diet isolate 7213-BHL032417-GBD18982_12134-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATAGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAA-TTTTTTCATAGTTATACCAATTTTAAATGGAGGATTCGGAAACTGACTTGTTTCCCTTATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCCTCTCTTACTCTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7215 Chironominae sp. water mite diet isolate 7215-BHL032417-GBD8062_21214-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCCGGTATAGTAGGAACTTCTTTAAGTATATTAATCCGAACGGAATTAGGTCATCCTGGCACATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATGCCTATTTTAATTGGAGGCTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTTCTGTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7218 Chironominae sp. water mite diet isolate 7218-BHL032417-GBD15275_2208-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCCGGAATAGTAGGAACTTCTTTAAGAATATTAATCCGAACTGAATTAGGTCATCCTGAAACATTTATTGGTTATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTTGAGGGTTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL722 Chironomus sp. water mite diet isolate 722-BHL072216-GBD15583_5181-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTTTATTTGGTATTTGAGCAGGGATGGTAGGGACTTCTTTAAGAATTCTCATTCGGGCTGAATTAGGACAAGCAGGAAGATTAATTGGTGATGATCAAATTTATAATGTAGTAGTAACTACCCACGCATTTATTATATTTTTTTTCATAGTTATACCAATTCTAATTGGTGGTTTTGGTAATTGAATTGTACCCTTAATATTAGGAGCCCCAGATATGGCTTTCCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTTACTCTTTTACTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID MF708883, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7221 Chironominae sp. water mite diet isolate 7221-BHL032417-GBD14956_28282-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCATGGATAGTAGGGACTTCTTTTAGAATATTAATCCGAACGGAATTAGGTCGTCCTGGAACATTTATTGGTGATGACTAAATTTATAATGTAATTGTTACTTCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7222 Chironomus sp. water mite diet isolate 7222-BHL032417-GBD2262_18235-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGCTCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACAAAATTTATAATGTTGTCGTTCCTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGAATTCAGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7223 Chironominae sp. water mite diet isolate 7223-BHL032417-GBD26568_9885-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTATGACTATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGTTTATTACCACTAATATTAGGAGCCCCATGATATGGCTTTTCCACGAATAAATAATATAAGAGTTTGATTATTACCACGATCGCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7224 Lebertia sp. water mite diet isolate 7224-BHL032417-GBD5215_22282-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAGTTGGAGCTAGATTAATAACGCTAATTCGACTTGAATTAGGACAACCAAGGTCACTCATAGGAAGTGAACAAATTTACAATACAATTGTAACTTCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAAAAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAGGATTTTGACTTCTTCCCCCATCCTTAACTCTACTTCTATCAAATTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7225 Chironominae sp. water mite diet isolate 7225-BHL032417-GBD27521_14117-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGTGCTTGATCAGGTATAGTAGGAACTTCTTTAAGATTATTAATGCGAACGGAATTAGGTCATCCTGGTACATTTATTGATGATGACCAATTTTATAATGTAATTGTTCCTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7227 Chironominae sp. water mite diet isolate 7227-BHL032417-GBD13959_17998-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTATATTTTAATTTTGGAGCTTAGTCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCACCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAACAAATAATATAAGATTTTGATTATTACGACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7228 Lebertia sp. water mite diet isolate 7228-BHL032417-GBD25086_20497-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAGTTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTGATAATCAGAGCCCCAGATATAGCCTTTCCACGAGAAAAAAAAATAAGAATTTGACTTCTTCCCCCATCCTTAACTCTACTTCTATCAAGGTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7229 Chironominae sp. water mite diet isolate 7229-BHL032417-GBD13249_12339-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCACTATATTTTATTTTTGGATCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATGTTAATTCGAACTGAATTATGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACCTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7232 Lebertia sp. water mite diet isolate 7232-BHL032417-GBD12430_12835-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTATTTTGTTTTTGGAGCATGATCCGGAATAGTTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATATAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAAAAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAAAAAATAATATAAGATTTCGGCTTCTTCCTCCATCCTTAACTCTTCTTCTAACAAGTTCCATTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7238 Chironomus sp. water mite diet isolate 7238-BHL032417-GBD6419_12483-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7240 Chironominae sp. water mite diet isolate 7240-BHL032417-GBD13435_4599-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTAGGAGCTTGAGCAGGTATAATAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAATTTTAGAATGTAATTGTTACTGCTCATGCTTTTATTATATTTTTTTTAATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7246 Chironominae sp. water mite diet isolate 7246-BHL032417-GBD12157_7883-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTCTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACCAATATTGGGAGCCCCTGAAAAGGCTTTTCCACCAAAAAATAATATAAGATTTTGATTATTACCACCATCTCTTACCTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7249 Chironominae sp. water mite diet isolate 7249-BHL032417-GBD3607_10407-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTATGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTAGATTATGACCACCAAGGCTTACTTAATTACTTGCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7251 Chironomus sp. water mite diet isolate 7251-BHL032417-GBD17991_14803-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGAGCTTGATCCGGAATAGTGGGAACTTCATCTAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTCC-TAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTGCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7254 Chironomus sp. water mite diet isolate 7254-BHL032417-GBD4495_12925-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTATGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAAGTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTT-TTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTGGTCCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGGTTCTGACTTTTACCCCCCTCTCTTACTCTGCTTCTTGCGAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7256 Chironomus sp. water mite diet isolate 7256-BHL032417-GBD2295_14717-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAAATTTATACATTATTTTGGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGAACAAAATTTATAATGTTGTAGTTACTGCACATGCTTTTTTTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATAGCTTGTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7260 Chironominae sp. water mite diet isolate 7260-BHL032417-GBD13635_22591-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATCTTTTATTTTTGGAGCTTGATCAGGTATAGTAGTAACTTCTTTATGTATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTAGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGAGTTTGATAATTACCACCATCTCTTACTTAATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7261 Chironomus riparius water mite diet isolate 7261-BHL032417-GBD13306_2902-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATCATTTTTGGGGCTTGATCCGGGATAGTGGGAACTGCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGAGACTGCACATGCTTTTATTATAATTTT-TTCATAGTTATACCAATTTTAATTGGAGGATTAGGAAACTGACTTGTCCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7266 Chironominae sp. water mite diet isolate 7266-BHL032417-GBD7896_21410-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAGTTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTCAATTGGAGGATTTTGAAATTTGTTATTACCACTAATATTAGGTGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTACTATCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7268 Psectrocladius sp. water mite diet isolate 7268-BHL032417-GBD29267_14489-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTTTATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAATTTGATTATTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTGCCCCCGTCATTAACTTTACAATTAGCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7274 Chironominae sp. water mite diet isolate 7274-BHL032417-GBD17921_26724-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTTATGACCAATTTTATAATGTAATTGTTACTGCTAATGCTTTTTTTATAATTTTTTTTATAGTAATACCGATTTTAATTGGAGGATTTGGAAATTGGTTATTTCCTCTAATATTAGGAGCTCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7275 Chironominae sp. water mite diet isolate 7275-BHL032417-GBD11944_13277-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCACCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCATGATATGCCTTTTACACGAATAAAAAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7276 Chironominae sp. water mite diet isolate 7276-BHL032417-GBD11796_4897-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGAAATTAGGTCATCATGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGGTACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATTCCTATTTTAATTGGAGGAATTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACGACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7283 Chironominae sp. water mite diet isolate 7283-BHL032417-GBD25138_16865-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGAGCTTGGTCAGGTATTGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCCTGCTTTTATTTTAATTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCTCATGATATGGCATTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7284 Chironominae sp. water mite diet isolate 7284-BHL032417-GBD19363_19504-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTTTTGGTAATGATCAAGTTTATAATGTCATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACCTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7290 Chironomus riparius water mite diet isolate 7290-BHL032417-GBD6984_15895-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGACTTTATACATTATTTTTGGGGCTCGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAACAGAATTAGGACGACCCGTAACTTTCATTGGAGATGACCAAATTTATATTGTTGTAGTTACTGCACATGCTTTTAATATAATTTT-TTCATAGTTATACCAATTTTAATTGAAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7292 Chironominae sp. water mite diet isolate 7292-BHL032417-GBD13461_15406-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTCTTGGAGCTTGATCAGGTATAGTAGGAACTCCTTTAAGTATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATACTGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGTCCCTGATATGGCTTTTCCACGAACAAATAGTATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7293 Chironominae sp. water mite diet isolate 7293-BHL032417-GBD19473_26392-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTATGGAGCTTGATCAGGTATAGTATGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATCGGTGATAACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTATGTACCCCTGATATGGTTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7296 Chironominae sp. water mite diet isolate 7296-BHL032417-GBD11558_27835-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTATTTTTGGAGCTTGATCAGTTATAGTAGGAACTTCTTTAAGACTATTAATCCGAACGGAATTAGGTCATCATGGAACATTTATTGGTGATGTCCAATTTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGACATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCTAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7298 Chironomus sp. water mite diet isolate 7298-BHL032417-GBD26519_21339-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGAAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCAGATGCTTTTATTATAA-TTTTTTCATAGATATACCAATTTTTATTGGAGGATTCGGGAAACTGACTTGTCCCCCTAATACTTGGAGCATCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCTCACTTACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7299 Chironomus sp. water mite diet isolate 7299-BHL032417-GBD12633_9417-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGTACTTCATTATGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTGTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCATCTTCTTGCTAATACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL730 Chironomus riparius water mite diet isolate 730-BHL072216-GBD8375_9501-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTGTTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACATGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTTCTACTATCTAGTTCTTTCGTAGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7302 Chironomus sp. water mite diet isolate 7302-BHL032417-GBD18121_11996-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACACTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGTAACTTTCATTGGAGATGACGAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATATCTTTTCCTCGAATAAATAATATAAATTTCTGACTTTTACTCCCCTATCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7303 Chironominae sp. water mite diet isolate 7303-BHL032417-GBD28168_12356-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGCAGGAAATTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGGTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTTGTTATTACCTCTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAAAAGACTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7305 Chironominae sp. water mite diet isolate 7305-BHL032417-GBD8014_17501-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATCGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAGTACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTAGCACTAATATTAGGAGCACCTGATATGGCTGTTCCACGAATAAGTAATATAAGATTTTGATTATTACCCCCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7308 Chironominae sp. water mite diet isolate 7308-BHL032417-GBD28495_16855-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATCTTTTATTTTTGGCGCTTGATCAGGTTTAGTAGGTACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAACCCCTGATATGGCTTTGCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTGCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7309 Lebertia sp. water mite diet isolate 7309-BHL032417-GBD27142_19669-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATACTTGGAGCTTGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCATTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTTGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGTTATAGCCTTTCCACGAAAAAAAAATATAAGATTTTGACTTCTTCCTCCATCCATAACTCTACTTCTAACAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7312 Chironominae sp. water mite diet isolate 7312-BHL032417-GBD24636_5629-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTTGGAGCTTGCTCAGTTATAGTAGAAACTTCTTTAAGATTATTAATCCGAACGGAATTAGTTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAAGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAGATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7313 Chironominae sp. water mite diet isolate 7313-BHL032417-GBD26574_16506-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTT-GGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTTATCCGGACGGGATTAGGTCATCCTTGAACATTTATTGGTGATGACCAAATTTTTAATGTAATTGTTACTGCTTATGCTTTTTTTATAATTTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACAACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7315 Chironomus riparius water mite diet isolate 7315-BHL032417-GBD22264_14369-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTATGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATATTGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTCATAATTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCGTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7316 Chironomidae sp. water mite diet isolate 7316-BHL032417-GBD28309_11068-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTATATTTTTGGAGCTTGATCAGGTATAGTAGGAATTTCTTTAAGAATATTAATCCGAACGGATTTAGGTCATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.3% identical to accession ID KR167490, identified in GenBank as Tanytarsus mendax. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7317 Chironominae sp. water mite diet isolate 7317-BHL032417-GBD20166_4960-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTGTATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATAGTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGAGTTTGATTATTCCCACCATCTCTTTCTTTATCACTTTCACGAAGAATAGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7318 Chironomus riparius water mite diet isolate 7318-BHL032417-GBD24569_18105-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTTGAGCAGAATTAGGACTACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGACTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTAACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCTTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7320 Chironomus sp. water mite diet isolate 7320-BHL032417-GBD19899_7883-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAGCTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTT-TTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACACTTCTACTATCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7322 Chironomus riparius water mite diet isolate 7322-BHL032417-GBD22103_22387-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTT-GGGGCTTGATCCGGAATTGTGGGAACTTCATTTAGAATGCTTATTTGAGCCGAATTTGGACGACCCAGAACTTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTACTTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7324 Chironominae sp. water mite diet isolate 7324-BHL032417-GBD26205_24472-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTTTTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTCCCACTAATATTAGGAGCCCCTGATATGGCTTCTCCACGAATAAATAATATAAGATTTTGATTAGTACCACCATCGCTAACTTTAGTACTTGCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7325 Lebertia sp. water mite diet isolate 7325-BHL032417-GBD5311_17348-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAGTTGTAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGCCTCACTCCTAGGAAGTTACTCAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGAATAGTTCTACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGAGTTTGACTTCTTCCTCCATCCTTAACTCTACATCGATCAAGTTCCTTTACAGGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7326 Chironominae sp. water mite diet isolate 7326-BHL032417-GBD18699_28782-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTTATTTTTGGAGCTTGATCCGGTATAGTAGGAACTTCATTAAGAATATTAATTCGAACGGAATTAGGCCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTAATTTCTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7327 Cryptochironomus sp. water mite diet isolate 7327-BHL032417-GBD13385_23349-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTTGGAGCTTGATCAGGTATATTAGGAACCTCATTAAGTATATTACTTCTAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACGAAATTTATAATGTAATTGTAACATCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCATTTTTAATTGGAGGATTTGGAAACTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7329 Chironominae sp. water mite diet isolate 7329-BHL032417-GBD9462_25141-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGGCATCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTATTGTTACTGCTTATGCTTTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATAGCATTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7330 Chironomidae sp. water mite diet isolate 7330-BHL032417-GBD22724_9739-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTAGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTAGATTATTTCCCCCGTCATTAACGTTATTATTATCGAGCTCTCTAGTTGAGAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7331 Chironominae sp. water mite diet isolate 7331-BHL032417-GBD18308_19378-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGCCCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATATCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCACTGAGATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCAGCGCTTACTTTATTACTTTCAAGAAGAAGAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7335 Chironominae sp. water mite diet isolate 7335-BHL032417-GBD28108_21376-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAATTGATTATTACCACTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCCTCTCTTACTTTATAACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7338 Chironomus riparius water mite diet isolate 7338-BHL032417-GBD18630_19298-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTATGACGACCCGGAACTTTCCTTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTT-CATTGTTATACCAATTTTAATTGGAGGATTCGGGAACTGACTTGTTCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTGTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7347 Chironominae sp. water mite diet isolate 7347-BHL032417-GBD27803_11711-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTGTGGAGCTTGATAAGGTATAATAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTTCCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7355 Chironominae sp. water mite diet isolate 7355-BHL032417-GBD20724_21125-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGACATCCTGGAACATTTCTTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTAGTTATTACCGCTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCATACTTTATTACATTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7365 Chironominae sp. water mite diet isolate 7365-BHL032417-GBD14600_2743-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCAGTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAAGTAGGTCAGCCTGGAACATTTATTGGTTAGGTCCATATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCACTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7369 Chironomus sp. water mite diet isolate 7369-BHL032417-GBD23328_13872-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGTTTGATCCGGAGTAGTGGGAACTTCATTAAGAATGCTTACTCGAGCGGAATTAGGACGACCCGGAACATTCATTGGAGATGGCCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTT-TTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCAACTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTGCTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL737 Chironomus sp. water mite diet isolate 737-BHL072216-GBD23416_5317-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTTTACATTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTCTTAGTATGCTTATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTAACTGCCCACGCATTTATTATAATTTTTTTCATAGTTATACCAATTCTAATTGGTGGTTTTGGTAATTGACTTGTACCCTTAATATTAGGAGCCCCAGATATGGCTTTCCCCCGAATAAATAATATAAGTTTTAGACCACTTCCCCCTACTCCTACACTTTAACAATCTAGTGCATTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR665396, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7370 Chironomus riparius water mite diet isolate 7370-BHL032417-GBD18213_5424-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGTAACTTTCATTGGAGATGACCATATTTAGAATGGTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCCCCTGACATAGCTTTTCCTCGCATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7380 Chironominae sp. water mite diet isolate 7380-BHL032417-GBD5751_22861-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATGTTATTGTTGAAGCTTGATAAGGTATAGTAGGAACTTCTTTAGGAATATTAATCCGAACGGAATTAGGTGATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTGATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7381 Chironominae sp. water mite diet isolate 7381-BHL032417-GBD24028_12341-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCCTGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCTTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGTTTATTACCACCATCTCTTACTTTACTACTTTCAAGAACAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7382 Chironomus riparius water mite diet isolate 7382-BHL032417-GBD22734_5960-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTATGGGGCTTGATCCGGAATGGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTAAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACCTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7384 Chironomus sp. water mite diet isolate 7384-BHL032417-GBD28021_20209-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATATATTATTTTTGGGGTTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTATTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTGATACTTGGAGCACCTGACATGGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTATTCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7389 Chironominae sp. water mite diet isolate 7389-BHL032417-GBD20774_4205-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTATTTTGGGAGCTTGCACAGGTAGAGTAGGAACTTCTTTAAGAATATTAATCAGCACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATGTTGATTATTACCATCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7396 Chironomus sp. water mite diet isolate 7396-BHL032417-GBD20451_12430-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAGAATTAGGACGACCGGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAA-TTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTGCTTCTATCTAGTACATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7397 Phaenopsectra sp. water mite diet isolate 7397-BHL032417-GBD14529_12482-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTTAGTATATTAATTCGAGCTGAATTAGGTCGCCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTACTTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGTAATTGATTAGTACCTCCAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCTTCTTTAACTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR293527, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7401 Chironominae sp. water mite diet isolate 7401-BHL032417-GBD8346_26209-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATAATTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATATTGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTT-ATAGTAATACCTATTTTAATTGGAGGATTTAGAAATTGGTTATTACCACTAATATTAGGATCCCCTGATATGGCTTTTCCACGAATAAATAATATAGGATTTTGATTATTACCACCATCTCTTACTTTATTACCTTTAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7402 Chironomus sp. water mite diet isolate 7402-BHL032417-GBD16722_8857-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAA-TTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCATCTGACATAGGTTTTCCTCAAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCGCTTACACGACTGCTGTCTAGTTCTTGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7406 Chironominae sp. water mite diet isolate 7406-BHL032417-GBD28217_17798-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGATCTTCTTTAAGAATATTAATCCGAACGGAATTAGGTGATCCTGGAACATTTATTGGTGATGAACAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATGATTTTTTTTTTATCGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCAATAATATTAGGAGCCCATGATATGGCTTTTCCACGAATAAATAATATAAAATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7407 Chironomus riparius water mite diet isolate 7407-BHL032417-GBD16540_4330-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGGTACTGCACATGCTTTTATTATAA-TTTTTTCATAGTTATACCAATTTTAATTGGAGGATTAGGAAACTGACTTGTCCACCAAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCTTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7408 Chironominae sp. water mite diet isolate 7408-BHL032417-GBD13090_2115-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTTAGTATATTAATTCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCATTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTAACTTTATTACTAGCAAGAAGAATAGGAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7412 Chironominae sp. water mite diet isolate 7412-BHL032417-GBD11674_23918-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTTATTCGAACGGAATTAGGTCAACCAAGAACTTTTATTGGTGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCGATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7415 Chironominae sp. water mite diet isolate 7415-BHL032417-GBD18107_22061-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTTAGAATATTAATTCGAACGTAATTAGGTCATCCTGTAACATTTATTGGTGATGACCAAATTTATAATGTCATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGTTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGAGTTTGATTATTACCACCGTCTCTAACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7416 Lebertia sp. water mite diet isolate 7416-BHL032417-GBD5845_20615-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAAATGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGTCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACATCTTCCTCCATCCTTAACTCTACTTCTATCAAGCTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7417 Chironominae sp. water mite diet isolate 7417-BHL032417-GBD26760_20920-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTTTATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTTAGAATATTAATTCGAGCGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTAATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATAATTACTACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7418 Chironomus sp. water mite diet isolate 7418-BHL032417-GBD23579_16724-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATGCTTATTCGCGCATAATTAGGACGACCCGGAACTTTCATTGGAGATAACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTTTTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTGCTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7419 Chironominae sp. water mite diet isolate 7419-BHL032417-GBD5212_7844-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGAATACTTATTCGAACAGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAACATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTATCACCATCTCTTACTTTATTACTTTCAAGAAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7425 Chironominae sp. water mite diet isolate 7425-BHL032417-GBD19528_26658-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTATTTTTGGGAGCTTGATCGGGTATAGGAGGAACTTCTTTAAGAATATTAATCCGAACGAAATTAGGTCATCCGGGAACTTTTATTGGTGATGACAAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCCCTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7428 Chironomus riparius water mite diet isolate 7428-BHL032417-GBD5982_12298-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGTTTGATCCGGAATAGCGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTTTTATAATTTTTTTCATAGTTATACCAATTTAAATTGGAGGATTCGGAAACTGACTTGTCCCTCTGAAACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTATTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7430 Cryptochironomus sp. water mite diet isolate 7430-BHL032417-GBD12518_13411-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACTACCAGGAACTTTTATTGGAGAAGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTAATACTGGGAGCCCCAGATTTAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTAACTCTACTTCTTTAAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7431 Chironomus sp. water mite diet isolate 7431-BHL032417-GBD25724_23431-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTACCTGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTTTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAGTAAATAATATAAGTTTCCGACTTTTACCCCCCGCGCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7432 Lebertia sp. water mite diet isolate 7432-BHL032417-GBD21439_7692-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAGTTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAAATGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATAAAGCTATTCCACGAAAAAAAAAAATAAGATTTTGACTTCTTCCCCCAGCCATAACCCTACTTCTAACAAGGTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7434 Chironominae sp. water mite diet isolate 7434-BHL032417-GBD29402_12686-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTGG-GCTTGATCAGGTATTGTAGGAAATTCTTTTAGAATTTTTATCCGGTCGGGATTTGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACGTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7435 Chironominae sp. water mite diet isolate 7435-BHL032417-GBD21657_23350-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGTTAATGACCAAATTTATAATGTAATTGTTACTGGTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAAATGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGGAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7436 Chironomus sp. water mite diet isolate 7436-BHL032417-GBD18709_21008-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCGGGAACTTTCATTGGAGATGACCAATTTTATATTGTTGTAGTTACTGCACATGCTTTTATTATAATTTT-TTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCCTCTACTTTCCAGTTCTTTCGTAGAGAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7437 Chironominae sp. water mite diet isolate 7437-BHL032417-GBD19027_28390-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACTAAATTTATAATGTAATTGTTACTGCTTATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAAGAGTTGGAAATTGATTATTACCCCTAATATTAGGAGCCCCTGATATGGTTTTTCTACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL744 Chironomus sp. water mite diet isolate 744-BHL072216-GBD23824_12519-Arr96 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTCTTTACATTATTTTTGGTGCTTGATCCGGAATGGTAGGGACTTCTCTTAGTATGCTTATTCGAGCAGAATTAGGACGTACTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACTACCCACGCATTTATTATATTTTTTTTCATAGTTATACCAATTCTAATTGGTGGTTTTGGTAATTGAATTGTACCCTTAATATTAGGAGCCCCAGATAAGACCTTCCCCCGAATAAATAATAAAAGTTTTTGACCTCTTCCCCCTTCTCTTACTCTTTTACTTTCTAGTTCATTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR665396, identified in GenBank as Chironomus maturus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL745 Cricotopus trifasciatus water mite diet isolate 745-BHL040916-GBD8706_25857-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGGACATCTCTAAGAATTTTAATCCGGGCCAAATTAGGACATGCTGGCTCATTAATTGGTGATGATCAAATTTATAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCTCTTACATTATTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KM933933, identified in GenBank as Cricotopus trifasciatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7452 Chironominae sp. water mite diet isolate 7452-BHL032417-GBD5694_24231-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAATGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGTTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTATCACCCCCATCTCTAACTTTATTACTATCAAACAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7462 Chironominae sp. water mite diet isolate 7462-BHL032417-GBD22076_5008-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTGATCCGAACTGAATGAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTAAACTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAGGATTTTGATTATTTCCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7468 Chironomus sp. water mite diet isolate 7468-BHL032417-GBD15101_5178-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTTCACATGCTTTTATTATAATTTTTTTCATAGTTATCCCAATTTTAATGGGCGGATTAGGAAACTGACTTGTCCACCTGATACTTGGATCACCTGACATAGCTTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACTCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7477 Chironominae sp. water mite diet isolate 7477-BHL032417-GBD28436_19642-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTCATCCGAACGGAATTAGGTCATCCTGGAACACTTATTGGTGATGACTAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTGTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTTACCTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7479 Chironomus sp. water mite diet isolate 7479-BHL032417-GBD7825_5041-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATAAAAATTTT-TTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCTTCACTAACTCTTCTTCTTTCAAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL748 Chironominae sp. water mite diet isolate 748-BHL040916-GBD18925_8424-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAAGTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTAACCCTTCTTATTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7482 Chironominae sp. water mite diet isolate 7482-BHL032417-GBD15586_7842-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTTGGAGCTTGATCCGGTATAGTAGGAACTTCTTTAAGAATGTTTATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATATAATTGTTACTGCTCATGCTTTTATTATAAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAGTTGATTAGTACCAATAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTATTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7484 Chironomidae sp. water mite diet isolate 7484-BHL032417-GBD28646_19639-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGATACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTTATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCCCGAATAAATAATATAAGGTTTTGATTACTTCCCCCCGTCATTAAATTGATTATTATCTAGCGCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL749 Psectrocladius sp. water mite diet isolate 749-BHL040916-GBD4178_11109-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCGTAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATGCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7492 Lebertia sp. water mite diet isolate 7492-BHL032417-GBD16437_28970-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTACTTTACTTTTGGAGCATGATCCGGAATAGTTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAAGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAAATGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCTGATATAGCTTTTCCCCGAATAAATAAAATAAGAATTTGGCTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCATTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7498 Chironominae sp. water mite diet isolate 7498-BHL032417-GBD28826_13456-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTT-GGAGCTTGATCCGGTATTGTAGGAACTTCTTTTAGAATTTTTATTCGGACGGTATTTGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTTTAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTAACTTTATTACTTTCAAAAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7499 Chironomus sp. water mite diet isolate 7499-BHL032417-GBD14921_9392-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCAGATGCTTTTATTATAATTTT-TTCATAGTTATACCAATTTTTATTGGAGGATTTGGAAACTGACTTGTTCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGGTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTACTGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7500 Lebertia sp. water mite diet isolate 7500-BHL032417-GBD20790_19526-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCTTGATCCGGAATAGTTGGAGCTAGATTTAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTACTAGGAAGTGACCAAATTTACAATGCAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGGTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAAAAATATAAGAATTTGGCTTCTTCCCCCATCCTTAACCCTACTTCTATCAAGTTGCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7501 Chironominae sp. water mite diet isolate 7501-BHL032417-GBD19116_18684-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAATAATATTAATCCGAACGGAATCAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTAGACATTGGTTATTATCACTAATATTAGGAGCCCCTGAAATGGCTTTTCCATGAATAAATAATATAAGA-TTTGATTATTACCACCATCTCTTGCTTTATTGCTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7503 Chironominae sp. water mite diet isolate 7503-BHL032417-GBD19959_5516-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTATTTTTGGAGCTAGATCAGGTATAGTAGGAACTCCTTTAAGAATATTAATCCAAACGGAATTAGGTCAACCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTGTTCCACGAATAAATAATATAAGATTTTGAATATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7504 Lebertia sp. water mite diet isolate 7504-BHL032417-GBD21408_6738-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAGTTGGCGCTAGATTAAGAATCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATAAAAGATTTTGACTTCTTACCCCATCCTTAACCCTACATCTAACAAGTACCTATACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7505 Chironomus riparius water mite diet isolate 7505-BHL032417-GBD27315_19639-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCATAATTAGGACGAGCCGAAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAA-TTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTCTCTTACTCTACTTCTGTCTAGTTCTTTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7507 Chironominae sp. water mite diet isolate 7507-BHL032417-GBD25271_13571-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTGTATTTTATTTTTGGAGCTTGATCAGGTATAGTAGTAACTTCTTTAAGAATTTTAATTCGAACGTAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGATTTGGAAATTGATTATTACCACTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCACTAACTTTATTACTATCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7508 Chironomus riparius water mite diet isolate 7508-BHL032417-GBD10574_26152-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATGGTGGGAACTTCATTAAGAATGCTTATTCGAGTAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTT-TTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGTAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTGTCTGACTTTTACCCCCCTCTCTTACTCTTCATCATTCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL751 Chironomidae sp. water mite diet isolate 751-BHL040916-GBD18448_21432-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAAAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7510 Chironominae sp. water mite diet isolate 7510-BHL032417-GBD13251_25429-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATGTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTTATGACCAAATTTAGATTGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGGTTATTACCACTAATATTTGGAGCACCTGATATGGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCACCATCTCTTACTTTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7516 Chironomidae sp. water mite diet isolate 7516-BHL032417-GBD28054_12676-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTTCATTATATTTTATTTTTGGAACTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATCACGTAATTGTTACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.0% identical to accession ID GU565708, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7517 Paratanytarsus sp. water mite diet isolate 7517-BHL032417-GBD9372_22210-Ldc29 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGTTCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTAAACCCTTCTTCTATCAAGAAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7519 Dicrotendipes sp. water mite diet isolate 7519-BHL040517-GBD21332_3185-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTAGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCAGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCCTTCTTCTTTCTAGATCAATTGAAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7520 Chironomidae sp. water mite diet isolate 7520-BHL040517-GBD7525_17376-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACAACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTCTCACTCTTTTACTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7521 Paratanytarsus sp. water mite diet isolate 7521-BHL040517-GBD18039_2026-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7522 Chironominae sp. water mite diet isolate 7522-BHL040517-GBD10712_26476-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATGTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCCGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTTATAGTTATGCAAATTTTAATTGGAGCTTTTGGAAATTGGCTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7523 Cryptochironomus sp. water mite diet isolate 7523-BHL040517-GBD25727_14586-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATATCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGTCCCAGATATAGCATTTCCCCCGAATAAATAATATAAGATTTTGACTTTTACCTCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7524 Chironomus sp. water mite diet isolate 7524-BHL040517-GBD18665_9635-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGTCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGCTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCATCTCACATAGCTTTTCCTCAAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACGCTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7525 Cricotopus sp. water mite diet isolate 7525-BHL040517-GBD8426_6616-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7526 Chironominae sp. water mite diet isolate 7526-BHL040517-GBD16498_21238-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAGATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTAGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7527 Chironomus riparius water mite diet isolate 7527-BHL040517-GBD8261_21314-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTAATTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAGTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCGTAGTTATACCAATTTTAATTGTAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGTACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7528 Chironomus riparius water mite diet isolate 7528-BHL040517-GBD14759_2190-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGCACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGTTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATCGGAGGTTTCGGAAACTGACTTGTCACCCTAATACTTGGAGCACCTGACATAGCTTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7529 Chironomus riparius water mite diet isolate 7529-BHL040517-GBD15684_13203-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTTTTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGTTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTATCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL753 Paratanytarsus sp. water mite diet isolate 753-BHL040916-GBD26575_7935-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGAACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCGTTAACCCATTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7530 Chironomus sp. water mite diet isolate 7530-BHL040517-GBD9231_17712-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTT-GGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGACTGCTTATTCGAGCAGGATTAGGACGACCCGAAACTTTTATTGGGGATGACCAAATTTATAATGTTGTAGTTACAGCACATGCTTTTAATATAATTTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7531 Dicrotendipes sp. water mite diet isolate 7531-BHL040517-GBD11722_27072-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7532 Chironomidae sp. water mite diet isolate 7532-BHL040517-GBD2057_15430-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7533 Dicrotendipes sp. water mite diet isolate 7533-BHL040517-GBD27265_15525-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATTCGAGCCTAAGTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7534 Chironomidae sp. water mite diet isolate 7534-BHL040517-GBD21928_11430-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7535 Chironomus riparius water mite diet isolate 7535-BHL040517-GBD17232_15886-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTGTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAAACTTTCATTGGAGATGACAAAATTTATAATGTTGTAGTTACTGCGCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTCTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7538 Paratanytarsus sp. water mite diet isolate 7538-BHL040517-GBD11459_7758-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGCACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGACCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7539 Chironomus riparius water mite diet isolate 7539-BHL040517-GBD20176_17719-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAAAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAAATTATAATGCTGTAATTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTATTTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7540 Chironomus sp. water mite diet isolate 7540-BHL040517-GBD21080_13945-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGATATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7541 Dicrotendipes sp. water mite diet isolate 7541-BHL040517-GBD24403_19231-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAATATACTTATTCGAGCCGAATTAGGTCGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTTATTGTTACAGTTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTAATCTAATTGGAGGTTTCGGAAATTGATTAGTCCCTTTTAATATTAGGAGCACCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7542 Chironominae sp. water mite diet isolate 7542-BHL040517-GBD10241_5628-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATGTTTTATTTTTGGAGCTTGTTATGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGTACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGGCCCAGATATGGATTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7543 Chironomus riparius water mite diet isolate 7543-BHL040517-GBD19835_23875-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGGCTTGATCCGGTATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACTAAATTTATAAGGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTCACATAGCTTTTCCTCAAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7545 Paratanytarsus sp. water mite diet isolate 7545-BHL040517-GBD20201_13624-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATCTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATCGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCCGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7546 Dicrotendipes sp. water mite diet isolate 7546-BHL040517-GBD22749_7031-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGTTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGTTTCGGAAATTGATTAGTCCCTTTTAATATTAGGAGCACCCGATATAGCTTTCCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7547 Chironomus riparius water mite diet isolate 7547-BHL040517-GBD16574_23592-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATGATCTTGTAGTTACTGCACTTGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCAAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCCTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7548 Chironomus riparius water mite diet isolate 7548-BHL040517-GBD25543_16647-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGTCTTGATCCGGAATAGTGGGAACTTTATTAAGAATGCTTATTCGAACAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGATATACCAATTTTAATTGGAGGATTCGGAAACTGACATGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTACTTTCTAGTTCTTTCATAGAAAATGGAGCTGGAACCGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7549 Chironomus sp. water mite diet isolate 7549-BHL040517-GBD8735_9321-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTCCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATCTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCCTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL755 Chironomidae sp. water mite diet isolate 755-BHL040916-GBD21636_21830-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7550 Chironomidae sp. water mite diet isolate 7550-BHL040517-GBD3401_19204-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGCAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7551 Chironomus sp. water mite diet isolate 7551-BHL040517-GBD6320_21786-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAAAGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTTATAGTTATCCCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGA---TTACCCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7552 Cryptochironomus sp. water mite diet isolate 7552-BHL040517-GBD20677_18005-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGCATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACTAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAATTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID KP954643, identified in GenBank as Cryptochironomus fulvus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7553 Paratanytarsus sp. water mite diet isolate 7553-BHL040517-GBD12500_2609-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7554 Dicrotendipes sp. water mite diet isolate 7554-BHL040517-GBD13480_21965-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCGTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCCTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7557 Chironominae sp. water mite diet isolate 7557-BHL040517-GBD9466_8493-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCTATAGTTATACCAATTTTAATTGGAGGGTTCGGAATTTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR692591, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7558 Dicrotendipes sp. water mite diet isolate 7558-BHL040517-GBD19370_27541-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCAAACAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTCCACATGCTTTTATTATAATTTTTTTTTATTGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCCTCTGCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7559 Chironomus riparius water mite diet isolate 7559-BHL040517-GBD21935_8891-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTAGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTGGGAGCACCCGACATAACTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7560 Chironominae sp. water mite diet isolate 7560-BHL040517-GBD23742_12157-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAA-TTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCTTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCCGCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7561 Chironominae sp. water mite diet isolate 7561-BHL040517-GBD11071_3163-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGCCTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7562 Chironomus riparius water mite diet isolate 7562-BHL040517-GBD6771_15018-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGAAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCACGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTTTTACTCCTCTTCTTTCAAGTACTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7563 Chironomus riparius water mite diet isolate 7563-BHL040517-GBD17691_9975-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGATTTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGTGGGTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGATTAAATAATATAAGTTTCTGACTTTTACCTCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7564 Chironominae sp. water mite diet isolate 7564-BHL040517-GBD21181_4359-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTCCATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAACCCCAGATACGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7565 Chironomus riparius water mite diet isolate 7565-BHL040517-GBD20074_4878-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGACTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTGGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTTTTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7566 Chironomus sp. water mite diet isolate 7566-BHL040517-GBD9349_7058-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATACAAGATTTTGACTTCTTCCCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7567 Chironomus sp. water mite diet isolate 7567-BHL040517-GBD19865_14285-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACTTTATTTTTGGGGCTTGATCCGGAACAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGTGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTGCCTCGAATAAAAAATATAAGATTCTGACTTTTACACCCCCCTCTCTTACTCTTCTTCGTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7568 Chironomus sp. water mite diet isolate 7568-BHL040517-GBD24985_20522-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAGATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCATCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGAATATTACCTCCTTCTCTAACCCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7569 Chironomus riparius water mite diet isolate 7569-BHL040517-GBD22888_13280-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATGCGGAACAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACACATCATCATTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL757 Orthocladiinae sp. water mite diet isolate 757-BHL040916-GBD27095_12455-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTAGGAGCTTGATCAGGAATAGTGGGAACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACAACCAGGCTCATTGATCGGAAACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTATTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7570 Chironomus riparius water mite diet isolate 7570-BHL040517-GBD6814_6050-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGACTAGTGGGAACTTCATTCAGAATGCTTATTAGAGCAGTATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGCTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCGTTCGTAGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7572 Psectrocladius sp. water mite diet isolate 7572-BHL040517-GBD7249_16825-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCTGTCACGCCGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCCCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7573 Chironomus riparius water mite diet isolate 7573-BHL040517-GBD9702_16663-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGATCCGGAACTTTCATTGGAGACGACTAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATATTTATACCAATTTTAATTGGAGGATTCGGAAAATGACTTATCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGGACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7575 Chironominae sp. water mite diet isolate 7575-BHL040517-GBD11172_24044-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7576 Paratanytarsus sp. water mite diet isolate 7576-BHL040517-GBD12744_17313-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAAATAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCATCTTTAACTCTTCTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7577 Dicrotendipes sp. water mite diet isolate 7577-BHL040517-GBD13039_18242-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTAGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGTCGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7578 Dicrotendipes sp. water mite diet isolate 7578-BHL040517-GBD11067_9269-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCTTGCTTTTAATATAATTTTTTTTATTGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTTCTGCTTTCTAAATCAATTGTAGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7579 Diaphanosoma sp. water mite diet isolate 7579-BHL040517-GBD7038_26069-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATATTTTATTTTTGGAGTTTGGTCCGGGATAGTTGGAACAGCCCTAAGTATACTTATTCGAGCTGAATTAGGGCAGTGTGGCAGACTTATTGGTGATGACCAAATTTATAATGTTATTGTAACCGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATGCCTATTCTCATTGGTGGCTTTGGTAATTGGCTGGTGCCTTTAATACTAGGTGCCCCTGATATGGCTTTTCCCCGTTTAAACAATTTAAGGTTTTGAATATTACCCCCCTTCTTTAACTCTTCTTTTGGTTGGAAGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID MG449615, identified in GenBank as Diaphanosoma sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7580 Cricotopus sp. water mite diet isolate 7580-BHL040517-GBD21278_20683-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7582 Paratanytarsus sp. water mite diet isolate 7582-BHL040517-GBD6330_6265-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATGCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACATCCAGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTATAGCTCATGCATTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.7% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7583 Chironomus riparius water mite diet isolate 7583-BHL040517-GBD10333_7213-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTTGGAACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAACCTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7587 Chironominae sp. water mite diet isolate 7587-BHL040517-GBD17186_28394-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGACTTTCCCTCGAATAAAAAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7588 Dicrotendipes sp. water mite diet isolate 7588-BHL040517-GBD13815_25908-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACAACCCGGGACATTTATTGGGGATGATCAAATCTACAGTGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATTGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAATCCCTTTAATATTTGGAGCCCCCGATATAGCTTTCCCACGGATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTGCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7589 Chironomus riparius water mite diet isolate 7589-BHL040517-GBD16130_4515-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTGTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGGTATAACAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTGGAAAATGGAGCCGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7592 Chironomidae sp. water mite diet isolate 7592-BHL040517-GBD17280_14449-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGACATGCAGGCTCATTAATTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGGTTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7593 Paratanytarsus sp. water mite diet isolate 7593-BHL040517-GBD27096_21427-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAATTCGAGCAGAATTAGGGCACCTTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGTGTGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATGGTTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7594 Chironomus sp. water mite diet isolate 7594-BHL040517-GBD11957_15640-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATATTTTATTTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7595 Chironomidae sp. water mite diet isolate 7595-BHL040517-GBD13594_21159-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCAAATAAATAATATAAGATTTTGATTATTACCCCCTTCATCAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7596 Chironomidae sp. water mite diet isolate 7596-BHL040517-GBD27307_9210-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGTTGATTTAGGTCACCCAGGTACATTAATTGGTGACGACCAAATTTATAATGCAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATCCCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCGCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7597 Chironomus sp. water mite diet isolate 7597-BHL040517-GBD6002_22041-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCTGAAACTGAATTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAACAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7598 Chironomus sp. water mite diet isolate 7598-BHL040517-GBD4877_6760-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGGGCTTGATCCGGAATAGTGGGTACTTTCTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACATGTCCTCCTAATACTTGGAGCACTTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCAAGTTCTTTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7599 Cryptochironomus sp. water mite diet isolate 7599-BHL040517-GBD24992_13710-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATATCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGTCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL760 Cricotopus sp. water mite diet isolate 760-BHL040916-GBD9903_15010-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATGAGGAATAGTAGGGACATCTCTAAGATTTTTAATCCGGGCCGAATTAGGACATGCTGGCTCATAAATTGGTGATGATCAAATTTATAATGTGATTGTTACAGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGTTCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTAACTACTTCCCCCTTCACTTACATTATTACTATCAAGTTCAATAGTAGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KM933933, identified in GenBank as Cricotopus trifasciatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7600 Chironomidae sp. water mite diet isolate 7600-BHL040517-GBD9112_16414-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACTTTATACATTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAAGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTTTAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCATGATATAGCTTTTCCTCGAATAAATAATGTAAGTTTCTGATTACTTCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7601 Chironomus riparius water mite diet isolate 7601-BHL040517-GBD26215_21586-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACATCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACTAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTCCCCCCCTCTCTTACTCCTCTACTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7602 Chironomidae sp. water mite diet isolate 7602-BHL040517-GBD7870_12382-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAATAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATCCCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR278209, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7603 Chironomus riparius water mite diet isolate 7603-BHL040517-GBD4068_22285-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCTTTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAAGTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCCTCTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7604 Chironomus riparius water mite diet isolate 7604-BHL040517-GBD19437_6025-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACTAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTAAAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATCTAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTCCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7605 Chironominae sp. water mite diet isolate 7605-BHL040517-GBD9798_17408-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGGGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTACTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTATCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7606 Chironomus riparius water mite diet isolate 7606-BHL040517-GBD10747_6415-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTTATTAAGAATGCTTATTCGAGCAGAATTAGGATGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTAAATTGGAGGATTCGGAAACTGACATGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTATCTAGGTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7607 Chironomus sp. water mite diet isolate 7607-BHL040517-GBD10408_16219-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTACTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCAGCCGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7609 Chironomus riparius water mite diet isolate 7609-BHL040517-GBD7785_5860-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGTAACAGTGGGAACTTCATTAAGAATGCTTATTCAAGCAGAATTAGGACAACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATGGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGTACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7610 Chironomus sp. water mite diet isolate 7610-BHL040517-GBD25755_10538-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTT-GGGGCTTGATCCGGAATAGTGAGAACTTCATTACGACTGCTTATTCGAGCAGAATTCGGACGACCCGGAACTTTCATTGGGGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTTATATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGTGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7612 Chironomus riparius water mite diet isolate 7612-BHL040517-GBD15564_3134-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAAGTAGGACGACCCTGAACTTTCATTGGAGATGACCAAATTTATAATGTTATAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGCAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7613 Paratanytarsus sp. water mite diet isolate 7613-BHL040517-GBD24415_19883-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGGGCCTGATCGGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCGTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTACTGCCTTTATTATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7614 Chironomus sp. water mite diet isolate 7614-BHL040517-GBD18106_27900-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAACAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTTTCATATTTATACCAATTTTAATTGGAGGATTCGGAAACTTACTTGTCCCTCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7616 Cryptochironomus sp. water mite diet isolate 7616-BHL040517-GBD11980_8855-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATATCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGTCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTAAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KJ207490, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7617 Chironomus riparius water mite diet isolate 7617-BHL040517-GBD12173_19440-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTTAGAATGCTTATTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTTTCCCACTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7618 Chironomus riparius water mite diet isolate 7618-BHL040517-GBD13135_24099-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGACTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATATATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAG-TTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTGCCCCCCTCTCTTACTCATCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7619 Chironomus riparius water mite diet isolate 7619-BHL040517-GBD18783_21855-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAGCTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGTAGAATTAGGACAACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCCTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7621 Chironomidae sp. water mite diet isolate 7621-BHL040517-GBD24160_24248-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGTATGGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACACTTTTACTTGCAAGTTCTATTGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7622 Chironomus riparius water mite diet isolate 7622-BHL040517-GBD26735_22012-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTCACATAGGTATTCCTCAAAAAAATAATATAAGTCTCTGAATTTTACCCCCCCTCTCTTACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7623 Orthocladiinae sp. water mite diet isolate 7623-BHL040517-GBD8071_21790-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTGGGCACTTCTTTAAGAATTTTAATTCGGCTAGAATTAGGACACCCAGGCTCATTGATCGGAGACGACCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTAATGCCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCCTTGATATTAGGAGCCCCTGATATAGCTTTTCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR291435, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7624 Chironomus riparius water mite diet isolate 7624-BHL040517-GBD3102_15360-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGTATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTATAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATCTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATTCTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAATTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7625 Chironomus riparius water mite diet isolate 7625-BHL040517-GBD20143_5932-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGTAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACCTGACAAAGCTTTTCCTCGAATAAAAAATATAAGTTTCTGACTTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTACGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7626 Chironomus sp. water mite diet isolate 7626-BHL040517-GBD8599_8290-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTGTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACACAGCCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTGCTTTCTAGATCAATTGTAAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7627 Chironomus riparius water mite diet isolate 7627-BHL040517-GBD27360_11862-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACCTTATTGTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTAGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7629 Dicrotendipes sp. water mite diet isolate 7629-BHL040517-GBD12115_23660-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTATGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCATGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7630 Chironomus riparius water mite diet isolate 7630-BHL040517-GBD23750_21152-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTATGACTGCTTATTCGCGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACTAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTGTCTGACTTTTACCCCCCATCTCTTACTCTGCTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7631 Chironomus sp. water mite diet isolate 7631-BHL040517-GBD9591_8060-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGCCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACACGCTTTTATTATAATTTTTTTTCATGGTTATATCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGTCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7632 Chironomus riparius water mite diet isolate 7632-BHL040517-GBD24879_6524-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGTAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTCCACATGCCTTTATTATAATTTTTTTCATAGTAATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCCCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTACTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7633 Dicrotendipes sp. water mite diet isolate 7633-BHL040517-GBD9861_27523-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTTTATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGGTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGGTTCGGAAATTGATTAGTCCCTTTTAATATTAGGAGCACCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCCTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7634 Chironomus riparius water mite diet isolate 7634-BHL040517-GBD24508_23697-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGAACGCCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCGCTTACTCTACTTCTTTCTAGTTCTTTCGTATAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7635 Dicrotendipes sp. water mite diet isolate 7635-BHL040517-GBD21183_12145-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAAAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGATGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7639 Chironomidae sp. water mite diet isolate 7639-BHL040517-GBD18217_4927-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTAATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGTAACATTAATTGGTGACGACCTAATTTATAATGTAATTTTTACAGCCCATGCTTTTATGATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGCGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7640 Cryptochironomus sp. water mite diet isolate 7640-BHL040517-GBD21833_7431-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAACTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATATCAATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7641 Chironomus sp. water mite diet isolate 7641-BHL040517-GBD9421_5137-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTGTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGACTGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTTCCCCTAATACTAGTAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTGCTAGTTCGTGCGTAGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7643 Chironomidae sp. water mite diet isolate 7643-BHL040517-GBD16637_12836-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCTTTAAGAATATTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAAATTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTTGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTATCTAGTTCAATTGTAGAAAATGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7644 Chironomus sp. water mite diet isolate 7644-BHL040517-GBD11496_22623-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGTATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATCGGAGATGATCAAATTTATAATGTTGTAGTTACTCCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGGAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCACTTACTCTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7645 Chironomus sp. water mite diet isolate 7645-BHL040517-GBD13190_6499-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGGGACTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACTAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACAATTACCTCCTTCTCTAACCCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7647 Chironomus riparius water mite diet isolate 7647-BHL040517-GBD22551_7358-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTTGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAACAGGGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCCAATAAATAAAATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTATTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7649 Chironomus riparius water mite diet isolate 7649-BHL040517-GBD16680_19935-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGACTTTATACATTATTTTTGGGTCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCATAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATCTTTTTCATAGTTATACCAATTTTAATTGGAGGTTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTACTGACTTTTACCCCCCCCCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7652 Chironomus riparius water mite diet isolate 7652-BHL040517-GBD20525_12626-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTGTACATTATTTCTGGGACTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGATGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAG-TTTTCCTCAAATAAATAATATAAGTTTCCGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7653 Chironominae sp. water mite diet isolate 7653-BHL040517-GBD27645_13274-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGAGCTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCTTACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7654 Chironomus sp. water mite diet isolate 7654-BHL040517-GBD22870_7497-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGGAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTCCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTTTCCCCCTAATACTTGGAGCACCTGACAAAGCCTTTCCCCGAAAAAATAATATAAGTATCTGACTTTTACCCCCCCTCTCTAACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7655 Chironomus riparius water mite diet isolate 7655-BHL040517-GBD21645_14701-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCACGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCAGCCTCCTTCTAGTACGTGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7659 Chironomus sp. water mite diet isolate 7659-BHL040517-GBD7074_13659-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCAAGCTGAACTAGGACATCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATATTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGCTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7662 Chironomus sp. water mite diet isolate 7662-BHL040517-GBD4233_7523-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCAATTTCGGTGCCTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACGTTTACCCCCCCTCGCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGTAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7664 Chironomus riparius water mite diet isolate 7664-BHL040517-GBD7500_20629-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATTCTTATTCGAGCAGAATTAGGACGCCCCGGAACTTGCATTGGAGATGAACAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7665 Dicrotendipes sp. water mite diet isolate 7665-BHL040517-GBD15955_26845-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTAGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGAAGACCCGGGATATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGTTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGTTTCGGAAAATGATTAGTCGCTTTTAATATTAGGAGCACCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7667 Cryptochironomus sp. water mite diet isolate 7667-BHL040517-GBD14143_26781-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCCTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGATGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATATCAATTTTAATTGGAGGATTCGGAAATTGATTGGTACCTCTTATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAACAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7668 Chironomus riparius water mite diet isolate 7668-BHL040517-GBD9246_18958-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGAGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTATTTTCATAGTAATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGGATAAAAAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7669 Dicrotendipes sp. water mite diet isolate 7669-BHL040517-GBD11207_11075-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATCTTTAGAGCTTGATCAGGAATAGTATGAACTTCTTTAAGTATACTTATTCGAGCCGAATTAGGACGAACCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTATTCCCTTTAATATTAGGATCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTACTTCTCTAACCCCTTCTTCTTTCTAGATCAATTGTAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL767 Paratanytarsus sp. water mite diet isolate 767-BHL040916-GBD23852_4343-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTATGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGTTCAAATCTTTAGTGTTATTGTTACAGTTCATGCTTTTATTATAATTTTTTTTATAGTTATATCTATTTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7670 Chironomus riparius water mite diet isolate 7670-BHL040517-GBD27620_11305-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACTAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTAGTTCCCCTAATACTTGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7672 Chironomus riparius water mite diet isolate 7672-BHL040517-GBD7656_16846-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTACGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATTGTTATACCAATTTAAATTGGAGGATTCGGAAACTGACTTTTCCCCCGAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTGCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7673 Cryptochironomus sp. water mite diet isolate 7673-BHL040517-GBD27123_16060-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTTATTTTTGGAGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTAACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTATTACCTCTTATACTGGGAGTCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGGTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7674 Dicrotendipes sp. water mite diet isolate 7674-BHL040517-GBD10012_16387-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATTGTTATACCCATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAACCCCCGATAAAGCCTTCCCACGAATAAATAATATAAGTATCTGACTATTACCTCCTTCTCTAACCCTTCTGCTTTCTAGATCAATTGTAGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7676 Chironomus riparius water mite diet isolate 7676-BHL040517-GBD18027_7087-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTAGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGACGACCAAATTTATAATGTTGTAGTTACTGCACATGCCTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCGTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCCTCTCTTACTCCTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7677 Chironominae sp. water mite diet isolate 7677-BHL040517-GBD27016_9965-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTCTGATTACTCCCACCTTCTCTTACTCTATTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR670143, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7679 Paratanytarsus sp. water mite diet isolate 7679-BHL040517-GBD19775_19042-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACCTCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCAACTTTAACCCTTCATCAATCAAGAAGATTAGTGGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7682 Chironominae sp. water mite diet isolate 7682-BHL040517-GBD8194_20216-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGTGCCTGATCGGGTATAGTAGGGACATCCCTAAGAATACTAATTCATGCTTAATTCGGTCGACCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR670143, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7685 Dicrotendipes sp. water mite diet isolate 7685-BHL040517-GBD25017_4949-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCGGAATTAGGACGACCCGGGACATTTATTGGAGATGATAAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTAGAGTATTGGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATACTATAAGTTTCTGACTATTACCTCCTTCTCTAACCCCTTCTTCTTGCTAAATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7689 Paratanytarsus sp. water mite diet isolate 7689-BHL040517-GBD16401_22429-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTCCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAAATTTTTTTCATAGTTATACCTATTTTAATTGGAGCTTTTGGAAATTGACTTATT-CCTTTAATGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7690 Chironomidae sp. water mite diet isolate 7690-BHL040517-GBD24594_4807-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTTGGGGCCTGATCGGGGATAGTAGGGATTTCTCTAGGAATACTAATTCGTGCTGAATTAGGTCACCCAGTAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGACCATGTTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7691 Dicrotendipes sp. water mite diet isolate 7691-BHL040517-GBD19610_19108-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7692 Chironomus riparius water mite diet isolate 7692-BHL040517-GBD16581_8676-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGTCCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCATTTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACACTACTTCTATCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7694 Dicrotendipes sp. water mite diet isolate 7694-BHL040517-GBD13920_18779-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGTCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAACTCTACAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTATTACCTCCTTCTCTAACTCTTCTTCTTTCTAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7696 Chironomidae sp. water mite diet isolate 7696-BHL040517-GBD21216_16558-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTTGGGGCCTGATCGGGAATAGTAGGGACATCTCTAAGATTACTATTTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGGGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTTATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7697 Chironomus riparius water mite diet isolate 7697-BHL040517-GBD4447_21605-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTACACATTATTTTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTAATTGGAGATGACCAAATTTATATTGTTGTTGTTACTGCACATGCTTTTCTTATAAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7698 Dicrotendipes sp. water mite diet isolate 7698-BHL040517-GBD4396_9327-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTCATTTTTGGTGCCTGATCAGGAATAGTGGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGAAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTATATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7701 Chironomus riparius water mite diet isolate 7701-BHL040517-GBD16965_25199-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACGTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACAACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATATCAATTTTAATTGGTGGATTTGGAAACTGACTTGTCCCTCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAAAATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7702 Dicrotendipes sp. water mite diet isolate 7702-BHL040517-GBD3479_14765-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGATTAGAGGGAATTTCCTTAAGTATACTTATTCGAGCCGAATTGGGAAGACCCGTTACATTTATTGGAGATGATCAAGTCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7703 Chironomus riparius water mite diet isolate 7703-BHL040517-GBD21134_9293-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTTGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAACTTTATAATGATGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCCATAGTTATACCAATTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTGCTGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7704 Dicrotendipes sp. water mite diet isolate 7704-BHL040517-GBD8681_5873-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCCTTAAGTATATTTATCCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCCACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7708 Chironomus riparius water mite diet isolate 7708-BHL040517-GBD13993_27879-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGGATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATTAATTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCTCCCTTACCCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7710 Dicrotendipes sp. water mite diet isolate 7710-BHL040517-GBD8975_25786-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCTAATTAGGACGACCCGGGACATTTATTGGAGATGATCGAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATTGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTTCCTCCTTCTCTAACCCATCTGCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7713 Chironomus riparius water mite diet isolate 7713-BHL040517-GBD18176_16739-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAGTTAGGACGACCCGGAACTTTCATTGGATATGACCAAATTTATAATGTTGTAATTATTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7715 Chironomus riparius water mite diet isolate 7715-BHL040517-GBD20663_25256-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACCTTATTTTTGGGGCTTGATCCGGAATAGTGGTAACTTCATTAAGAATTCTTATTCGAGCAGAATTAGTCCGACCCGGAACTTTCATTGGAGATTACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7716 Dicrotendipes sp. water mite diet isolate 7716-BHL040517-GBD9936_12427-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGTTCATGCTTTTATTATAATTTTTTTTTTATGGTGATACCTATTCTAATTGGAGGTTTCGGAAATTGATTAGTCCCTTTAATATTGGGAGCACCCGATATAGCATTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTACTATTATCTAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7717 Dicrotendipes sp. water mite diet isolate 7717-BHL040517-GBD27088_10234-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGCCCCGGGACATTTATTGGAGATGACCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTAATGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAAAATAAGTTTCTGACTATTACCTCCCTCTCTAACCCCTACTACTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7719 Chironomidae sp. water mite diet isolate 7719-BHL040517-GBD12258_25830-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACTTCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGATTTTATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGGATAAATAATATAAGTTTCTGATTACTCCCTACTTCTCTTTCTCTATTACTGTCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL772 Leucophenga sp. water mite diet isolate 772-BHL040916-GBD12814_10547-Ldc69 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTTTATTTTATATTTGGAGCATGAGCAGGAATAGTCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGCGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAATAATATAAGTTTTTGACTTCTTCCTCCTTCACTTACACTATTATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.3% identical to accession ID JX887648, identified in GenBank as Leucophenga sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7720 Chironomus sp. water mite diet isolate 7720-BHL040517-GBD8373_25345-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTGTTGGGGCTTGATCAGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGTGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7721 Dicrotendipes sp. water mite diet isolate 7721-BHL040517-GBD11722_13289-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTCCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGTTCATGCTTTTATTATAATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGTTTCGGAAATTGATTAGTCCCTTTTAATATTAGGAGCACCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTGGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7722 Chironominae sp. water mite diet isolate 7722-BHL040517-GBD29387_17717-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGTCCACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCATACGCTTTTATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCCTTTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7724 Chironomus riparius water mite diet isolate 7724-BHL040517-GBD10488_13728-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCGTTGGAGATGACTAAATTTTTATTGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGAAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGCTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7726 Chironominae sp. water mite diet isolate 7726-BHL040517-GBD14389_26457-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGTAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAACAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTCTTCCTTTAATTTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTATTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7727 Dicrotendipes sp. water mite diet isolate 7727-BHL040517-GBD7131_25376-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCCGGAATAGTAGGAACTTTCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAAAAAATAATATAAGTTTCTGCCTATTACCTCCTTATCTAACTCTTCTTCTTTCTAAATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7729 Dicrotendipes sp. water mite diet isolate 7729-BHL040517-GBD19372_2139-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAGTCTACAATGTAATTGTTACAGCTCATGCTTTTCTTATAATTTTTTTTTATGGTTATACCTATTCTAGTTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCACTAACCCTACTTCTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7734 Chironomus riparius water mite diet isolate 7734-BHL040517-GBD3489_20431-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGTAATAGTGGGAACTTCATTAATAATGCTTATTCGAGCAGAATTAGTACGACCCAGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGGTATACCAATTTTAATTGTAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGTAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7735 Chironomus riparius water mite diet isolate 7735-BHL040517-GBD17456_2022-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCTGGTATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACTAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7737 Chironomus riparius water mite diet isolate 7737-BHL040517-GBD13280_28031-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTATATACATTATTTTTGGGGCTTGATCCGGGATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTCTTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACGTTTACCCCCCTCTCTTACTCTTCTTCGTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7739 Chironomidae sp. water mite diet isolate 7739-BHL040517-GBD19916_14485-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACTTCCCTAAGAATACTAATTCGTGCTGAATTAGGACACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAAATTTTTTTATAGTTATACCAATTTTTAATTGGAGGATTCGGAAATTGACTATTTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCCCCTTCTCTTACTCTTTTACTTTCTAATTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7742 Dicrotendipes sp. water mite diet isolate 7742-BHL040517-GBD13545_26234-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTATGAACTTCCTTTAGTATACTTATTCGAGTCGTATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAGTGTAATTGTTACAGTTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGTTTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCACCCGATATAGCTTTCCCACGATTAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7743 Chironomidae sp. water mite diet isolate 7743-BHL040517-GBD13654_14559-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAGTTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAACTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTTATAGTTATACCAATTTTAATCGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCGTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.4% identical to accession ID KR658416, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7746 Chironomidae sp. water mite diet isolate 7746-BHL040517-GBD28092_17967-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTTGGTGCCTGATCGGGGTTAGTAGGGACGTCCCTAAGATTACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATCATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTATCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGATGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7747 Chironomus riparius water mite diet isolate 7747-BHL040517-GBD27095_19275-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGCGATGACCAAATTTACAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGTTTCGGAAACTGACTTGCCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7751 Dicrotendipes sp. water mite diet isolate 7751-BHL040517-GBD18258_13037-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTTTTCGAGCCGAATTAGGACGACCCGGGACATATATTGGAGATGCTCAATTCTACAATGTAATTGTTACAGCTCATGCTTTTTTTATATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACTCTTCTTCTTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7756 Chironomus riparius water mite diet isolate 7756-BHL040517-GBD19349_9942-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACCTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGGTGTAGTTACCGCACATGATTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCTCCCTAATACTTGGATCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7758 Chironomus riparius water mite diet isolate 7758-BHL040517-GBD15443_13021-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATGCGGAATAGTGTGAACTTCATTAGGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTTTTAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAGTACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7762 Dicrotendipes sp. water mite diet isolate 7762-BHL040517-GBD8712_13630-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGAACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAAATTTTTTTATGGTTATACCTATTTTAAATGGAAGATTCGGAAATTGATTATTCCCTTTAATATTAGGTGCCCCCGATATAGCTTTCCCACGAATAAAAAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTTCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7766 Dicrotendipes sp. water mite diet isolate 7766-BHL040517-GBD18973_22069-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTTATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGTTCATGCTTTTATTATAATTTTTTTTTTATTGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAACTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCGCCTTCTCTAACCCTGCTGCTATCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7769 Dicrotendipes sp. water mite diet isolate 7769-BHL040517-GBD6341_10387-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGCGCCGAATTCGGACGACCCAGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTATGAGCCCCCGATACAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTGCTTCTTTCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7770 Chironomus riparius water mite diet isolate 7770-BHL040517-GBD19864_24051-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTATGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAAATTTCATTGGAGATGAACAAATTTATAATGGTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATATTAATTGGAGGATTCGGAAACTGACTTGTCACCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7772 Chironomus sp. water mite diet isolate 7772-BHL040517-GBD27769_12992-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTT-GGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGACTGCTTATTCGAGCAGCATTAGGACGACCCGGAACTTTCATTGGGGATGACCAAATTTTTAATGTTGTAGTTACTGCACTTGCTTTTAATATAATTTTTTTCATAGTTATATCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCCTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7778 Chironomidae sp. water mite diet isolate 7778-BHL040517-GBD14613_5415-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGGGCTGAATTAGGTCACCCATGAACATTAATTGGTTACGACCTAGTTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTTATAGTTATACCAATTTCAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGAAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7780 Chironomus sp. water mite diet isolate 7780-BHL040517-GBD11330_20233-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGTCGACCCGGAACTTTCATTGGAGATGTCCAAATTTATAATGTTGTAGTTACTGCAGATGCTTTTATTATAAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACACTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7787 Chironomus sp. water mite diet isolate 7787-BHL040517-GBD15943_28263-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTT--GGGGCTTGATCCGGAATAGTGGGAACTTCATTCAGACTGCTTATTCGAGCAGCATTAGGACTACCCGGAACTTTCATTGGGGATGACCAATTTTATAATGTTGTAATTACTGCACATGCTTTTAATATAATTTTTTTCATAGTTATACCAATTTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7791 Chironomus sp. water mite diet isolate 7791-BHL040517-GBD6983_21131-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGAGTTTGTTCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCTCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7795 Dicrotendipes sp. water mite diet isolate 7795-BHL040517-GBD6535_7431-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATATTTATTCGAGCCGGATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGCAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7796 Dicrotendipes sp. water mite diet isolate 7796-BHL040517-GBD24106_18486-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTACTTTATTTTTAGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATTTAAAATGTTATTGTTACAGCTCATGCTTTTATTATAAATTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCCGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAAAAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7799 Chironomus riparius water mite diet isolate 7799-BHL040517-GBD22829_20164-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATTCATTATTTTTGGTGCTTGATCCGGAATAGTGAGAACTTCATTAAGAATGCTTATTAGAGCAGAATTAGGACGACCCGGAACTTTCATTGAAGATGACCAAATCTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAACTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7801 Chironomus riparius water mite diet isolate 7801-BHL040517-GBD16509_5791-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTAGGACACTGACTTGTCCCCCTAATACTTGGAGCACCTCACATAGTTTTTCCTCGAATAAATAATATAAGTTTCTGAATTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7802 Diptera sp. water mite diet isolate 7802-BHL040517-GBD17860_19471-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACACTTTATTTTATATTTGGAGCATGAGCAGGAATAATCGGAACTTCTCTAAGAATTTTAATTCGTGCTGAATTAGGACACCCTGGAGCATTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCATGCATTTGTAATAATTTTTTTTTATAGTTATACCAATTATAATTGGTGGATTCGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCCTTTCCACGAATAAACAATATAAGGGTTTGACTTCTTCCTCCTTCACTTACACTAGCATTAGTAAGAAGTATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 88.6% identical to accession ID KC292439, identified in GenBank as Leucophenga sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7803 Chironominae sp. water mite diet isolate 7803-BHL040517-GBD10252_25959-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCAGGAACATTAATTGGTGACGACCAATTTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGCTTCAGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR658416, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7804 Chironomus sp. water mite diet isolate 7804-BHL040517-GBD9381_27315-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGGAACTTCATTAAGATTTCTTATTCGAACGGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCATTTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCTCTCTTACTCCACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7806 Chironomus riparius water mite diet isolate 7806-BHL040517-GBD26819_23428-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTGATTGGAGATGAGCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTCATTGTAGGATTCAGAAACTGACTTGTCTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7811 Dicrotendipes sp. water mite diet isolate 7811-BHL040517-GBD17320_5619-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCCTTACATTTATTGGATATGGTCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATGAGGAGCTCCCGATATAGCTTTCCCACGAATAAATAATAAAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7813 Chironomus sp. water mite diet isolate 7813-BHL040517-GBD23970_19743-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTT--GGGGCTTGTTCCGGAATAGTGGGAACTTCTTTATGACTGTTTATTCTAGCAGAATTATGACGACCCGGAACTTTCATTGGGGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTAATATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGTCATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7818 Dicrotendipes sp. water mite diet isolate 7818-BHL040517-GBD24473_17305-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTAGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGGCACGGGACATTTATTGGAGATGATCAAATCTACAATGTACTTGTTACAGCTCTTGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAAATGGTGGATTCGGAAAATGATTATTCCCTTTAATATTAGGAGCTCCCGATATAGCTTTCCCACGAAAAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7820 Chironominae sp. water mite diet isolate 7820-BHL040517-GBD17142_3825-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCTTTAAGTAGGCTAATTCGAGCAGAACTTGGACTACCTGGTACTTTTATTGGAGATGACCTAATTTACAAGGTAATTGTCACAGCAGACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7824 Dicrotendipes sp. water mite diet isolate 7824-BHL040517-GBD3324_16374-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCAAGCCGAATTAGGACGACCCGGTTCATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCGCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTACTTCTTTCTAAATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7828 Chironomus riparius water mite diet isolate 7828-BHL040517-GBD7843_25338-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGAGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCTCCTAATACTTGGAGCACCTCACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7830 Chironominae sp. water mite diet isolate 7830-BHL040517-GBD20867_20245-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCTTTAAGTATGCTAATTCGAACAAAATTTGGACAACCTGGTACTTTAATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACACTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7831 Chironominae sp. water mite diet isolate 7831-BHL040517-GBD14905_26230-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAACAGTACTTGGACGACCTTGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTTTTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCAAATAAATAATATAAGTTTTTGACTTCTTCCCCCTCCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7832 Chironomus riparius water mite diet isolate 7832-BHL040517-GBD22322_13387-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATCTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCATTTTTAATTGGAGGATTCGGAAACTGATTTGGCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACGCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7835 Chironomus sp. water mite diet isolate 7835-BHL040517-GBD24555_6936-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTT-GGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGACTTCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTTGGGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTAATATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCGTCTTCTTTCTAGTACTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7836 Chironomus riparius water mite diet isolate 7836-BHL040517-GBD22039_22099-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGTCTTGATCCGGAATAGTGGGAACTTCACTAAGAATGCTTATTAGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAAATTTAATTCGAGGATTCGGAAACTGACTTGTCCCCCTAATACCTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7837 Chironomus sp. water mite diet isolate 7837-BHL040517-GBD6428_18352-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTTAGAATGCTTATTCGAGTAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATATTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTTGTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7839 Chironomus riparius water mite diet isolate 7839-BHL040517-GBD7269_24045-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAATACTGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTAATATAATTTTTTTCATAGTTATACCAATTTAAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTAACCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7840 Dicrotendipes sp. water mite diet isolate 7840-BHL040517-GBD14225_9132-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCCGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACCGCTCATGCTTTTATTATAATTTTTTTGTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTGCTCTAACCCTGCTGCGTTCTAGAGCAATTGTAGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7843 Chironomidae sp. water mite diet isolate 7843-BHL040517-GBD6123_7947-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACTTCCTTAAGAATTTTAATTCGTGCTGAATTAGGTCACCCTGGATCATTAATCGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTGTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7847 Chironomidae sp. water mite diet isolate 7847-BHL040517-GBD21078_25987-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTTGGGGCCTGCTCGGTGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTGTAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGGTTCTGATTTCTCCCTCCTTCTCTTTCTCCTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7848 Chironomus riparius water mite diet isolate 7848-BHL040517-GBD26601_6848-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAGCTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTCTATTATAATTTTTTTCATAGTTATACCAATGTTAATGGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTACCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7851 Chironomus riparius water mite diet isolate 7851-BHL040517-GBD28879_18543-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATGCGGTATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATCGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACAGAGCTTTTCCTCGAAGAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7854 Dicrotendipes sp. water mite diet isolate 7854-BHL040517-GBD17253_16820-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTTTATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGAGATTTATTGGAGATGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTAATACCAATTATAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACTCTACTTCTTTCTAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7857 Chironomidae sp. water mite diet isolate 7857-BHL040517-GBD16454_2840-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGGGGTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACTAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTACGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTATCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.8% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7860 Chironomus riparius water mite diet isolate 7860-BHL040517-GBD25335_11823-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACACTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTCTCATTGGAGATGACCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTCTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAGTAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGGAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7867 Chironomus riparius water mite diet isolate 7867-BHL040517-GBD5034_6582-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGCATAGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATCTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTCACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7870 Chironomus riparius water mite diet isolate 7870-BHL040517-GBD18727_22621-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATATTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCATTTTTAATTGGATGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTCACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCCGCTTCTTTCTAGTTCCTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7871 Dicrotendipes sp. water mite diet isolate 7871-BHL040517-GBD28106_21803-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCATTAAGTATACTTATTCGAGCCGAATTAGGACGACCCTGGACATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACAGTTCATGCTTTTATTATAATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGTTTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7873 Chironominae sp. water mite diet isolate 7873-BHL040517-GBD26185_8880-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTTGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGTTACTTTTATTGGAAATGACCAAATTTATAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTGTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACGCTTTGACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7874 Chironomidae sp. water mite diet isolate 7874-BHL040517-GBD10279_15709-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACAACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGGGTCGGAAATTGAATTTTACCTTTAATATTAAGAGCCCCTGATATAGCTTTTCCTCCGATAAAAAATAAAAGTTTCTGATTACTCCCTCCTTCTCCTTCCCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7877 Dicrotendipes sp. water mite diet isolate 7877-BHL040517-GBD1915_16674-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCGTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGATCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAGTTGTTACAGCTCATGCTTTTATGATAATTTTTTTTTATTGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAACTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAGCCCTTCTGCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7880 Chironominae sp. water mite diet isolate 7880-BHL040517-GBD13006_28159-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGAACTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTATAGTGATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTAACTTCTTCCCCCTTCATTAACTCTTTTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7884 Chironomidae sp. water mite diet isolate 7884-BHL040517-GBD15000_8386-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATCTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCTCTAAGAATACTAATTCGTGCTGAATTATGTCACCCAGGAACATTTATTGGTGATGACCAAATTTATAATGTTATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTGGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTTCCCCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGTTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7886 Dicrotendipes sp. water mite diet isolate 7886-BHL040517-GBD26567_7242-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCAAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGTTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGTTTCGGAAATTGATTAGTCCCTTTTAATATTAGGAGCACCCGATAGAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCGCTAACCCAGCTTCTTGCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7890 Chironominae sp. water mite diet isolate 7890-BHL040517-GBD13272_12055-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACCTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAGTTGGAGCCTTTGGAAATTGACTCATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCCTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7893 Chironomus sp. water mite diet isolate 7893-BHL040517-GBD12713_9066-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCTCATGTTTTTATTATAATTTTTTTCATATTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTTCCTCGAATAAATAATATAAGTTTCTGACTCTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7902 Chironomus riparius water mite diet isolate 7902-BHL040517-GBD27703_9656-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCGTGATCCAGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACTAAATTTATAATGTTATAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCAGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTATTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7905 Dicrotendipes sp. water mite diet isolate 7905-BHL040517-GBD19692_15031-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGCATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGTTCATGCTTTTATTATAATTTTTTTTTTATGGTTATACCTATTCTAATTGGAGGTTTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCACCCGATATAGCTTGCCCACGAAGAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCGACATCTTTCTAAATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7908 Chironomidae sp. water mite diet isolate 7908-BHL040517-GBD15196_3142-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTAGGGGCATGAGCGGGGATAGTAGGGACATCCCTAAGAATACTAATGCGTGCTGAATTAGGTTACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCTGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7910 Chironomus riparius water mite diet isolate 7910-BHL040517-GBD20621_4516-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGCCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAAGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATCTTGTAGTTACTGCACATGCTTTTATTATAAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTCACCCTCCTCTCTTACCCTACTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7915 Chironomidae sp. water mite diet isolate 7915-BHL040517-GBD25208_9472-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCATGAACATTTATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGATCCCCTGATATAGCTTTTTCCTCGAATAGATAATATAAGTTTCTGATTACTCCCTCCTCCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR278209, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7918 Chironomus sp. water mite diet isolate 7918-BHL040517-GBD6644_23741-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATTTTATTTTTGGAGCTTGATCTGGAGTAGTGGGAACTTCATTAAGAATGCTTATTCGAACAGAATTAGGACGACCCGGAACTTCCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTGTTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTTTTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7921 Cricotopus trifasciatus water mite diet isolate 7921-BHL040517-GBD21407_20550-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATCTTCGGAGCATGATCAGGAATAGTAGGGACATCTCTAAGAATTTTTATCCGGGCCTAATTAGGACATGCTGGCTCATTAATTGGTGATGATCAAATTTATAATGTGATTGTTACAGCACATGCTTTCGTTATAATTTTTTTTATAGTTATACCTATTTTAATTGGTGGGTTTGGAAATTGATTAGTTCCTCTAATATTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTATTGACTTCTTCCCCCTTCTCTTACATTATTACATTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KM933933, identified in GenBank as Cricotopus trifasciatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7922 Chironomus riparius water mite diet isolate 7922-BHL040517-GBD4662_23879-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACTACCCGGAACTTTCATTGGAGATGACCAAATTTATAATTTTGTAGTTACTGCACATGTTTTTATTATAATTTTTTTCTTAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7923 Chironominae sp. water mite diet isolate 7923-BHL040517-GBD15482_26144-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATTTTTGGTGCTTGATCAGGAATGGTAGGGACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID MG449442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7925 Chironomus sp. water mite diet isolate 7925-BHL040517-GBD14048_26071-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCGGGATTAGTGGGAACTTCATTAAGATTGCTTTTTCGGGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTAAAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCACAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTACCCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL793 Cricotopus sp. water mite diet isolate 793-BHL100916-GBD28504_19602-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATTAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGAGGCTCCTGATATAGCATTCACTCGAATAAATAATATAAGTGTTTGATTATGACCCCCTTCTCTCACCTAACTTCATTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGGA	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7931 Chironomus sp. water mite diet isolate 7931-BHL040517-GBD10703_11457-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGGACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTGTTACCCCCCTCTCTTACTCCTCTTCTTTCTAGTTCTTTCGTAGGAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7933 Chironomidae sp. water mite diet isolate 7933-BHL040517-GBD26472_10166-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTTGGGGCCTGATCGGGGATAGTTGGGACTTCTTTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATATAGTTATACCATTTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCTTGATATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR278209, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7934 Chironomidae sp. water mite diet isolate 7934-BHL040517-GBD13932_2487-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTATTTTTGGGGCCGGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGGGCTGAATTAGGTCACCCAGTAACATTAATTGGTGACGTCCTAATTTATAAGGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCACTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7936 Chironominae sp. water mite diet isolate 7936-BHL040517-GBD20860_11358-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTTGGAGCTTGATCTGGTATAGTGGGTACTCCTTTAAGTATGCTATTTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTCATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTATTGTTAGGAACCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAATTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7937 Dicrotendipes sp. water mite diet isolate 7937-BHL040517-GBD26985_19624-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTAGAGCTTGATCTGGAATAGTAGGAATTTACTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGAGACATTTATTGGAGATGATAAAATCTACAATGTAATTGTTACAGATAATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTACTTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGACCCCGATATAGCTTTCCCACTAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTGACCCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL794 Chironomidae sp. water mite diet isolate 794-BHL100916-GBD8274_14712-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGACTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAGTTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTATTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7943 Chironomus riparius water mite diet isolate 7943-BHL040517-GBD14942_11689-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAAATTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCTGAAACTGACTTGTCCCCCTCATACTTGGAACACCTGTCATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7946 Dicrotendipes sp. water mite diet isolate 7946-BHL040517-GBD7230_6634-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTAGTGTTATACCAATTCTAATGGAAGGATTCGAAAATTGATTAGTCCCTTTAATATTAGAAGCCCCCGATATAGCTTTCCCACAAATAAAAAATAAAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTGCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL795 Cricotopus sp. water mite diet isolate 795-BHL100916-GBD18216_4016-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGGGCTTGGTCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGTCATGCCGGCTCATTGATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCCCATGCTTTCGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCTTTAATACTTGGGGCACCAGATATAGCCTTTCCCCGGATAAATAACATAAGTTTTTGACTTCTACCCCCATCATTAACTCTTTTGCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR670938, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7951 Chironomus sp. water mite diet isolate 7951-BHL040517-GBD12104_19278-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGATCTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATCGGAGGTTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCCTCATTTACTCTTCTACTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7952 Chironomus riparius water mite diet isolate 7952-BHL040517-GBD8316_10808-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCCTTAAGAATGCTTATTCGATCAGAATTAGGACGACCCGTAACTTTCATTGGAGATGACTAAATTCATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL796 Psectrocladius sp. water mite diet isolate 796-BHL100916-GBD26864_9421-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTACATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7965 Chironomidae sp. water mite diet isolate 7965-BHL040517-GBD18191_16890-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTGGG-GCTTGATCCGGAATAGTGGGAACTTCATAAAGACTGCTTATTCGAGCAGGATTAGGACGACCCGGAACTTTCATTGGGGATGACCAAATTTATAATGTTGTAGTTACAGCATATGCTTTTAATATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCATGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.8% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7968 Chironomus riparius water mite diet isolate 7968-BHL040517-GBD14060_2141-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGATCTTTCCTTGGAGATGACCAAATTTATAATCTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTACACCAATTTTAATTGGAGGATTTGGAAACTGTCTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTGCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL797 Cricotopus sp. water mite diet isolate 797-BHL100916-GBD17773_17778-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGCGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACTTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGCGGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7971 Chironomus riparius water mite diet isolate 7971-BHL040517-GBD18190_15724-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTGTTGGGGCTTGATCCGGAATAGTGGGAACTTCATAAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAACCTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACTCCCCTCTCTTACTCTTCTTTTTTCTAGTTCTTTCGTAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7974 Dicrotendipes sp. water mite diet isolate 7974-BHL040517-GBD17641_27969-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATGATTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCCAATATAGCTTTCCCACGAATAAATAATATAAGGTTCTGACTATTACCTCCTTCTCTAACCCAGCTACTTTCTAAAACAATTGTAGAAAATGGAGCTGGAGCAG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7977 Chironomus riparius water mite diet isolate 7977-BHL040517-GBD15389_27034-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCATGATCGGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGTAGAATTAGGACGACCCGGATCTTTCATTGGAGATGACTAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7979 Chironomidae sp. water mite diet isolate 7979-BHL040517-GBD9816_26416-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTACTTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTATCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTACACATTAACAATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL798 Cricotopus sp. water mite diet isolate 798-BHL100916-GBD13934_24226-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGGGCTTGATCAGGAATAGTAGGAACTTCCCTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGAT--------------TTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.0% identical to accession ID KR643248, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL7981 Chironomus riparius water mite diet isolate 7981-BHL040517-GBD23105_15596-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGGAATAGTGGGAATTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCAATGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACTTACTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCCTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7984 Chironomus riparius water mite diet isolate 7984-BHL040517-GBD21625_14690-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGTAGAATTATGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCCCGAATAAATAATATAAGGATCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCCTTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7989 Chironomus riparius water mite diet isolate 7989-BHL040517-GBD13798_8747-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGTCCAAATTTATAATGTTGTAGTTACTGCAGATGCTTTTATTATAAATTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAACACCTGACATAGCCTTTCCCCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTAACTCTTCTTCGTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7994 Chironomus riparius water mite diet isolate 7994-BHL040517-GBD8249_25446-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTGTACATTATTTTTGGGACTTGATCCGGAATAGTGGGGACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGAAACTTTCATTGGAGATGACCAAATTTATAATCTTGTAGTTACCGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTCACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7997 Chironomus riparius water mite diet isolate 7997-BHL040517-GBD17774_4178-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCCTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGGTATACCAATTTTTAATTGGAGGATTGGGAAAGTGACGTGTCCCCCTAATACTTGGAGCACCTCACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTCCTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL7999 Chironomus riparius water mite diet isolate 7999-BHL040517-GBD17230_5812-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTGTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACTACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTAGACCAATTTGAAATGGAGGATTGGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTCCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGA	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8003 Chironominae sp. water mite diet isolate 8003-BHL040517-GBD27882_21805-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGTACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCATCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTCCCTCCTTCTCTTTCTCTATTACTTTCTAGTACAATAGTATAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR670143, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL801 Cricotopus sp. water mite diet isolate 801-BHL100916-GBD11725_27089-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTTATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAAATGATTAGTTCCTTTAATGTTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCCTTCTCTAACCTTACTTCTATCAAGTTCAATCGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8012 Chironomus sp. water mite diet isolate 8012-BHL040517-GBD5849_20048-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCGGGATTAGAGGGAACTTCATTAAGATTGCTTATTCGAGCGGAATTAGGACGACCCGGAACTTTCTTTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTCTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTACCTAGTTCTTTCGTAGAAAATGGATCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8013 Chironomus sp. water mite diet isolate 8013-BHL040517-GBD26487_23014-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACTAAATTTATAATGTTGTAGTTACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTCTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTAACTCTACTACTATCTAGATCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8015 Chironomus sp. water mite diet isolate 8015-BHL040517-GBD5396_22460-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTTATTTTTGGGGCTTGATCCGTACTAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGACTTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTGTAATTTTTTTCATAGTTATACCAATTTTAATTAGAGGATTCGGAAACTGACTTGTCCCACTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8016 Paratanytarsus sp. water mite diet isolate 8016-BHL040517-GBD28985_19306-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGTACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATACTAGGAGACCCAGATATAGCCTTTCCTCGAAAAAATAATATAAGATTATGACTTCTGCCCCCCATCTTTAACTCTATTACTTTCAAATAGAATAGTGGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8017 Chironomidae sp. water mite diet isolate 8017-BHL040517-GBD22021_6812-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGTGCCTGATCGGG-ATTGTAGGGACATCCCTTAGAATACTTATTCGTGCTGGATTAGGTCACCCAGGAACATTAATTGGGAACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTACTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8018 Chironominae sp. water mite diet isolate 8018-BHL040517-GBD18395_22611-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTAGGACGCCCAGGTACTTTTATTGGTTATGATCAAATTTATAATGTAATTGTAACTGCTCACGCTTTTATTATAATTTTTTTTATGGTTATGCCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTAATACTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGGTTTTGACTTTTACCACCCTCTTTAACTCTTTTACTTTCAAGAACAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR289362, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL802 Chironomidae sp. water mite diet isolate 802-BHL100916-GBD4570_16090-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAACCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8024 Dicrotendipes sp. water mite diet isolate 8024-BHL040517-GBD8155_10867-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCTTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGGCGAATTAGGACGACCCGGTACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGTTCATGCTTTTATTATATTTTTTTTTTATGGTTATACCTATTCTAATTGGAGGTTTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCACCCGATATAGCGTTCCCACGAATAAATAATATAAGTTTCTGACTATTGCCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8025 Chironomus sp. water mite diet isolate 8025-BHL040517-GBD27113_15584-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTT-GGGGCTTGATCCGGAATAGTGGGAAATTCATTTAGACTGCTTAATCGAGCAGGATTTGGACGACCCGGTACTTTCATTGGGGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTAATATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGGTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8026 Chironomus riparius water mite diet isolate 8026-BHL040517-GBD27541_20639-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCTAAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTATTGCACATGCTTTTATTATAATTTTTTTCATACTTATACCAATTTTAATTAGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCTCCTCTCTTACTCCTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8028 Chironomus riparius water mite diet isolate 8028-BHL040517-GBD23515_10216-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATCTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACGTTTACCCCCCTCTCGTACTCTACTTCTATCTAGTTCGTTCGTGGAAAAGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8029 Dicrotendipes sp. water mite diet isolate 8029-BHL040517-GBD7799_9139-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTGTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGAAGATCAAGTTTATAATGTAATTGTTACAGCTCATGCTTTTATTATATTTTTTTTTTATGGTTATACCTATTTTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTACTTCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL803 Cricotopus sp. water mite diet isolate 803-BHL100916-GBD25164_18383-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8032 Chironominae sp. water mite diet isolate 8032-BHL040517-GBD23085_25817-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGGGCCTGATCGGGTATGGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAAAATTAATTGGTGACGACCGAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTGTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTGCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR670143, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8034 Chironomus sp. water mite diet isolate 8034-BHL040517-GBD20519_28444-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCCAGCTGAATTAGGACGACCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCATTTTTAATTGGAGGATTCGGAAACTGACTTTTCCCCCTAATACTTGGAGCACCAGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTAACTCTTCTACTTTCTAGTACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8035 Chironominae sp. water mite diet isolate 8035-BHL040517-GBD13204_23900-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTATTTCGTGCTGAATTTGGCCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGCAATTGTTACAGCCCATGATTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGATCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR670143, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8038 Chironomus riparius water mite diet isolate 8038-BHL040517-GBD28797_19148-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGTGGCTTGATCCGGAATAGTGGGAACTTCATTAAGACTGCTTATTCGAGCAGAATTAGGACGACCCTGAACTTTCATTGGAGATGACTAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCACTTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTATTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8039 Chironomidae sp. water mite diet isolate 8039-BHL040517-GBD18840_13937-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCCTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR475554, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL804 Paratanytarsus sp. water mite diet isolate 804-BHL100916-GBD9950_22340-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGGTCAGGAATAATCGGAACATCCTTAAGTATACTAAATCGAGCAGAATTAGGGCACCCTGGAACATTTATTGGAGATGACCAAATCTATAATGTAATTGTTACAGCTCATGCTTTTATTACAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCTCCCGATATAGCTTTTCCCCGTATAAATAACATAAGTTTTTGATTACTTTCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KM988017, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8044 Chironomidae sp. water mite diet isolate 8044-BHL040517-GBD23179_17366-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACCTTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACTTCCTTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGAACAAATTTATAATGTAATTGTTCCAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCATCTCTTTCTCGATTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8046 Chironomus riparius water mite diet isolate 8046-BHL040517-GBD10187_8878-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACAACCCGGAACTTTCATTGGAGATGACTAAATTTATAATGTTGTAGTTATTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8047 Chironomus sp. water mite diet isolate 8047-BHL040517-GBD19290_7839-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATCTTTTTCATAGTTATACCAATTTTAATCGGGGGTTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTAACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8048 Dicrotendipes sp. water mite diet isolate 8048-BHL040517-GBD13524_14998-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTTATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL805 Cricotopus sp. water mite diet isolate 805-BHL100916-GBD7512_9659-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTTGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAATTTTTGATTATTACCCCCTTCTCTCACCTTGCTACTTTCAAGTACAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8052 Chironomus riparius water mite diet isolate 8052-BHL040517-GBD26773_22665-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGAGCAGGAACTTTCATTGGAGATGACTAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGAATCGGAAACTGACTTGTCCTCCTAATACTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL806 Chironominae sp. water mite diet isolate 806-BHL100916-GBD11379_14543-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTCGGAGCTTGATCTGGAATAGTAGGAACATCACTTAGTATATTAATTCGAGCAGAACTTGGTCACCCTGGAACTTTTATTGGTGATGATCAAATTTACAATGTTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTTATAGTTATACCTATCCTAATTGGTGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGTCCCTGATATAGCTTTTCCACGAATAAATAATATGAGATTTTGATTACTTCCCCCTTCTTTATCTCTTCTTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR155923, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8060 Chironomus sp. water mite diet isolate 8060-BHL040517-GBD21908_21850-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGACCTTTATACCTTATTTTTTGGGGCTTGCTCCGGAATAGTGGGAACTTCATTTAGAATGCTTATTCGAGCCGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTAGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACGCCTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8061 Chironomus sp. water mite diet isolate 8061-BHL040517-GBD23390_26654-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTT-GGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGACTGCTTATTTGAGCTGAATTAGGAAGACCCGGAACTTTCATTGGGGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTAATATGATTTTTTTCATAGTTATACCCAGTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL807 Paratanytarsus sp. water mite diet isolate 807-BHL100916-GBD16789_15466-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGGAACTGATTATTTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTATTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8071 Chironomus riparius water mite diet isolate 8071-BHL040517-GBD21908_27496-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTTCGACCAGACTTAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGTTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCGTACTCCTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8077 Dicrotendipes sp. water mite diet isolate 8077-BHL040517-GBD22765_23723-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTTATCTGGAATAGTAGGAACTTCCTTAAGTATCCTTATTCGAGCCGTATTAGGACGACCCGTGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTTGATTAGTCCCTTTAATATTAGGAGCACCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8078 Chironomus sp. water mite diet isolate 8078-BHL040517-GBD7930_6757-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCATAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTGAGACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATGAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL808 Chironomidae sp. water mite diet isolate 808-BHL100916-GBD15218_22569-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATAAAGATATTGGAACACTATATTTTATTTTTGGGGCTTGGTCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTAAATTAGGTCATGCCGGCTCATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCCCATGCTTTCGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCTTTAATACTTGGGGCACCAGATATAGCCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID JF412070, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8080 Chironomidae sp. water mite diet isolate 8080-BHL040517-GBD22663_22716-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATACTTCATTTTCGGTGCCTGATCAGGTATAGTGGGAACTTCCTTAAGAATATCAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACTAAATGTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KM993958, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8082 Chironomidae sp. water mite diet isolate 8082-BHL040517-GBD25056_15232-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGATCTTGATCAGGGATATTAGGAACCTCATTCAGTATATTAATTCGCGCAGGATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACGTTCTAGTTCAATTGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KM993958, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL809 Chironomidae sp. water mite diet isolate 809-BHL100916-GBD5354_21852-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGGGCTTGGTCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGTCATGCCGGCTCATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCCCATGCTTTCGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.7% identical to accession ID KJ167864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL810 Chironomidae sp. water mite diet isolate 810-BHL100916-GBD3559_20744-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTCACAGCACATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGGAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8104 Chironomus riparius water mite diet isolate 8104-BHL040517-GBD22611_7599-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGTATGCTTATTCGATCAGAATTTGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTTCCCCTAATACTTGGAGCGCCTGACATAGCGTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8108 Chironomus riparius water mite diet isolate 8108-BHL040517-GBD14210_14732-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCTTATACATTATTTTTTGGGGCTTGATTCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACGGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTCACTCTTCTTCGTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL811 Cricotopus sp. water mite diet isolate 811-BHL100916-GBD13727_10367-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTTATTAATCGGAGACTATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCTTTAATACTTGGGGCACCAGATATAGCCTTTCCCCGGATAAATAACATAAGTTTTTGACTTCTACCCCCATCATTAACTCTTTTGCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID KR670938, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8110 Dicrotendipes sp. water mite diet isolate 8110-BHL040517-GBD3214_17570-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTATTTAAGTATACTTATTCGAGCCGAATTAGGATGTCCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACGTCCTTCTCTAACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8111 Chironomidae sp. water mite diet isolate 8111-BHL040517-GBD7572_17888-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACTTCCTTAAGAATACTAATTCGAGCTGAATTAGGTCAACCAGGAACATTAATTGGTGAAAACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATACCTTTTCCTCGAATAAATAATATAAGATTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR278209, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8112 Chironomus riparius water mite diet isolate 8112-BHL040517-GBD13525_22487-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTTTGGGGCTTGATCCGGAACAGTGGGAACTTCATTAAGAATGCTGATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGATGACCAAATTTATAATGTTGTAATTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCATTTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCTCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8123 Dicrotendipes sp. water mite diet isolate 8123-BHL040517-GBD4270_10841-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTACTTAAGTATACTTGTTCGAGCCGCAGTAGGACGACCCGGGACATTTCTTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACTCTTCTTCTTTCTAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8126 Chironomus riparius water mite diet isolate 8126-BHL040517-GBD5465_12078-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTGTTGGGGCTTGATCCGGAATCGTGGGAACTTCATTAGGAATGCTTCTTCGAGCAGAATTAGGACGACCCAGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTCGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAGTAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8130 Chironomus sp. water mite diet isolate 8130-BHL040517-GBD10986_23694-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGAGCCGGAATAGTGGGAACTTCATTAAGAATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTAAATGGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTTTCTAATGCATTCGTAGAAAATGGAGCTTGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8140 Paratanytarsus sp. water mite diet isolate 8140-BHL040517-GBD17638_14001-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCTTGATCTGGAATTGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR272133, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8145 Chironomus riparius water mite diet isolate 8145-BHL040517-GBD18085_2219-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGGCCCGTATCTTTCATTGGAGATGACCAAATTTAGAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAGGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCCAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8148 Dicrotendipes sp. water mite diet isolate 8148-BHL040517-GBD9416_3078-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATATTAGGAACTTCCTTAAGTATACTTACTCGAGCCGAATTAGGACGACCCGGTACATTTATTGACGATGATCAAATCTACAATGTAATTGTTACAGTTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGTTTCGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCGAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL815 Cricotopus sp. water mite diet isolate 815-BHL100916-GBD25799_21615-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGAACTTACTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATTAAATTTATAACGTTATTGTTACAGATCATGTTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGAAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAGTTGTTTAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8150 Dicrotendipes sp. water mite diet isolate 8150-BHL040517-GBD25309_5429-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCATTAAGTATATTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTAGTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAACAAATAAAATAAGTTTCTGACTATTACCCCCTTCCCTAACCCCTACTACTTTCTAGTTCAATTGTAGAAAACGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8151 Chironomus riparius water mite diet isolate 8151-BHL040517-GBD18513_28941-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTGGGTACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACTAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCACTTTTAATTGGAGGATTCGGAAACTGACTTGTCTCCCTAATACTTGGAGCACCTGACATGGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCGCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8153 Chironomus sp. water mite diet isolate 8153-BHL040517-GBD26112_9063-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTT-GGGGCTTGATCCGGAATTGTGGGAACTTCATTAAGACTGCTTATTCGCGCCGGATTAGGACGACACGGAACTTTCATTGGGGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTTATATAATTTTTTTCATAGTTATACCAATTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCATACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8155 Chironomus riparius water mite diet isolate 8155-BHL040517-GBD24783_24075-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTGTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATCTTGTAGTTACTGCACATGCTTTTATTATATTTTTTTTTCTTAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTTTCCCCCTAATACTTGGAGCACCTGACATAGCATTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8156 Chironomus sp. water mite diet isolate 8156-BHL040517-GBD10356_9058-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTAAACATTATTTT-GGGGCTTTATCCGGAATAGTGGGAACTTCATTTAGACTGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGGGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTAATATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTGCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8157 Paratanytarsus sp. water mite diet isolate 8157-BHL040517-GBD24270_4466-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTTCATTTTTGATGCCTGATCAGGAATAGTAGGAACTCTCCTATGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACTAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGTAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCGTTTCCTCGAAGAAATAATATAAGATTTTTGACTTCTTCCCCCCTCTTTAACTCATTTACTTTCAAGTAGAATAGTGGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8158 Dicrotendipes sp. water mite diet isolate 8158-BHL040517-GBD28110_9180-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATGGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCGTTCCCACGAAAAAATAAGATAAGTGTCTGACTATTACCTCCTTCGCTAAACCCTTCTTCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8161 Chironomus riparius water mite diet isolate 8161-BHL040517-GBD16071_4606-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGAGCCGGAATAGTGGGAACTTCATTAAGAATGCTTATGCGAGCAGAATTAAGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTGACTGCACATGCTTTTATGATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTAGGAGACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8169 Chironomus riparius water mite diet isolate 8169-BHL040517-GBD15965_17321-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGTCTAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAAATTTTTTCATAGTTATACCAATTTTAAATGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGTGCACCGGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTTCTAGTTCTTTCGTAGAAAGTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL817 Psectrocladius sp. water mite diet isolate 817-BHL100916-GBD25352_7128-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCTTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGCTCCTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8170 Chironomidae sp. water mite diet isolate 8170-BHL040517-GBD13744_10519-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACC	Using NCBI BLASTN in June 2018, this sequence was 99.0% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8174 Chironomus riparius water mite diet isolate 8174-BHL040517-GBD20146_7639-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGTACTTCATTAAAAATGCTTATTCGAGCAGAATTAGGACGACCCGTTACTTTCATTGGAGATGACCAAATTTATAATCTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8175 Chironomus sp. water mite diet isolate 8175-BHL040517-GBD22918_25290-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTT-GGGGCTTGATCCGGAATTGTGGGAACTTCATTTAGACTGCTTATTTGAGCAGAATTTAGACAACCCGGAACTTTCATTGGGGATGACCAAATTTACAATGTTGTAGTTACTGCACATGCTTTTAATATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8177 Chironomus riparius water mite diet isolate 8177-BHL040517-GBD17145_26812-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTTATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTGTAATCTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGAATTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAGATAATATAAGTTTCTGACCTTTACCCCCCTCTCTTACTCTTCTTCTTACTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL818 Dicrotendipes sp. water mite diet isolate 818-BHL100916-GBD16881_5053-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTGTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGATATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATTGTTATACCTATTCTAATTTGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAACTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTGCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8182 Chironomus riparius water mite diet isolate 8182-BHL040517-GBD19774_27958-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTAATTAAGAATGCTTATTCGAGCAGAATTAGGACGACACGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTGATTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTTCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8199 Chironominae sp. water mite diet isolate 8199-BHL040517-GBD23166_25891-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTTGGGGCTTGATCTGGTTTAGTAGGTACTTCTTTAAGTATGCTATTTCGAGCAGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTATTTGTCACAGCATACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAGTAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8200 Dicrotendipes sp. water mite diet isolate 8200-BHL040517-GBD6019_20082-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCAGAATTGGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTATTCCCTTTAATATTAGGAGCTCCCGAAATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8203 Chironomus sp. water mite diet isolate 8203-BHL040517-GBD14281_21573-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGAGACTTTACACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACTACCCGGAAATTTCATTGGAGATGACTAAATTTATAATGTTGTATTTACTGCACATGCTTTTATTATAATCTTTTTCATAGTTATACCAGTTTTAATCGGAGGTTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8207 Chironomidae sp. water mite diet isolate 8207-BHL040517-GBD13747_16525-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCTTAAGAATACTAATTCGTGCTGAATTAGGTCAACCAGGAACATTAATTGGTGACGACTAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAACCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTTCCACCTTCTCTTTCTCTTTGACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL821 Chironomidae sp. water mite diet isolate 821-BHL100916-GBD12356_2717-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAACTCTCTAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 91.1% identical to accession ID KM102730, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8210 Chironomus sp. water mite diet isolate 8210-BHL040517-GBD28221_19951-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTGTATACATTATTTTTGGG-CTTTATCCGGAATTGTTGGAACTTCATTCAGACTGCTTATTCGAGCAGAATTAGGACGAACCGGAACTTTCATTGGGGATGACCAAATTTATAATGTTGTAGTTACAGCACATGCTTTTAATATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL822 Paratanytarsus sp. water mite diet isolate 822-BHL100916-GBD16598_27008-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTACTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8222 Chironomidae sp. water mite diet isolate 8222-BHL040517-GBD20085_7930-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAGTAGGTACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATACTTTTTTTTATAGTTATACCAATTTTAATTTGAGGGTTCGAAAATTGACTTTTACCTTTAATATTAGGAGCCCCATGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCATTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8223 Paratanytarsus sp. water mite diet isolate 8223-BHL040517-GBD3507_11430-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTTCATTATACTTCATTTC-GGTACCTGATCAGGGATAGTGGGTACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTTATAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTCTAACTGGAGGATTTGGGAACTGATTACTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR292109, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8227 Dicrotendipes sp. water mite diet isolate 8227-BHL040517-GBD8721_10842-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTCAGAACTTCCTTAAGTATACTTATTCGAGCCTAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTATAGCTCATGCTTTTATTATAATTTTTTTATTGTTATACCTATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAACTTTCCCATGAATAAATAATATAAGTTTCTGACTATGACCTACTTCTCTAACCCTTCTGCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL823 Cricotopus sp. water mite diet isolate 823-BHL100916-GBD28673_20508-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATCTTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTCGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTTGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCCCGAATAAATAATATAAGTTTTTGATTATTACCCCCCTTCTCTCACCTTACTACTTTCAAGTGCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8236 Chironominae sp. water mite diet isolate 8236-BHL040517-GBD12970_18587-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTATGTATGCTAATTCGAGCAGAACTTGGACCACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGGATACGCTTTTATTATAAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTGTTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTCTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL824 Cricotopus sp. water mite diet isolate 824-BHL100916-GBD15522_3883-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTCGAGAATCTTAATTCGAGCTGAATTAGGTCATTCCTTATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGAGTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTCCCCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8248 Chironomus sp. water mite diet isolate 8248-BHL040517-GBD12373_25600-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTGTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTTTTCGAGCAGAATTAGGACGACGCAGAACTTTCAATGGAGATGAGCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATAACAATTTTAATTGGAGGATTCGGAAACTAACTTGTCCACCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8249 Chironomus riparius water mite diet isolate 8249-BHL040517-GBD18467_9053-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACTAAATTTATAATGTTGTAGTTACTGCACATGCTTTTAGTGTAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGAATTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCGTACTCTTCTTCTTTCTAGTTCTCTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL825 Chironomidae sp. water mite diet isolate 825-BHL100916-GBD14345_23669-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTTAGAATTCTAATTCGAGCAGAATTAGGACATGCAGTGTGATTAATTAGAGACGATCAAATTTATAATGTAATTGTTACAGCTGATGCTTTTGTAATAATTTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAACTGACTAGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGTTTTTGAATGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8250 Chironomus sp. water mite diet isolate 8250-BHL040517-GBD7495_17922-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACAAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATATTTATTCCAATTTTAATTGGAGGATTCGGAAACTGTCTTCTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCCCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8255 Chironomus riparius water mite diet isolate 8255-BHL040517-GBD26068_6815-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCAGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTTTTTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACATGTCCCCCTAATACTTGGGGCACCTCACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTATTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8256 Chironomus sp. water mite diet isolate 8256-BHL040517-GBD4215_16360-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACAAAATTTATAATCTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAATACTTGGAGCACCTGACATAGCTTTTCCACGAATAAATAATATAAGTTTCTGACTTTCACCCCCCTCACTTACTCTACTTCTATCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8258 Chironomus sp. water mite diet isolate 8258-BHL040517-GBD27028_22105-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGGACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAGTGCTTATTCGAGTAGAATTAGGACGACCCGGAACTTTAATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATCGGAGGTTTCGGAAACTGATTTGTTCCCCCTAATACTGGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTAACTCTTCTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8261 Dicrotendipes sp. water mite diet isolate 8261-BHL040517-GBD26414_22311-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGTCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAGTTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGTTTCGGAAATTGAATAGTCCCTTTTAATATTAGGAGCACCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8262 Chironomus riparius water mite diet isolate 8262-BHL040517-GBD29535_16844-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGAGGCTTGATCCGGAATAGTTGGAACTTCATTAAGCATGCTTATCCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACTAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCGTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCACTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8264 Chironomus sp. water mite diet isolate 8264-BHL040517-GBD25357_24677-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTT-GGGGCTTGATCCGGAATTGCGGGGACTTCATTTAGACTGCTTATTCGAGCTGGATTAGGACGACCCGGAACTTTCATTGGGGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTTATATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTATCTAGTTCTTTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8267 Chironomus riparius water mite diet isolate 8267-BHL040517-GBD4106_10656-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTGTTGGGGCTTGATCCGGAATAGAGGGAACTTCATTAAGAATGCTTATTCAAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGTTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTGTCCCCCTAATAATTGTAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8270 Chironomus sp. water mite diet isolate 8270-BHL040517-GBD20159_16586-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGGTCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAACATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCGTAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCCGACTTTTACCCCCCCGCTCTTACACTTCATCTGTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8271 Chironomus sp. water mite diet isolate 8271-BHL040517-GBD21157_14197-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGTTTGATCCGGTATAGTGGGAACTTCCTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGGGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTGACCCCCCTCTCTTACACGACTTCTTTCTAGTGCTTTCGTAGAGAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8277 Dicrotendipes sp. water mite diet isolate 8277-BHL040517-GBD2883_9941-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTAAATTTTTGGAGATTGATCTGGAATAGTATGAACTTCCTGAAGTATACTTATTCGAGTTGCATTAGGACGACCCGTGACATTTATTGGAGATGATCAAGTCTACAATGTAATTGTTACAGCTCATGCTTTTTTTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGACCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAAATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8279 Chironomus riparius water mite diet isolate 8279-BHL040517-GBD25571_10594-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGCTCAGGAATAGTGGGTACTTCATTATGAATGCTTATTCGAGCAGAATTAGGACGAGCCGGAACTTTCTTTGGAGATGACCAAATTTAAAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL828 Cricotopus sp. water mite diet isolate 828-BHL100916-GBD7501_9662-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACACTATATTTTATTTTTGGGGCTTGGTCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGTCATGCCGGCTCATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCCCATGCTTTCGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCTTTCTCTCACCTTACTTCTTTCAAATTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8286 Dicrotendipes sp. water mite diet isolate 8286-BHL040517-GBD16855_22585-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCTGAATTAGGACGACCCGGGACATTTATTGGTGATGATCAAATCTACAATGTAATTGTTACAGTTCATGCTTTTATTATATTTTTTTTTTATGGTTATACCTATTCTAACTGGAGGTTTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCACCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8288 Chironomus riparius water mite diet isolate 8288-BHL040517-GBD21632_20813-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGACTTGATCCGGGATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCTTAAAACTTGAAGCACCTGACATAG-TTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTATCTAGTTCTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL829 Chironomidae sp. water mite diet isolate 829-BHL100916-GBD22338_19889-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTTGGGGCCTGATCGGGGATAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTATTTGGTGACGACCAAATTTACAAAGTATTTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTTCTCTTTTACTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8297 Dicrotendipes sp. water mite diet isolate 8297-BHL040517-GBD15241_1951-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTGATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGGGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATCATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCATCTCTAACCCTACTACTATCAAGAACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL830 Chironomidae sp. water mite diet isolate 830-BHL100916-GBD5214_22065-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATATTTTTATTTTTGGAGCATGATCAGGACTAGTTGGAACTTCCTTAAGAATATTACTTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTATTGCACATGCTTTCTTTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTAGCCCCATCTCTAACATTATTACTATCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8301 Dicrotendipes sp. water mite diet isolate 8301-BHL040517-GBD18332_11348-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATCCTTATTCGAGTCGAATTAGGCCGACCCGGGGCATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTAATGCTTTTATTATAATTTTTTTTTATGATTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCTCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8305 Chironomus riparius water mite diet isolate 8305-BHL040517-GBD15772_6873-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATAACCAAATTTATAATGTTGTAGTTTCTGCACATGCTTTTATTATAATTTTTTTCGTAGTTATACCAATTTTAATTAGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAATACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8308 Chironomus sp. water mite diet isolate 8308-BHL040517-GBD24733_23347-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTGTTTT-GGGGCTTGATCCGGAATAGTTGGCACTTCATTTAGACTTCTTATTCGAGCAGAATTAGGACGACCCGGAACTGTCATTGGGGATTACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTAATATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8309 Chironominae sp. water mite diet isolate 8309-BHL040517-GBD21933_11263-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGGGCCTGATCGGGGTTAGTAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGACCAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTT-ATAGTTATACCAATTTTAATTGGTGGGTTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCTCTTACCCTTTGACTTTCAAGTGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR670143, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL831 Chironomidae sp. water mite diet isolate 831-BHL100916-GBD27168_18784-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAAAATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8310 Chironomus riparius water mite diet isolate 8310-BHL040517-GBD25538_11687-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTT-GGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGTACGGCCCGGAACTTTCATTGGAGATGACCAAATTTATAATCTTTTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCCTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8311 Paratanytarsus sp. water mite diet isolate 8311-BHL040517-GBD4690_7707-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATCTTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGCATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTATAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCCTTTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAATAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL832 Cricotopus sp. water mite diet isolate 832-BHL100916-GBD1868_17271-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGAACCTCTCTTAGAATTTTAATTCGAGCAAAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTTTAATAATTTTTTTTATAGTAATACCAATTCTAATTGTAGGATTTGGAAATTGATTAGTCCCTTTAATACTAGGAGTCCCAGATATAGCATTCCCTCGAATAAATAACATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8322 Dicrotendipes sp. water mite diet isolate 8322-BHL040517-GBD29008_16567-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCAAGCTTTTATTATATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCTGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATGAGTTTCTGACTATTACCTCCTTCTCTAACCCGTCTTCTTTCTAAATCAATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8323 Dicrotendipes sp. water mite diet isolate 8323-BHL040517-GBD22492_18862-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGCACTTCCTTAAGTATACTTATTCGAGTCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGTTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGTTTCGGAAATTGATCAGTCCCTTTTAATATTAGGAGCACCCGATATAGCTTTCCCACGAATAAATAATATAAGATTCTGACTATTACTTCCTTCTCTAACCCTTCTTCTATCTAAATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8326 Chironominae sp. water mite diet isolate 8326-BHL040517-GBD28894_19385-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATACTTCATTTTCGGTGCCTGGTAAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTAGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGTCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8328 Chironomus sp. water mite diet isolate 8328-BHL040517-GBD21430_7137-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTT-GGGGCTTGATCCGGAATAGTGGGAACTTCCTTTAGGCTGCTTTTTTGGGCAGAATTTGGACGACCCGGAACTTTCATTGGGGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTAATATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL833 Chironomidae sp. water mite diet isolate 833-BHL100916-GBD18082_2080-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACACTATATTTATTTTTGGGGCTTGGTCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGTCATGCCGGCTCATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCCCATGCTTTCGTAATAATTTTTTTTATAGTAATACCTATTTTTATTGGAGGATTTGGGAATTGATTAGTTCCTTTAATACTTGGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.6% identical to accession ID KM102730, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8332 Chironominae sp. water mite diet isolate 8332-BHL040517-GBD28552_13154-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTATGTATGTTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGATCATATTTACAATGTAATTGTCACAGCATACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGCTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTATAAAATGGAGCTGGAACA	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8333 Chironomus sp. water mite diet isolate 8333-BHL040517-GBD13779_21850-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCTTTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTCCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTATTTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATACAAGTTTCTGACTTCTACCCCCCTCTCTGACTCTTCTTCTTTCTAGTTCATACGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8338 Chironomus riparius water mite diet isolate 8338-BHL040517-GBD23445_25989-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGAGCCTGATCTTTCATTGGAGATGACTAAATTTATAATTTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATGAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8352 Chironomidae sp. water mite diet isolate 8352-BHL040517-GBD10906_8802-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGGGCCTGATCGGGGATAATAGGGACATCCCTAAGAATACTAATTCGTGCTGAATTAGGTCACCCAGGAACATTAATTGGTGACGAACAAATTTATAATGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAATTGACTTTTACCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTAGAATAAATAATATAAGTTTCTGATTACTCCCTCCTTCACTATCTCTTTTACTATCTAGTTCAAATGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR290422, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8365 Dicrotendipes sp. water mite diet isolate 8365-BHL040517-GBD3557_8583-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTCTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGTACATTTATTGGAGATGATCAAATCTATAATGTAATTGTTACAGTTAATGCTTTTATTATAATTTTTTTTATGGTTATACCCATTCTAATTGGAGGTTTCGGAAATTGATTAGTCCCCTTTAATATTAGGAGCTCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8366 Chironomus sp. water mite diet isolate 8366-BHL040517-GBD23889_4707-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGACTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTCTTATAATTTTTTTTCTTAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTTTCCCCCTAATACTTGGAGCTCCGGACAAAG-TTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8369 Chironomus riparius water mite diet isolate 8369-BHL040517-GBD18967_22873-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGTTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACTAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCAAAGTTATACCCATTTTAATTGGAAGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACCCTTCTTCTTTCTAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8371 Chironomus riparius water mite diet isolate 8371-BHL040517-GBD12739_12330-Ldc67 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAAATTTATACATTATTTTTGGGGCTTGATCCGGAACAGTGGGAACTTCATTATGAATGCTTATTAGAGCAGAATTAGGACGACCCGGAACTTTCATTGAAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTAACTTTTACCCCCCTCTCTTACTCTTCGTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8374 Oligochaeta sp. water mite diet isolate 8374-BHL101416-GBD16207_16981-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTGCCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTTCTAATTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL8375 Chironomus riparius water mite diet isolate 8375-BHL101416-GBD25857_19453-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTAACTTGT-CCCATAATACTAGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGGCTTTTACCCCCCTCTCATACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8378 Amphichaeta raptisae water mite diet isolate 8378-BHL101416-GBD13594_21742-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL8379 Chironomus crassicaudatus water mite diet isolate 8379-BHL101416-GBD8557_10954-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAGTTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTTGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAATTCATTTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8380 Chydorus brevilabris water mite diet isolate 8380-BHL101416-GBD21444_21434-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCAGTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCCCGTCTTAATAAATTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTGGGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8381 Oligochaeta sp. water mite diet isolate 8381-BHL101416-GBD18933_16680-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACCCTATACTTAATTTTAGGAGTTTGAGCCGGAATAATTGGAACCGGAACTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTCCTAGGGAGAGATCAGCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTTTAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTATTACTTGGAGCACCAGATATGGCCTTCCCACGACTTAACAATTTAAGATTTTGACTTCTACCACCTTCACTAATCCTACTAGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL8382 Chironominae sp. water mite diet isolate 8382-BHL101416-GBD12740_19749-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATTAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTACTCATGCATTTATTATATTTTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTCTCAAGTTCGATTGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8383 Chironomus crassicaudatus water mite diet isolate 8383-BHL101416-GBD8480_7376-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATATTATTTTGGTGCTTGCTCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAGTTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGATCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTCTTGACTTCTCCCCCCATCCTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.1% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8384 Chironomidae sp. water mite diet isolate 8384-BHL101416-GBD21573_16830-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCGTGATCGGGAATAGTAGGAACTTCTCTTAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAAATTTAATTGGAGATGATCAAATTTATAATGTTATTGTAACAGGCCATACTTTTATTATAATTTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTAGTGCCATTAATATTAGGAGCACCTGATATGGCATTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCTTCCTTAACATTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR754220, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8385 Lebertia sp. water mite diet isolate 8385-BHL101416-GBD22359_12472-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGAAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTAAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATTAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCCTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8386 Chydorus brevilabris water mite diet isolate 8386-BHL101416-GBD22839_25659-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTCTTTGGAATTTGAGCTGGTATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATAAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTCTTAGTAGGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8387 Chironomus sp. water mite diet isolate 8387-BHL101416-GBD22697_19494-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTCTAGGGGCTTCACCCGGAATAGTGGTAACTTCATTAAGAATGCTTATTCGAGCAGATTTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCAACTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8388 Oligochaeta sp. water mite diet isolate 8388-BHL101416-GBD27297_11431-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAAGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTTCCTAATAATTTTCTTTATGGTTATACCAGTATTTATTGGAGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGAATAAACAATTTAAGATTCTGACTACTACCACCTTCACTAACCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL8390 Chironomus riparius water mite diet isolate 8390-BHL101416-GBD26041_14341-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACGTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTGTTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAATTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTCGTCCCACTAATACTTGGAGCACCTGACGTAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTGTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8391 Chironomus sp. water mite diet isolate 8391-BHL101416-GBD12626_17340-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTGGGAACTTCATTAAGAATGCTTGTTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTCGTCCCCCTAATACTTGGAGCACCTGACGTAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACCTTTACCCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8392 Chironominae sp. water mite diet isolate 8392-BHL101416-GBD21071_15972-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAAGAATGGTAGGAACTTCTTTAAGTATACTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAACGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGGCTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8393 Chironomus sp. water mite diet isolate 8393-BHL101416-GBD23817_10486-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCCGGAAATTTCATTGGCGATGACCAAATTTATAATGTTGTAGTTACTGCACATGGTTTTATTATAATTTTTCTCATAGTTATACCAATTTTAATTGGAGGGTTCGGAAACTGACTTGTCCCCCTAAGACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGCTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8394 Chironomus sp. water mite diet isolate 8394-BHL101416-GBD25338_25324-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGGGGCTTCATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACTAAATTTATAATGTTGTAGTTAGTGCACATGCTTTTATTATAATTTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTCTCTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8395 Psectrocladius sp. water mite diet isolate 8395-BHL101416-GBD21527_25221-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTCATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAGTAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8396 Phaenopsectra sp. water mite diet isolate 8396-BHL101416-GBD6357_19314-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR723136, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8397 Chironominae sp. water mite diet isolate 8397-BHL101416-GBD10784_18612-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8398 Chironominae sp. water mite diet isolate 8398-BHL101416-GBD22958_6691-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTAGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTCCCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8400 Chironomus sp. water mite diet isolate 8400-BHL101416-GBD4215_15758-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACACTATACTTTATTTTTGGTCCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATCACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCTTTTAATATTTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8401 Phaenopsectra sp. water mite diet isolate 8401-BHL101416-GBD17100_7762-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCCTCTCTTACTCGTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8402 Chironomus riparius water mite diet isolate 8402-BHL101416-GBD21793_20932-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGAAATAGTGGGAACTTCATTAAAAATGCTTATTCGAGCAGAATTAGGACGATCCGGAACTTTCATTGGAGGTGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTAGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGTTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8403 Chironomus sp. water mite diet isolate 8403-BHL101416-GBD17238_23764-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATAATTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8405 Chironomus sp. water mite diet isolate 8405-BHL101416-GBD10051_12899-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGGGGCTTCATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGAAGACCCGGGACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCCTAATTCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8407 Chironominae sp. water mite diet isolate 8407-BHL101416-GBD10479_15350-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATATTTTTTTTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGAATATTAATCCGAACGGAATTAGGTCATCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTAGAAATTGGTTATTACCACTAATATTAGGAGCCCCTGATATGGCTTTTCCACGAATAGATAATATAAGATTTTGATTATTACCACCATCTCTTACATTATTACTTTCAAGAAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR661442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8408 Chironomus sp. water mite diet isolate 8408-BHL101416-GBD12604_8302-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGGTTTTATTATAATTTTTCTCATAGTTATACCAATTTTAATTGGAGGGTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGCTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8409 Chironominae sp. water mite diet isolate 8409-BHL101416-GBD16198_12104-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGTCGGACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCACGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8412 Phaenopsectra sp. water mite diet isolate 8412-BHL101416-GBD23752_14539-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATAAAGCATTTCCTCGGATAAAAAATATAAGTATTTGACTTTTACCCCCCTTCTTTAACTTTACTTCTTTCTACTACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8414 Chironomus sp. water mite diet isolate 8414-BHL101416-GBD15239_5482-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGAGCCGAAATAGTGGGAACTTCATTAAGAATGCTTATGCGAGCAGAATTAGGACGATCCGGAACTTTCATTGGAGATGACCAATTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTGGGAAACTGACATGTCCCCCTAATACTTGGAACACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8416 Phaenopsectra sp. water mite diet isolate 8416-BHL101416-GBD5856_19047-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGGTTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.7% identical to accession ID KR274695, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8418 Oligochaeta sp. water mite diet isolate 8418-BHL101416-GBD25313_7665-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACCCTATACTTAATTTTAGGAGTTTGAGCCGGAATAATTGGAACCGGAACTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTCCTAGGGGAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGC-TTTCCTACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL8419 Chironomus sp. water mite diet isolate 8419-BHL101416-GBD27961_10108-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAACTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACACCCCTCTCATGCTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL842 Chironomidae sp. water mite diet isolate 842-BHL100916-GBD7684_22063-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTGTTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAAAACTCGATCACGCTGATTCTTTCATCGGAGAAGATCAAATTTATAATGTAATTGTTACCGCTCATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTATTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR752938, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8422 Oligochaeta sp. water mite diet isolate 8422-BHL101416-GBD19681_26852-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAACTGGAACAGGAACTAGAATATTAATTCGGATTAAATTATCTCAACCAGGATCATTACTATGGAAGAGATCAACTAGATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCGTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL8424 Chironomus sp. water mite diet isolate 8424-BHL101416-GBD20151_8827-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAACTTATAATGTTGTAGTTACTGCACATGCTTTTATTATATTTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACATTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KC750313, identified in GenBank as Chironomus nepeanensis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8426 Chironomus sp. water mite diet isolate 8426-BHL101416-GBD27330_16804-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTATTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTCTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAACACCAGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8427 Cricotopus sp. water mite diet isolate 8427-BHL101416-GBD21524_16189-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGAATAGTGGGTACCTCTCTTAGAATTTTAATTCGAGCAGAATTAGGTCATGCGGGTTCTTTAATTGGAGATGATCAAATTTACAATGTAATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTAATACCAATTCTAATTGGAGGATTTGGAAATTGATTAGTCCCTCTAATACTAGGAGCCCCAGATATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTATTACCACCTTCTTTAACATTATTATTATCAAGATCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR656807, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8428 Chironomus sp. water mite diet isolate 8428-BHL101416-GBD13973_12701-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACGTTATACTTTATTCTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGTATGCTTGTTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTCGTCCCCCTAATACTTGGAGCACCTGACGTAGCTTTTCCTCGAATAAATAATAAAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTGCTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8429 Phaenopsectra sp. water mite diet isolate 8429-BHL101416-GBD14320_11225-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCGTGATCGGGAATAGTAGGAACTTCTCTTAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAAATTTAATTGGAGATGATCAAATTTATAATGTTATTGTAACAGCCCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTCTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAGATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR723136, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL843 Cricotopus sp. water mite diet isolate 843-BHL100916-GBD11757_20659-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTATCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGTGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCTTCGAATAAATAATATAAGTTTTTGATTATTACCCCCCTTCTCTCACCTAACGTCTTTCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8433 Oligochaeta sp. water mite diet isolate 8433-BHL101416-GBD14009_10259-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACCTAATCTTAGGAGTTTGAGCTGGAAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGGTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTGTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTAGTAGTTGCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL8434 Chydorus sp. water mite diet isolate 8434-BHL101416-GBD13737_24214-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTAATTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAACGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGGTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCGTTCCCTCGTCTTAATAAATTAAGTTTCTGGCGTCTTCCCCCAGCTTTAACCCTTCTTTTAGAAGGGAGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8435 Phaenopsectra sp. water mite diet isolate 8435-BHL101416-GBD4063_18566-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTTGGTACTTCTTTAAGTATGCTAATTCGAGCAGATCTTGGACGACCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTGTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR274695, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8436 Oligochaeta sp. water mite diet isolate 8436-BHL101416-GBD16760_5797-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAGTCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATAAAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTTGTTATACCATTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCCCCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.4% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL8437 Chironomus sp. water mite diet isolate 8437-BHL101416-GBD27616_16925-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTAACTAGT-CCCTTTATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCCTTACTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8439 Phaenopsectra sp. water mite diet isolate 8439-BHL101416-GBD5283_21744-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTTTGGAGCTTGATAAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGGGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR769945, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8440 Chironomus sp. water mite diet isolate 8440-BHL101416-GBD7315_16703-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAGCTTCCCTTAGATTATTTATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTTGGTGATGACCAAATTTATAATGTATTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGATCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTCTTGACTTCTCCCCCCATCCTTAACTCTACTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8441 Chironomus sp. water mite diet isolate 8441-BHL101416-GBD24983_17920-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGAAAACTAACTTGT-CCCATAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTTTTACCCCCCTATCTAACTCTACTAATTTCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8442 Chironominae sp. water mite diet isolate 8442-BHL101416-GBD25256_5984-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGTGGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAATAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8444 Chironomus sp. water mite diet isolate 8444-BHL101416-GBD29111_15313-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTCGGACGACCTGGATCTTTTATTGGTTATGACCAAATTTATAATGTAGTTGTTACAGCTCACGCATTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTAACTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8446 Chironomidae sp. water mite diet isolate 8446-BHL101416-GBD21425_25842-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTTATTCGACTCGAATTAGGACACCCAGGCTCATTAATCGGAGAAGAACAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCGTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8447 Chironominae sp. water mite diet isolate 8447-BHL101416-GBD20246_15945-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGCAGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8448 Chironominae sp. water mite diet isolate 8448-BHL101416-GBD21521_19523-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACCTCCTCCATCTCTAACACTACTTCTTTCAAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8449 Chironomus sp. water mite diet isolate 8449-BHL101416-GBD22518_14953-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGAGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGGTTTTATTATAATTTTTCTCATAGTTATACCAATTTTAATTGGAGGGTTCGGAAACTGACTTGCCCCCCTAATACTTGGAGCACCTGACATAGCTTCTCCTCGAATAAATAATATAAGCTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL845 Cricotopus sp. water mite diet isolate 845-BHL100916-GBD18138_14574-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTAAAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTAATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAAAAATAAAAGTTTTTGATTATTCCCCCCTTCTCACACCTTACTTCATTCAAGTGCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8453 Chironomus sp. water mite diet isolate 8453-BHL101416-GBD20373_8490-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTTGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACTGG	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8454 Chironomus sp. water mite diet isolate 8454-BHL101416-GBD8111_23015-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8455 Oligochaeta sp. water mite diet isolate 8455-BHL101416-GBD3151_16979-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATCGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCCTTCCCACGATTTAACCATTTAAGATTCTGACTACTACCACCTTCCCTAATCCTATTAGTTTCTTCTGCCGCCGTAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL8460 Phaenopsectra sp. water mite diet isolate 8460-BHL101416-GBD3552_13420-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTGTAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGATCTTGGACGACTTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR274695, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8461 Chironomus sp. water mite diet isolate 8461-BHL101416-GBD19449_17936-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGCTATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTACTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAATTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTTTCCTCGAATAAATAATATAAGCTGCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8473 Chironomus sp. water mite diet isolate 8473-BHL101416-GBD11982_17182-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTAGAGCTTGATCAGGAATAGTAGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTTAATGCTTGGAGCATATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCATCTTCTTTCTAGTTATTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8477 Oligochaeta sp. water mite diet isolate 8477-BHL101416-GBD16896_20122-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGATTAAACCAGTATTTATTGGGGGAGTTGAAAATTGACTTCTACCTCTAATACTTGGAGCATCAGATATAGCTTTCCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL8478 Chironomus riparius water mite diet isolate 8478-BHL101416-GBD19352_27814-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGAGGCTTCATCCGGAATATTGGGAACTTCATTAAGAATGCTTATTCGAGCATAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATTCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCATCTTCTGTCTAGTTCTTGCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8483 Chironominae sp. water mite diet isolate 8483-BHL101416-GBD16417_5250-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTAATCAGGAATGGTAGGAACTTCTTCAAGGATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8489 Chironomus sp. water mite diet isolate 8489-BHL101416-GBD19172_11638-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTAAAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATACAAGTTTCTGACTTTGACCCCCCTCTCTTACGCGTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL849 Chironomidae sp. water mite diet isolate 849-BHL100916-GBD18055_8318-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTTTATTTTATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTTTAAGAATTCTAATTCGAGCAGAATTAGGATATGCAGGCTCATTATTTGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAATTGACTCGTTCCTTTAATATTAGGAGCACCTGATATGGCTTTCCCACGAATAAATAATATAAGATTTTGATTGTTGCCCCCATCATTAACTTTATTATTATCTAGATCAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KM964594, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8490 Chironomidae sp. water mite diet isolate 8490-BHL101416-GBD11780_19114-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTAATCTTAGGAGTATGAGCAGGAATAGTTGGTACAAGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGTTATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KR723136, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8492 Chironomus sp. water mite diet isolate 8492-BHL101416-GBD9942_20697-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCATTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTGTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8495 Oligochaeta sp. water mite diet isolate 8495-BHL101416-GBD22933_23760-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAATTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAAATTATATCAACCAGGATCATTCCTAGGAAGAGATCAACTTTTTAATACTCTAGTAACTGCACATGCTTTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGACTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL8496 Phaenopsectra sp. water mite diet isolate 8496-BHL101416-GBD11739_25220-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACTCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATATGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8498 Chironominae sp. water mite diet isolate 8498-BHL101416-GBD27540_12920-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGAAGCTTGACCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACTTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8500 Chironominae sp. water mite diet isolate 8500-BHL101416-GBD23615_26607-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTTGGAACTTGGTCAGGAATGGTGGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTATTTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCCTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8504 Chironomus sp. water mite diet isolate 8504-BHL101416-GBD17356_28909-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTCTGGGGCTTCATCCGGAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTTCATAGTTAGACCAATTTTATTTGGAGGATTCGGAAACTGACTTTTCCCCCTAATGTTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCACTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8509 Chironomus sp. water mite diet isolate 8509-BHL101416-GBD24295_20371-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGG-AACTGACTTGTCCCCCTAATGCTTGGAACACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8510 Oligochaeta sp. water mite diet isolate 8510-BHL101416-GBD12435_15255-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATCATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTATGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAACCCTATAAGAATCTTCTGCTGCCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 85.7% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL8521 Chironomidae sp. water mite diet isolate 8521-BHL101416-GBD16869_11523-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAAC---CCTTCTTT-TAGTGGGGGGGGGCA---GTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.8% identical to accession ID KR769945, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8523 Phaenopsectra sp. water mite diet isolate 8523-BHL101416-GBD27139_17794-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATTTTAATTCGAGCAGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGTAATTGATTAGTACCTCTAATATTGGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTTCCCCCGTCTTTAACTTTACTACTATCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8524 Chironomus sp. water mite diet isolate 8524-BHL101416-GBD9428_20258-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTACCCTATACTTTATTTTTGGAGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTCTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTAACATGT-CCCATAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8529 Chironominae sp. water mite diet isolate 8529-BHL101416-GBD26348_23409-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTTGGAGCTTGATCAGGAATGGTAAGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATACTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8532 Chironomus sp. water mite diet isolate 8532-BHL101416-GBD26701_23039-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGGGGCTTCATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGTACTTTCATTGGAGATGACAAAATTTATAATGTTGAAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGCATTCGGAAACTTTCTTGTCCCCCTAATGCTTGGATCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTATCCCCCTCTCTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL854 Cricotopus sp. water mite diet isolate 854-BHL100916-GBD15843_6486-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGGGCTTGGTCAGGAATAGTAGGAACTTCTTTAAGAATTTTAATTCGAGCTGAATTAGGTCATGCCGGCTCATTAATTGGTGACGATCAAATTTATAATGTAATTGTTACAGCCCATGCTTTCGTAATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGGAATTGATTAGTTCCTTTAATACTTGGGGCACCAGATATAGCCTTTTCCGCGAATAAATAATATAAGATTTTGACTATCACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR670938, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8542 Chironomidae sp. water mite diet isolate 8542-BHL101416-GBD24338_11106-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 83.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8544 Chironomidae sp. water mite diet isolate 8544-BHL101416-GBD6376_13530-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCC------ATCACTAATTCTAT-TAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.3% identical to accession ID KR769945, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8545 Chironominae sp. water mite diet isolate 8545-BHL101416-GBD23546_15511-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTATTTTTGGAGCGTGATCGGGAATAGTAGGAACTTCTCTTAGAATATTAATTCGAGCTGAATTAGGATATCCTGGAAATTTAATTGGAGATGATCAAATTTATAATGTTATTGTAACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8546 Chironomidae sp. water mite diet isolate 8546-BHL101416-GBD23627_4541-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGACCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGTCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAACAATAAAAGTTTTTGATTTCTTCCTCCATCTCTAACTCTTCTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KJ166684, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8547 Chydorus sp. water mite diet isolate 8547-BHL101416-GBD22933_6642-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATAAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8549 Chironomidae sp. water mite diet isolate 8549-BHL101416-GBD4998_20214-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTATTTTTGGCGCCTGATCTGGGATAGTCGGGACTTCTCTAAGAATGCTTACTCAAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGC-TTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8555 Phaenopsectra sp. water mite diet isolate 8555-BHL101416-GBD27698_12003-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTAGTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTACACTAATCCAATTAGTTTCTTCTGCTGC---CGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL856 Cricotopus sp. water mite diet isolate 856-BHL100916-GBD22767_24069-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTAAGAATCTTAATTCGAGCTGAATTAGGTCATGCTGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGAAATAGCTTTCCCCCGAATAAAAAATATAAGTTTTTGATTAATACCCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8561 Oligochaeta sp. water mite diet isolate 8561-BHL101416-GBD23332_24006-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAAATTATCTCAACCAGGATCATTCCTAGGAAGAGTTCAACTTTATAATACTCTAGTAACTGCACAGGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCCTCACTAAACCTATTAGTTTCTTCTGGGGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.2% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL8562 Phaenopsectra sp. water mite diet isolate 8562-BHL101416-GBD16110_13472-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAAATTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGTAATTGATTAGTACCACTAATATTAGGAGCCCCTGATATAGCATTTCCACGAATAAATAATATAAGTTTTTGACTATTACCACCATCTCTAACTTTACTTCTTTCAAGAACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR723136, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8563 Polypedilum sp. water mite diet isolate 8563-BHL101416-GBD14321_13584-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCGTGATCGGGAATAGTAGGAACTTCTCTTAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAAATTTAATTGGAGATGATCAAATTTATAATGTTATTGTAACAGCCCATGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGCTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID MG449714, identified in GenBank as Polypedilum sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8570 Phaenopsectra sp. water mite diet isolate 8570-BHL101416-GBD23497_23812-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTCATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCACCTGATATAGCATTTCCCCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTAACCGTACTTCTTTCAAGTACAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR723136, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8571 Chironomus sp. water mite diet isolate 8571-BHL101416-GBD22090_27588-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTGGGGCTTCATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCTGAATTAGGACGACCCGGGACTTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAAATGGAGGATTCGGAAACTGATTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCACGAATAAATAATATAAGTTTCTGACTGTTACCCCCCTTCTCTAACTCATCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8573 Chironomus sp. water mite diet isolate 8573-BHL101416-GBD13253_24058-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAGGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAAAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGGGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8574 Chironomus riparius water mite diet isolate 8574-BHL101416-GBD24199_22520-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGTTCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGTACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAACACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTACTGACTTTTACCCCCCTCTCTTACTCATCTTCTTTCTAGTACTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8578 Chironomidae sp. water mite diet isolate 8578-BHL101416-GBD19868_7999-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCGTGATCGGGAATAGTAGGAACTTCTTTTAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAAATTTAATTGGAGATGATCAAATTTATAATGTTATTGTAACAGCCCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTCGGAAACTAACTTGTCCCA-TAATACTTGGAGGACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR754220, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8580 Oligochaeta sp. water mite diet isolate 8580-BHL101416-GBD21512_11110-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTAGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTATCTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTTGGAAATTGACTTTTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACATTATAAGATTCTGACTACTACCCCCTTCATTAACCCTATTAGTTTCTTCTGCAGCCGTAGAAAATGGAGCTAGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.

>RL8582 Chironomus sp. water mite diet isolate 8582-BHL101416-GBD26744_15814-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGGTTTTATTATAATTTTTCTCATAGTTATACCAATTTTAATTGGAGGGTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCCTTTCCCCGAAAAAAAAAAAATAAGCTTCTGAATTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8589 Phaenopsectra sp. water mite diet isolate 8589-BHL101416-GBD28206_9485-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTAGGGAGCATGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTATTACCCCC------ATCACTAATTCTAT-TAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.2% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL859 Cryptochironomus sp. water mite diet isolate 859-BHL100916-GBD3525_15969-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATGTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACAAACAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATATCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGTCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8591 Phaenopsectra sp. water mite diet isolate 8591-BHL101416-GBD14923_17700-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAACTCGGCCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGGTTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCATTAACTTTACTACTATCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8600 Chironomidae sp. water mite diet isolate 8600-BHL101416-GBD28939_15856-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACGTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCCTGTTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTATTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGATTTTGATTACTTCCTCCATCTCTATCCCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.7% identical to accession ID GU944724, identified in GenBank as Chironomus circumdatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8602 Lebertia sp. water mite diet isolate 8602-BHL101416-GBD11542_26900-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGATTTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTCTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTACACTAATAATCAGAGCCCAAGATATAGCTTTTCCACGAAAAAATAATATAAGATTATGACTTCTTCCTCCATCCTTAACACTACTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8609 Chironomus sp. water mite diet isolate 8609-BHL101416-GBD5097_12440-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCAGGAATAGTAGGAACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGGTTTTATTATAATTTTTCTCATAGTTATACCAATTTTAAAATGGAGGCTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGCTTCTGACGTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8611 Lebertia sp. water mite diet isolate 8611-BHL101416-GBD17180_4142-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAATTCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCATTTCCACGAATAATTAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTATTTCTATCAAGTTCCTTTACCGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8615 Chironomidae sp. water mite diet isolate 8615-BHL101416-GBD18118_8460-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCGTGATCGGGAATAGTAGGAACTTCTCTTAGAATATTAATTCGAGCTGAATTAGGACATCCTGGAAATTTAATTGGAGATGATCAAATTTATAATGTTATTGTAACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGATATTGACTAGTGCCATTAATGTTAGGAGCACCTGATATGGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCATTCGTAGAAGATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR754220, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8616 Chironominae sp. water mite diet isolate 8616-BHL101416-GBD12513_6409-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATACATTATTTTTGGGGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGTCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTGTTTTATAGTTATACCTATTTTAATTGGAGG-TTTGGATATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8617 Culex pipiens water mite diet isolate 8617-BHL101416-GBD3323_14037-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCTTATATGGCCTTTCCTCGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACACTTCTACTTTCAAGTAGTTTAGTATAAAATGGCGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.4% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8620 Chydorus sp. water mite diet isolate 8620-BHL101416-GBD21640_5621-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCATAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAACGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGACACCTGATATAGCCTTCCCTCGTCCTAATAATTTAAGTTTCTGGCTTCTTTCCCCCAGCTTTAACCCTACTTATAGTAGGGGGGGCAGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8622 Chydorus brevilabris water mite diet isolate 8622-BHL101416-GBD6011_23008-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTTGGGGCTTGATCCGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCAAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTATGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.8% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8630 Phaenopsectra sp. water mite diet isolate 8630-BHL101416-GBD20854_16478-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTTATAGTAATACCAATTTTAATTTGAGGATTCGGAAACTAACTTGT-CCCATAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.1% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8639 Oligochaeta sp. water mite diet isolate 8639-BHL101416-GBD26015_15507-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTATGAGTTTGAGCTGGAATAATTGGAACAGGAACCAGAATATTAATTCGGATTGAATTATCTCAACCAGGGTCATTCCTAGGAAGAGATCAACTATATAGTACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGATTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 81.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL8644 Culex sp. water mite diet isolate 8644-BHL101416-GBD11749_10795-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTATTTTTGGGGCTTGATCAGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAGGTCAACCAGGTGTATTTATTGGAAATGGTCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTTATAGTAATACCAATTATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGACCTTTCCTCGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL865 Cricotopus sp. water mite diet isolate 865-BHL100916-GBD20176_24251-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGTAATAGTAGGTACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGATGTGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATAACTATTTTAATTGGAGGATATTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTGACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8656 Oligochaeta sp. water mite diet isolate 8656-BHL101416-GBD21688_24794-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATATTTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATATTATGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.2% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL866 Cricotopus sp. water mite diet isolate 866-BHL100916-GBD27885_17254-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATAAGGAATAGTAGGGACTTACTTGAGAATCTTAATTCGAGTTGAATTAGGTCATGACGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTGCTTTCAAGTTCAATTGTTTAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8663 Psectrocladius sp. water mite diet isolate 8663-BHL101416-GBD8577_15214-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCCTGATCAGGCATAGTAGGCACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCCGGTTCCTTAATTGGAGATGAACAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTCCCGTTAATATTAGGAGCCCCCGACATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.1% identical to accession ID KR739843, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8667 Chydorus sp. water mite diet isolate 8667-BHL101416-GBD24116_23339-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAATGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTTGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCCTTTGTTATAATCTTTTTTATAGTTATACCCATTTTAATTGGGGGGTATGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGACATAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8670 Phaenopsectra sp. water mite diet isolate 8670-BHL101416-GBD24411_24034-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGTTGAATTATGTCAACCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGACTATTACCCCCATCTCTAACTTTACTACTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8671 Phaenopsectra sp. water mite diet isolate 8671-BHL101416-GBD21915_19318-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATACTTTATTTTTGGAGCCTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTTAGTAATACCTATTTTTAATTGTGGGATTTGGAAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCATTAACTTTACTACTATCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8676 Phaenopsectra sp. water mite diet isolate 8676-BHL101416-GBD22875_13078-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATACTTTATTTTTGGGGCTTGATCCGAAATAGTGGGAACTTCATTAAGTATGCTTATTCGAGCAGACTTAGGACGATCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATCATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.2% identical to accession ID KR274695, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8678 Chydoridae sp. water mite diet isolate 8678-BHL101416-GBD10067_16901-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTCGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCTTAATATTAGGGGCACATGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTAACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATC-GTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.9% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8681 Phaenopsectra sp. water mite diet isolate 8681-BHL101416-GBD14579_12902-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTTTACTTTATTTTTTTGGAGCTTGATCAGGACTAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTCTTTGACTTTGACCCCCTTCTTTAACATTACATCAATCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8684 Chironominae sp. water mite diet isolate 8684-BHL101416-GBD21672_26345-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTCTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAATTTGGCCATCCGGGTACCTTTATTGGAGAAGACCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTAACTCTTCTTCTTTCAAGTTCAATTGTAGAAAGTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8686 Phaenopsectra sp. water mite diet isolate 8686-BHL101416-GBD20790_9019-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATACTTTATTTTTGGAGCTTGATCAGGAATAGTGGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGACACCCCGGAACTTTCATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCCTCTTTAACTTTACTTCTTTCTAGTTCGATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8688 Chydorus brevilabris water mite diet isolate 8688-BHL101416-GBD5919_6196-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTTTTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCGTTATTGGAGATGATCAAATTTACAATGTTATTGTCATTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGTGGGGTTTGGAAACTGACTCTTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGACAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8697 Phaenopsectra sp. water mite diet isolate 8697-BHL101416-GBD9441_25190-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGTTCAGGAATAGTAGGAACTTCTTTAACTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTTATAGTTACTGCACATGGTTTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATCTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGTATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8706 Chironomus sp. water mite diet isolate 8706-BHL101416-GBD11455_7316-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGGCTGATCCGGAATAGTGGGCACTTCATTAAGAATACTTATTCGAGCAGAATTAGGACGACCCGGAACTTTTCATTGGAGATGACCAAATTTACAATGTTGTAGTTACTGCACATGGTTTTATTATAATTTTTCTCATAGTTATACCAATTTTAATTGGAGGGTTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGCTTCTGACTTTTACCCCCGTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL871 Cricotopus sp. water mite diet isolate 871-BHL100916-GBD19094_23898-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTGAGTATCTTAATTCGAGCTGAATTAAGTCATGCCGTATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTACCTTTAATGTTAGGAGCTCCTGATATAGCTTTCCCCCGAATAAATAATATAAGTTTTTGATTATTACCCCCCTTCTCTCACCTTACTACTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8714 Chironomus sp. water mite diet isolate 8714-BHL101416-GBD6870_8778-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGCACTTTATATTTTATTTTTGGTACTTGATCAGGAATAGTTGGAACTTCCCTTAGAATATTAATTCGAGCAGAACTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAAATTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTTCCTTTAATATTAGGAGCTCCAGATTTGGCCTTCCCATCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCTTTTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8718 Chydorus brevilabris water mite diet isolate 8718-BHL101416-GBD16810_24834-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAATAGGGACCCTTATTGGAGATGATCAAATTTAGAACGTTACTGTCACTGCACATGCTTTTGTTATAATCTTTTCTATAGTTATACCCATCATAATTGGTGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGAGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8726 Chironomus sp. water mite diet isolate 8726-BHL101416-GBD12614_21012-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTT-GGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAACAATATAAGTTTTTGATTACTTCCTCCATCTCTATCTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.1% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8730 Lebertia sp. water mite diet isolate 8730-BHL101416-GBD9610_4168-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTAAATCGACTTGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCGTGCTTTCGTTATAATTTTCCTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTATTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCCTTCTTTATCTTTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8731 Oligochaeta sp. water mite diet isolate 8731-BHL101416-GBD24315_17984-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGCGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGCATCATTCCTAGGAAGAGATCAACTATTTAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTTCTGGTTATACCAGTATTTATTGATGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGATTTAACAATTTAAGATTCTGACTACTACCCCCTTTACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.9% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL8734 Diptera sp. water mite diet isolate 8734-BHL101416-GBD15269_21757-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTACATTATATTTTATTTTTGGAGCTTGATTAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTTATAGTAATACCTATTTTAATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATGGCATTCCCACGACTTAACAATATAAGATTTTGACTTCTACCACCTTCACTAACCCTACTGGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACTGG	Using NCBI BLASTN in June 2018, this sequence was 87.0% identical to accession ID JF966742, identified in GenBank as Anopheles claviger. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8737 Chironomidae sp. water mite diet isolate 8737-BHL101416-GBD7191_17693-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACTTCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTAGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGCACCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCATCATTAACCTTATTATCAACTAGAACACTAGCTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KJ207864, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8740 Chironominae sp. water mite diet isolate 8740-BHL101416-GBD21457_10516-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAACTTGGCCATCCAGGTACCTTTATTGGAGATGACCAAATTTATAATGTTTTTGTAACTGCTCATGCATTTATTATAATTTTTTTTTATAGTTTTACCTATTTTAATTGGAGGATTTGGAAATTGATTTGTACCTCTTATATTAGGAGCCCCTGATATAGCTTTTCCACGAATAAACAATATAAGATTTTGATTACTTCCACCATCTCTAACTCTTCTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR289330, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8742 Chironominae sp. water mite diet isolate 8742-BHL101416-GBD11601_27027-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTTAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGAACAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTTTTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCTTCATTAACTCTATTACTTTCAAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8745 Phaenopsectra sp. water mite diet isolate 8745-BHL101416-GBD9409_17973-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTATGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTATTTCGAGCTGAATTGGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCTTTTATTATATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTTTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCCTCTTTAACTTTACTACTATCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8746 Lebertia sp. water mite diet isolate 8746-BHL101416-GBD8584_8438-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTCTTGGAGCATGATCCGGAATAATTGGAGCTAGATTAAGAACCCTACTTCGACTTGGATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTTTAACTGCTCATGCTTTCGTTATAATTTTCTTCATAGTAATACCAATGATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGACTTCTTCCTCCATCCTTAACTCTACTTCTATCAAGTTCCTTTACAAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8748 Oligochaeta sp. water mite diet isolate 8748-BHL101416-GBD22030_24545-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTTAACCAGGATCATTCCTGGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTATCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTATAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCATTAATCTTATTAGTTTCTTCTGCTGTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL8751 Oligochaeta sp. water mite diet isolate 8751-BHL101416-GBD24122_16692-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATAGTTTATCTTAGGAGTTTGAGCTGGAATAATTGGTACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATTAACTATACAATACTCTAGTAACTGCACATGCATTCGTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGATGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.8% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL8756 Chironominae sp. water mite diet isolate 8756-BHL101416-GBD18532_2668-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACTGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTTTTTTACTTTCAAGTGCTACTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8759 Phaenopsectra sp. water mite diet isolate 8759-BHL101416-GBD26833_14431-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACATTATCCTTTATTTTTGGAGCTTAATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGTAATTGAATAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCGTCTTTAACTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR293527, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8761 Phaenopsectra sp. water mite diet isolate 8761-BHL101416-GBD25821_20988-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTACGTATATTAATTCGAGCTGAATTAGGTCACCAAGGAACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATGCTTGGAGCACATGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8767 Chironomidae sp. water mite diet isolate 8767-BHL101416-GBD5891_20847-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCTTGATCAGGAATGGTAGGAACTTCTTTAAGTATATTAATTCGAGCCGAACTTGGCCATCCAGGTACCTTTATTGGAGATGAGCAAATTTATAATGTTATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGCACCAGATATGGCCTTCCCACGACTTAACAATTTAAGATTTTGACTTCTACCACCTTCACTAATCCTACTGGTTTCTTCTGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.9% identical to accession ID KT104776, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8768 Chironomus riparius water mite diet isolate 8768-BHL101416-GBD12587_7296-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTGTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATTGTTATACCAA-TTTAATTGGAGGATTCGGAAACTAACTTGT-CCCCTGATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGAC-TTTATCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8773 Chironomus sp. water mite diet isolate 8773-BHL101416-GBD20849_8979-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGCATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTAACTTGT-CCCATAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCGCGCTTACACTACTGCTGTCTAGTGCTTGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8778 Chironomus riparius water mite diet isolate 8778-BHL101416-GBD11686_4770-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGCGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGAGTTGGAAACTGACTTGTCCCCCTAATACTTGGAACACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTCTTACCCCCCCTCTCTTACTCGTCTTCTGTCTAGTTCTTCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8781 Chydorus brevilabris water mite diet isolate 8781-BHL101416-GBD11774_5177-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAAAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATGTAGCCTCCCCTCGTCTTAATAATTGAAGTTTCTGGGTCCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGTGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8788 Oligochaeta sp. water mite diet isolate 8788-BHL101416-GBD3360_15151-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAATTTTCATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTA--TCT-TTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.0% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL8794 Oligochaeta sp. water mite diet isolate 8794-BHL101416-GBD26839_22673-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCATCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTAATAACAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTTGGAGTACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTATAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 86.3% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL8797 Chironominae sp. water mite diet isolate 8797-BHL101416-GBD27041_9089-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATACTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTCTAAGTATGCTAATTCGAGTAGATCTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGCAATTGTCACAACACATGCTTTTATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGATTTATTCCTTTAATGTTAGGACCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.8% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8799 Chironomus sp. water mite diet isolate 8799-BHL101416-GBD28116_15117-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACTTTATATATTATTTTTGGTACTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGATGTCCTGGAACTTTTATTAGTGATGACCAAATTTATAATGTAGTAGTTATAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTAAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCTTTCCCTTGAATAAATAAAATAAGTTATTGACTTCTCCCCCCAATCTTTAACTCTT-ATCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 95.9% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8808 Phaenopsectra sp. water mite diet isolate 8808-BHL101416-GBD9633_27875-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCAGGATCTTTAATTGGAGATGATTAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCATTAACTTTGCTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8809 Chironomus sp. water mite diet isolate 8809-BHL101416-GBD27760_19474-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAAAGTTATACATTATTTTTGGGGGCTTGATCCGGAATAGTGGGAACTTCATTAGGAATGCTTGTTCGAGTAGAGTTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGATACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAAGATTCGGAAACTGACTCGTCCCCCTAATACTTGGAGCACCTGACGTAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8812 Chironomus sp. water mite diet isolate 8812-BHL101416-GBD6485_25389-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGATCTTGGACGACCTGGTACTTTAATTGGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACATGT-CCCCTAATACTTGGAGCACCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATAGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8814 Chironomus sp. water mite diet isolate 8814-BHL101416-GBD9945_26388-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTCTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTAACTTGT-CCCATAATACTTGGAGCACCTGACATAGCTTTTCTTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTGTCTTTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8821 Chironomus sp. water mite diet isolate 8821-BHL101416-GBD6605_16857-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATATATTATTTT-GGTGCTTGGTCAGGAATAGTAGGAACTTCCCTTGGAATATTAATTCGAACAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTAACTTGT-CCCATAATACTTGGAGCACCTGACATAGCTTTTCCTAGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8827 Phaenopsectra sp. water mite diet isolate 8827-BHL101416-GBD23838_18586-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTATACTATACTTTATTTTTGGAGCTTGATCAGGTATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTGAATTAGGTCACCCTGGTTCTTTAATTTGAGATGATCAAATTTATAATGTAATTGTAACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGAAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCGTCTTTAACTTTACTACTATCTAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR276936, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL883 Dicrotendipes sp. water mite diet isolate 883-BHL100916-GBD24821_15072-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTAGAGCTTGATCCGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTAATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACTCTTCTTCTTTCTAAATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8835 Oligochaeta sp. water mite diet isolate 8835-BHL101416-GBD7714_25383-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CACCCTATACTTAATTTTAGGAGTTTGAGCCGGAATAATTGGAACCGGAACTAGAATATTAATTCGGATTGAATTAGCTCAACCAGGATCATTCCTAGGGAGAGATCAGCTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTTTAGTTATACCAGTATTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCTTCTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.1% identical to accession ID LT904771, identified in GenBank as Chaetogaster diastrophus. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL8837 Chironomus sp. water mite diet isolate 8837-BHL101416-GBD7356_11797-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGAGGCTTGATCCGGAATAGTGGTAACTTCAATAAGATTACTTATTCGAGCATAATTAGGACAACCCGGAACTTTCATTGGAGGTGACCAAATTTATAATGTTGTAGTTACTGCACATGGTTTTAATACAATTTTTCTCATAGTTATACCAATTTTAATTGGAGGGTTCGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGCTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTATCTAGCTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8842 Lebertia sp. water mite diet isolate 8842-BHL101416-GBD17317_22005-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTCTTTACTTTGCTTTTGGAGCATGCTCCGGTATAATTGGAGCTAGATTAAGAACCCTAATTCGACATGAATTAGGACAACCAGGCTCACTCCTAGGAAGTGACCAAATTTACAATACAATTGTAACTGCTCATGCTTTCGTTATAATTTTTTTCATAGTAATACCAATAATAATTGGAGGTTTTGGAAACTGATTAGTTCCACTAATAATCAGAGCCCCAGATAAAGCCTTTCCACGAATAAATAAAATAAGATTTTGACTTCTTCCCCCATCCTTAACTCTGCTTCTATCAAGTTCCTTTACAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG773262, identified in GenBank as Lebertia sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8850 Phaenopsectra sp. water mite diet isolate 8850-BHL101416-GBD24680_8231-Lqhc59 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATATATTATTTTTGGAGCTTGATCAGGAATAGTAGGAACTTCTTTAAGTATATTAATTCGAGCTAAATTAGGTCACCCAGGAACTTTAATTGGGGATGATCAAATTTTTAATGTAATTGTAACTGCCCATGCATTTATTATAATTTTTTTTATAGTAATACCTATTTTAATTGGGGGATTTGGTAATTGATTAGTACCTCTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGACTTTTATCCCCCTTTTTTATCTTTACTTCTTTCTAGTTCAATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR723136, identified in GenBank as Phaenopsectra sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8853 Paratanytarsus sp. water mite diet isolate 8853-BHL101416-GBD20599_22775-Lq60 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTGCTGCCTTTAATATTAGGAGCCCCAGAAATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8857 Chydorus brevilabris water mite diet isolate 8857-BHL101416-GBD3988_12120-Lq60 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTCATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGGTTTGGAAACTGACTTGTCCCCTTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTACTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8863 Cryptochironomus sp. water mite diet isolate 8863-BHL101416-GBD23028_12606-Lq60 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTCTTATACTGGGAGCACCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTAGCCCCCATCTTTGACCCGTCTTCTTTCAAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8866 Chironominae sp. water mite diet isolate 8866-BHL101416-GBD7517_18541-Lq60 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATATTAGGTACTTCTTTAAGTATGCTTATTCGAGCAGAACTTGGACGACCTGGTACTTTCATTGTAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTT-ATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCGGATATGGCTTTCCCTCGAGTAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8870 Chironominae sp. water mite diet isolate 8870-BHL032417-GBD13493_13287-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACATGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACACTTTTATTATATTTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8871 Dicrotendipes tritomus water mite diet isolate 8871-BHL032417-GBD18900_20356-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCATATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTAAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAAATCAATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8872 Chironomus riparius water mite diet isolate 8872-BHL032417-GBD29684_15845-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTGTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACCTTCATTGGGGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTGTCTGACTTTTACCCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8874 Paratanytarsus sp. water mite diet isolate 8874-BHL032417-GBD13469_6342-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCCGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 99.1% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8877 Chironominae sp. water mite diet isolate 8877-BHL032417-GBD23573_8815-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAATAGGTACTTCTTTAAGTATGCTAATTCGAGCAAAACTTGGACGACCTGGTACTTTTATTAGAGATGACCAAATTTACAATGTAATTTTCACAGCACACCCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTTTTCCTTTAATTTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTTTTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8879 Chironomus riparius water mite diet isolate 8879-BHL032417-GBD27592_11352-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATATTCCATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTTTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8880 Culex pipiens water mite diet isolate 8880-BHL032417-GBD24398_8260-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAAACAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAA-TTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAAGAAATAATATAAGTTATTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 98.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8881 Lebertia quinquemaculosa water mite diet isolate 8881-BHL032417-GBD17850_19136-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATACTTCGCTTTTGGGGCTTGATCAGGAATGGAGGGAGCAAGACTAAGAACTTTAATCCGTTTAGAATTAGGACAACCAGGAACTCTCCTAGGAAGAGACCAAATTTATAATACTATCGTAACAGCTCACGCCTTCGTTATAATTTTCTTTATAGTTATGCCAATAATAATTGGAGGATTCGGAAATTGACTAGTCCCATTGATAATTAGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGACTTTTACCCCCCCTCTTTAACTCTTCTACTATCTAGTTCTTTTACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID MG773261, identified in GenBank as Lebertia quinquemaculosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8882 Paratanytarsus sp. water mite diet isolate 8882-BHL032417-GBD15006_2108-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAACGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8883 Chironominae sp. water mite diet isolate 8883-BHL032417-GBD11962_14720-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGGCCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCCCATGCTTTTACTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGCTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACACTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID MG449442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8884 Paratanytarsus sp. water mite diet isolate 8884-BHL032417-GBD3054_11868-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGATCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGGTTTTGATTACTTCCCCCATCGTTAACCCTACTTCTATCAAAAAGATTAGTATAAAGTGGAGCTGAAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8885 Dicrotendipes sp. water mite diet isolate 8885-BHL032417-GBD9753_16791-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACGACGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.0% identical to accession ID KR286332, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8887 Glyptotendipes sp. water mite diet isolate 8887-BHL032417-GBD11835_4865-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACCTTATATTTTATTTTTGGGGCATGATCAGGAATACTTGGGACTTCTTTAAGAATGATTATTCGAGCTGAACTAGGACGACCAGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACTGCACATGCATTTATTATAATTTTTTTTTATAGTTATACCTATTTTATTTGGAGGGTTTGGAAATTGACTAGTTCCTTTAATATTGGGGGCACCTGATATAGCGTTCCCTCGAATAAATAATATAAGATTTTGACTTTTACCTCCATCTTTAACCCTTTTACCTTCAAGTTCAATTGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.6% identical to accession ID KP954649, identified in GenBank as Glyptotendipes meridionalis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8888 Paratanytarsus sp. water mite diet isolate 8888-BHL032417-GBD10992_25032-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCTTTATATTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR276527, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL889 Cricotopus sp. water mite diet isolate 889-BHL100916-GBD7149_8887-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCCGGAATAGTAGGGACTTCCTTGAGAATGTTAATTCGAGCTGAATTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAAGATTTGGAAACTGATTAGTTCCTTTAACGTTAGGGACTCCTGATAAAGCCATCCCTCCAATAAATAATAAAAGTTTTTGATTATTAACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8890 Paratanytarsus sp. water mite diet isolate 8890-BHL032417-GBD19039_11975-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCGTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR758568, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8891 Chironomus riparius water mite diet isolate 8891-BHL032417-GBD23648_10523-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTTGACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8892 Chironominae sp. water mite diet isolate 8892-BHL032417-GBD15549_15101-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTAATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTTCCCCCTTCTCTTACTCTACATCTTTCTAGAGCAGTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8893 Chironominae sp. water mite diet isolate 8893-BHL032417-GBD11482_22792-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGAATTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTGCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8894 Dicrotendipes sp. water mite diet isolate 8894-BHL032417-GBD24758_12263-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTATTTTCGGAGCTTGATCAGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCAATCTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8895 Chironomus riparius water mite diet isolate 8895-BHL032417-GBD4401_11213-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCGCTTTATACATTATTTTTGGGGCTCGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTACTTGCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8896 Chironominae sp. water mite diet isolate 8896-BHL032417-GBD9964_11755-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAAAACTTGGACGACCCGGAACTTTTACTGGAAATGATCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTATTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8898 Paratanytarsus sp. water mite diet isolate 8898-BHL032417-GBD10097_19372-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAACTTGATCTGGAATAGTAGGTACTTCTTTAGGTATGCTAATTCTAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACGTTCCCCATCTTTAACCCATCTTCTATCTATAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.1% identical to accession ID KR758568, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8899 Chironomus sp. water mite diet isolate 8899-BHL032417-GBD14141_19133-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAACTTTAATTGGAGGATTCGGAAATCGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTGGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL890 Chironomidae sp. water mite diet isolate 890-BHL100916-GBD12766_21145-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGCACTTCCTTAAGAATTTTAATTCGACTAGAATTAGGACACCCTGGCTCATTAATCGGAGACGATCAAATTTATAATGCAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCCATTTTAATTGGAGGAGTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCCATCTCTCACCTTACTTCCATCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8900 Glyptotendipes sp. water mite diet isolate 8900-BHL032417-GBD11830_4890-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACCTTGTATTTTATTTTTGGGGCATGATCAGGTATAGTTGGGACTTCTTTAAGAGTGCTTATTCGAGCTGAACTAGGACGACCAGGAACTTTTATTGGTGATGATCAAATTTACAATGTAATTGTTACTGCACATGCATTTATTATAATTTTTTTTTTATAGTTATACCTATTTTATTTGGAGGGTTTGGAAATTGACTAGTTCCTTTAATATTGGGGGCCCCTGATATAGCTTTCCCTCGAATAAATACTATAAGTTTTTGACTTTTTCCTCCTTCTTTAACACTATTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID KP954649, identified in GenBank as Glyptotendipes meridionalis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8901 Paratanytarsus sp. water mite diet isolate 8901-BHL032417-GBD25142_10311-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTCAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR743912, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8903 Chironominae sp. water mite diet isolate 8903-BHL032417-GBD14018_9538-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACGACGTGGTACTTTTATTGGAGATGACCAAATTTACAACGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTCAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAAAAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8905 Chironominae sp. water mite diet isolate 8905-BHL032417-GBD17001_20198-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTGATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.3% identical to accession ID MG449215, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8906 Chironominae sp. water mite diet isolate 8906-BHL032417-GBD8394_10096-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTCCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCCTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG449442, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL891 Chironomidae sp. water mite diet isolate 891-BHL100916-GBD17631_27370-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTACTTTTGGAGCTTGATCGGGAATAGTTGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGGGACGGTCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTATGGGCTCCTGATATAGCTTTTCCGCGAATAAAAAAAATAAGATTTTGATTATTGCCCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8910 Chironominae sp. water mite diet isolate 8910-BHL032417-GBD19139_23592-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTT-AGTATTGTTATTTGAGGCAGAATTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGAAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8912 Chironominae sp. water mite diet isolate 8912-BHL032417-GBD4111_11236-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACGACGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTCTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8914 Dicrotendipes sp. water mite diet isolate 8914-BHL032417-GBD19938_21863-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAGTATTAGTGGGCGCCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8916 Chironominae sp. water mite diet isolate 8916-BHL032417-GBD17768_13916-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACGGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8917 Dicrotendipes sp. water mite diet isolate 8917-BHL032417-GBD9061_17074-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTACTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATACTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGGAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR155429, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8918 Chironomus riparius water mite diet isolate 8918-BHL032417-GBD24949_16881-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTGAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACTAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATTTAAGTTTCTGACTTTTACCCCCCCTGTCTTACTCGACTGCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8920 Chironomus sp. water mite diet isolate 8920-BHL032417-GBD13795_24708-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCTTTATATTTTATTTTCGGAGCTTGATCGGGAATAATCGGAACATCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTTTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8921 Chironominae sp. water mite diet isolate 8921-BHL032417-GBD26448_13397-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCTGAACTTGGACGACCTGGTACTTTTACTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTCTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTGTTTGACTTACTACCCCCTTCTCTTACTCTTCTTCTTTCTAAATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8924 Dicrotendipes sp. water mite diet isolate 8924-BHL032417-GBD18450_8641-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATCTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8927 Chironominae sp. water mite diet isolate 8927-BHL032417-GBD12156_3888-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGGTTGCTAATTCGAGCAGAACTTGGACGCCGTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACCCTTTTTCTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8930 Glyptotendipes meridionalis water mite diet isolate 8930-BHL032417-GBD13094_17693-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTACCTTATATTTTATTTTTGGGGCATGATCAGGAATAGTTGGGACTTCTTTAAGAATGCTTATTCGAGCTGAACTAGGACGACCAGGAACTTTTCTTGGTGACGATTAAATTTACAATGTAATTGTTACTGCACATGCATTTATTATAATTTTTTTTATAGTTATACCTGTTTTATTTGGAGGGTTTGGAAATTGACTAGTTCCTTTAATATTGGGGGCCCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTTTACCTCCTTCTTTAACTCTTTTACTTTCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KP954649, identified in GenBank as Glyptotendipes meridionalis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8932 Paratanytarsus sp. water mite diet isolate 8932-BHL032417-GBD7275_21195-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATCTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGTATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTACCCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8937 Chironomus sp. water mite diet isolate 8937-BHL032417-GBD19038_12424-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTGGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTCTGACTATTACCCCCCTTACTTACCCTTCTTCTATCTAGTTCATTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8939 Chironomus riparius water mite diet isolate 8939-BHL032417-GBD23065_20346-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAACTGACTTGTCCCCCTAATACTTGGAACCCCTGACATAGCTTTTCCTCGAATAAATAATAAAAGTTTCTGGCTTTTACCCCCCCCTTCTAACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8941 Dicrotendipes sp. water mite diet isolate 8941-BHL032417-GBD12534_17626-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTCCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGCCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTAC--CCCCCCTTTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8942 Dicrotendipes tritomus water mite diet isolate 8942-BHL032417-GBD12603_23378-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAGTTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCCTTCTCTTACACTTCTACTTTCTTGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8944 Dicrotendipes tritomus water mite diet isolate 8944-BHL032417-GBD12708_24590-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGTACTTCTTTAAGTATATTTATTCGAGCAGAAGTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAACTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTACTCCTTTCTAGATCAATTGTAGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8946 Psectrocladius sp. water mite diet isolate 8946-BHL032417-GBD23020_10271-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCCTGATCAGGTATAGTAGGTACATCTTTAAGAATTTTAATTCGAGCAGAACTCGGTCACGCTGGTTCTTTAATCGGAGACGATCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTGGGAGTACCTGATATAGCATTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCGTCATTAACTTTACTATTATCTAGCTCTCTAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID KR750166, identified in GenBank as Psectrocladius sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL895 Cricotopus sp. water mite diet isolate 895-BHL100916-GBD21486_6314-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATTATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGATGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGTCTCCTGATATAGCTTTCCCTCGCATAAATAATATAAGTTTTTGATTATTACCCCCCTTCTCTAACCTGACTTCGTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8951 Chironomus riparius water mite diet isolate 8951-BHL032417-GBD23255_16510-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACAAAGCCTTTCCCCGAATAAATAATATAAGGTTCTGACCTTTACCCCCCCTCTCTTACTCTTCTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8954 Dicrotendipes tritomus water mite diet isolate 8954-BHL032417-GBD4866_6834-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGTCAGCCTGGAACTTTTATTGGTGACGATCAAATTTAAAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATAAAGCATTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR296575, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8957 Chironominae sp. water mite diet isolate 8957-BHL032417-GBD16146_23301-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGTTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTACTGGAGATGACCAAATTTACAATGTTATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAACATAAGTTTTTGACTACTTCCCCCATCATTAACTCTTTTACTATCAAGTTCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8958 Chironominae sp. water mite diet isolate 8958-BHL032417-GBD5403_13136-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAATTTGGACGACGTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCATCACTAACTCTATTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8972 Chironomus sp. water mite diet isolate 8972-BHL032417-GBD7649_8119-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAGACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATGGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8973 Dicrotendipes tritomus water mite diet isolate 8973-BHL032417-GBD2892_17080-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTGTCCCTCGGATAAAAAATATAAGTATTTTATGACTACCCCCCTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8976 Chironomus sp. water mite diet isolate 8976-BHL032417-GBD26231_15965-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATCCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTCTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCCCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCATTTCTAACTCTACTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8977 Chironominae sp. water mite diet isolate 8977-BHL032417-GBD26887_17393-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACTACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTACTTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAAAATAAGTTTTTGACTTCTTCCACCTTCATTAACTCGTTAACTGTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL8980 Chironomus riparius water mite diet isolate 8980-BHL032417-GBD24855_10099-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGTGCAGCTGACATAGCTTTTCCTCGAGTAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCATCCTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8982 Chironomus riparius water mite diet isolate 8982-BHL032417-GBD8375_9454-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACTACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCAAATGATTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGGAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8986 Chironominae sp. water mite diet isolate 8986-BHL032417-GBD13594_27105-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATTTGGACGACCTGGTACTTTTATTGGAGATGATCAAATTTACAATGTCATTGTTACAGCACATGCTTTTATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTTTTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8987 Chironominae sp. water mite diet isolate 8987-BHL032417-GBD8248_9548-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGAACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCACATGCTTTTATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGCTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTCCTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8989 Chironominae sp. water mite diet isolate 8989-BHL032417-GBD24816_22854-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTTTATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACCTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTTATTGTCACAGCACATGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTATTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8992 Chironominae sp. water mite diet isolate 8992-BHL032417-GBD21421_11113-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTCACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTCTTGACTTCTTCCCCCTTCATTAACTCATTTTCAATCAAGTGCTATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8993 Chironomus riparius water mite diet isolate 8993-BHL032417-GBD6428_18961-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGTTCCGGAATAGTGGGAACTTCATTAAGATTGCTTATTCGAGCAGAATTAGTACGACACGGAACTTTCATTGGAGATGACCAATTTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL8997 Dicrotendipes tritomus water mite diet isolate 8997-BHL032417-GBD14068_14406-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTAATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCCGTCCCTCGGATAAATAATATAAGATTTTGATTACTACCCCCTTCTCTTACTCTTCTTCTTCTCTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9001 Chironominae sp. water mite diet isolate 9001-BHL032417-GBD18053_28892-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATACTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACTGCACACGCTTTTATTATAAATTTTTTTTATAGTTATGCCATTTTTAATTGGAGGTTTTGGAAATTGACTTTTTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTATTACTATCAAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9005 Dicrotendipes tritomus water mite diet isolate 9005-BHL032417-GBD25680_21280-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGCTCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTACTTGTTACAGCTCATGCTTTTATTAGAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCTACTTCTTTCTAGATAAATTGTAGGAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR282179, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL9009 Chironominae sp. water mite diet isolate 9009-BHL032417-GBD6983_16426-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACGACGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAAGAGCCCCAGAAATGACTTTCCCTCGAATAAAAAATATAAGTTTTTGACCTCCTCCCCCTTAATTAACTCTTTTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9014 Chironominae sp. water mite diet isolate 9014-BHL032417-GBD11424_2310-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTCCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACATTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTCTTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTATGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTTACTCTCCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9016 Chironominae sp. water mite diet isolate 9016-BHL032417-GBD27672_11981-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTGCTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAAGTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCCGATATGGACTTCCCCCGAATAAAAAATATAAGTTTTTGAACTCTTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9022 Chironominae sp. water mite diet isolate 9022-BHL032417-GBD28761_13474-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATCTTTTATTTTTGGAGCTTGATCTGTTATAGTAGGTACTTCTTTAATTATGCTAATTCGAGCAGAACTTGGTCGACCTGGTACTTTTTTTGGAGATGACCAAATTTACAATGTAATTGTCACATCACACGCTTTTATTATAATTTTTTTTATATTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATAAAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9026 Chironominae sp. water mite diet isolate 9026-BHL032417-GBD19630_23096-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCCTTCCCCCGAAAAAATAATAAAAGTTTTTGGCTTCTTCCCCCTTCATTAAACCTTTTTCTTTCCAAGTTCCATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9035 Dicrotendipes tritomus water mite diet isolate 9035-BHL032417-GBD19024_27640-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGTACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTTGTGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGATTTCCCCCGGATAAAAAAAATAAGTTTTTGATTACTACCCCCCTTCACTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL904 Cricotopus sp. water mite diet isolate 904-BHL100916-GBD22265_13571-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GATCATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCTGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTTATTGGAGGATTTGGAAACTGATTAGTTCCTTTAAAGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTATTTGATTATTACCCCCCTTCTCTCACCTTACTTCTTTCAAGTACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9044 Paratanytarsus sp. water mite diet isolate 9044-BHL032417-GBD26074_8134-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACTTCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGAACATTTATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGGAATTGACTTCTTCCTTTAATATTAGGAGCCCCCGAAATAGCCTTTCCCCGGATAAAAAAAATAAGTTTTTGAATACTTCCCCCATCTTTAACCCTTCTTCTATCAAGAAGATTAGGGGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9046 Dicrotendipes tritomus water mite diet isolate 9046-BHL032417-GBD5474_23295-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATACTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGGAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCCAATTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCACGGATAAATAATATAAGTTTTTGATTACTACCCCCCTTCTCTAACTCTACTACTTTCTAGAGCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9050 Chironomus riparius water mite diet isolate 9050-BHL032417-GBD9746_23570-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATACTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATTACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCACTTTTAATTGGAGGATTCGGAAACTGACTTTTCCCCCTAATACTTGGATCACCTGACATAGCTTTTCCCCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTTTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL9061 Chironominae sp. water mite diet isolate 9061-BHL032417-GBD12675_13357-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCTGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCTATTTTAATTGGAGGTTTTGGAAATTGAATTATTCCTTTAATGTTAGGAGCCCCAGATAAGACTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCCTTCATTAACTCTTTTACTTTCAAGTACAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9066 Dicrotendipes sp. water mite diet isolate 9066-BHL032417-GBD19016_27657-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TGGCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGTACTTCTTTATGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATATCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGATTTCCCCCGGATAAAGAATAAAAGTTTTTGATTACTTCCCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR155720, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9073 Dicrotendipes tritomus water mite diet isolate 9073-BHL032417-GBD27960_19543-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTCGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGAACTGGAACTTTTATTGGTGACGATCAAATTTAAAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACAAATTTTAATTGGAGTATTTGGAAATTGATTTGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCGAACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9078 Chironominae sp. water mite diet isolate 9078-BHL032417-GBD18605_14353-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTACCTCGAATAAATAATATAAGTTATTGACATCATCCCCCTTCATTAACACTATTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9099 Chironominae sp. water mite diet isolate 9099-BHL032417-GBD11864_15331-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGGACTTTTACTGGAAATGACCAAATTTACAATGTAATTGTCACAGCACACGGTTTTTTTATAAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTCATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL910 Cricotopus sp. water mite diet isolate 910-BHL100916-GBD22742_15764-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGATCTTGATCAGGAATAGTAGGGACTTCCTTGTGTATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGAGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTAACCTCTTTCAAGTACAATTGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9112 Chironominae sp. water mite diet isolate 9112-BHL032417-GBD2813_18665-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAATAGGTACTTCTTTAAGTATGCTAACTCGAGCAGAACTTGGGCGACCTGGTACTTTTATTAGAGATGGCCAAATTTACAATGTAATTGTCACATCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCGGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9113 Chironominae sp. water mite diet isolate 9113-BHL032417-GBD27658_8529-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGAACACCTGGTACATTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGATTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTATTACTTGCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9118 Dicrotendipes sp. water mite diet isolate 9118-BHL032417-GBD8430_23426-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTCGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCAGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAAATGATTGGTTCCTTTAATATTAGGTGCACCAGATATAGCTTTCCCTCAGATAAAAAAAATAAGTTTTTGATTACTACCCCCCTTCCCTTACTCTCCTTCTATCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9124 Chironomus riparius water mite diet isolate 9124-BHL032417-GBD4388_20480-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCCTTAAGAATGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCATGTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTTGCTTACTCGACTTCTTTCTAGTGCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL9126 Culex sp. water mite diet isolate 9126-BHL032417-GBD16698_23378-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTT-ATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTCCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9128 Chironominae sp. water mite diet isolate 9128-BHL032417-GBD13343_17143-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATGTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAGGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCATTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATAGCTTTGCCTCGAATAAATAATATAAGTTTTTGATTACGTCCTCCTTCTCTTACTCTACCTCTTTCTAGCTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID MG449381, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9129 Chironominae sp. water mite diet isolate 9129-BHL032417-GBD4118_11258-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTATGTTTGCTAATTCGAGCAGAACTTGGACGAAGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCAAATTTTAATTGGAGGTTTTGAAAATTGACTTATTCCTTTAATGTTAGGAGACCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTCTGACTTCTTCCCCCTTCATTAACTCTTTTACTATCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9137 Chironominae sp. water mite diet isolate 9137-BHL032417-GBD22074_8237-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAATTTGGACGACCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGTTTTGGAAATTGACTTATACCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCAAATAAATAATATAAGTTTTTGACTTCTTCCCCCTGCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9143 Chironominae sp. water mite diet isolate 9143-BHL032417-GBD5488_13303-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGATCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGGTTTGGAAATTGACTAATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACCCTATTACTTACAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9146 Culex sp. water mite diet isolate 9146-BHL032417-GBD13662_18984-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTT-ATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAGGTAGTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.5% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9150 Chironomus sp. water mite diet isolate 9150-BHL032417-GBD14396_4493-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAAAATTAGGCCGACCCTGAACTTTCAGTGGAGATGACCAAATTTATAAGGGTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGGCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTCCCCCCCTTTCTTCCTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTTGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.8% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9151 Chironomus sp. water mite diet isolate 9151-BHL032417-GBD18781_25667-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCATAATTAGGCCGACCCGGAACTTTCATTGGTGATGATCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGATCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTGTCTGACTTTTACCCCCCCTTTCTTACTCGACTTCTATCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.1% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL916 Cricotopus sp. water mite diet isolate 916-BHL100916-GBD23745_24251-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTTATTGGAGATGATCAAGTTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAAAGTTAGGGGCTCCTGATATAGCTTTCCCCCGAATAAATAAAATAAGTTTTTGATTATTACCCCCCTTCTCCCACCTTACTTCTTTCAAGTACAATTGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9163 Chironominae sp. water mite diet isolate 9163-BHL032417-GBD11623_21915-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGTATAACTTGGACGACGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTGTCCCTCGAATAAATAATATAAGGTTTTGACTTCTTCCCCCTTCAGTAACTCTTTTACTTTCAAGTTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL9165 Chironominae sp. water mite diet isolate 9165-BHL032417-GBD17293_7500-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTTGGGGCTTGATCTGTTATAGTAGGTACTCTTTTAGGTATGCTATTTCGAGCAGAACTTGGACAACCTGGTACTTTTACTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9167 Dicrotendipes tritomus water mite diet isolate 9167-BHL032417-GBD2974_19002-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCCGGAATAGTTGGGACTTCTCTAAGTATACTTATTCGAGCAGAGCTGGGGCGACCTGGAACTTTTATTGGTGACGATCAAATTTAAAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTATTTATAGTTATACCAATTTTAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATATTAGGGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCTCTTACTCTACTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9170 Culex sp. water mite diet isolate 9170-BHL032417-GBD15360_6827-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTCCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAA-TTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL918 Cricotopus sp. water mite diet isolate 918-BHL100916-GBD26401_9070-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACCTTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTTCCTTGAGTATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTTATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATCATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGTGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGAGTATTACCCCCCTTCTCACACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9189 Dicrotendipes sp. water mite diet isolate 9189-BHL032417-GBD25207_18433-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGGGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATATTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAAATGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGGCACCAGATATAGCATTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCTTCTCTCACTCTACTACTTTCTAGATCGATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9210 Chironominae sp. water mite diet isolate 9210-BHL032417-GBD23799_18624-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGTCCTGTTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTAATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATGGACTTATTCCTTTAATGTTAGGGGCCCCAGATATGGCTTTCCCTCGAATAAAAAATATAAGCTTTTGACTTCTGCCCCCTGCATTAACGCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL925 Cricotopus sp. water mite diet isolate 925-BHL100916-GBD26306_15044-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCCGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCGGGATCATTCATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTTTTCATAGTTATACCTATTTTAAATGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGGTTTTGATTATTTCCCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9250 Chironominae sp. water mite diet isolate 9250-BHL032417-GBD25950_21294-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACGACGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTCTTATAATTTTTTTTTATAGTTACGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCTTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTATTACTGTCAAGATCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9258 Chironomus riparius water mite diet isolate 9258-BHL032417-GBD23405_20114-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAATTTCATTAAGAATGCTTATTCGAGCATAATTAGGACGACCCGTAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACGCGTCTTCTGTCTAGTTCGTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9264 Chironominae sp. water mite diet isolate 9264-BHL032417-GBD2287_17666-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTTGGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTTCTTTTATTGGAGATGAACAAATTTACAATGTAATTGTCACAGCTCATGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACACTTTTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL9281 Chironominae sp. water mite diet isolate 9281-BHL032417-GBD5926_20872-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTAGTACTTTTATTGGAGATGACCAATTTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGTTTTTGTAAATTGACTTATTCCTTTAATGTTAGAAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCCTGCATTAACTCTTTGACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9285 Chironominae sp. water mite diet isolate 9285-BHL032417-GBD11300_12375-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTTTATTTTATTTTTGGAACTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACACTTTAACAATAAAGTGCTAGAGTAGAAAATGGAGCTGAAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9287 Dicrotendipes sp. water mite diet isolate 9287-BHL032417-GBD23093_21904-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GCACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTATGTATACTTATTCGAGCAGAACTAGGCCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCCATTTTAATTGGAAGATTTGGTAATTGATTGGTTCCTTTAATATTAGGGAGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGATTACTTCCTCCCTCTCTAACTCTACTTCTTTCTAGAACAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID KR282179, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9296 Dicrotendipes tritomus water mite diet isolate 9296-BHL032417-GBD27359_9551-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGATCGACCTGGAACTTTTATTGGTGACGATCAAATTTATAACATAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTCGGGGCACCAGATATAGCGTTCCCTCGGATAAATAATATAAGTTTTTGATTACTACCCCCCTTCTCTTACTCTTCTTCTATCTAAATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9309 Dicrotendipes tritomus water mite diet isolate 9309-BHL032417-GBD25880_24623-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTAATACCAATATTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGTGTTTGATTACTACCCGCTTCTCTTACTCTGCTTCTTTCTAGAACAAGTGTATAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL931 Chironomidae sp. water mite diet isolate 931-BHL100916-GBD25703_18400-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATCTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTCGAATTAGGACACCCAGGCTCATTAATCGGAGACGAAAAAATTTTTAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAAATGGAGGCTTTGGAAATTGATTAGTTCCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAAAAAAATAAGATTTTGATTAATACCCCCGTCATTAACCTTACTTTTATCAAGATCAATAGTAGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9310 Paratanytarsus sp. water mite diet isolate 9310-BHL032417-GBD10166_20240-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCTTTATATTTTATTTTCGGAGCTTGATCAGGAATAATCGGAACCTCCTTAAGTATATTAATTCGAGCAGAATTAGGACACCCTGGATCATTTATTGGAGAAGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTTTAATTGGAGGTTTTGGAAATTGACTATTTCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCCCGAATAAATAATATAAGTTTTTGATTACTTCCCCCATCGTTAACCCTACTACTATCAAGAAGATTAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR740048, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9326 Chironominae sp. water mite diet isolate 9326-BHL032417-GBD3203_15845-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGAGATGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACGACGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACATTCAATTTCTATTGTATAAAATGGAGCTGAAACA	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9361 Chironominae sp. water mite diet isolate 9361-BHL032417-GBD25062_7560-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACGACGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTTATTGTCACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTAAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCACTTACCCTTTTACTTTCAAGTTCTATCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9368 Chironominae sp. water mite diet isolate 9368-BHL032417-GBD18673_25986-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTACTGGAGATGACCAAATTTACAATGTAATTGTCACAGCGCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCACGAATAAATAAGATAAGTTTTTGACTTCGTCCCCCTTCATTAACTCTTTAACTATCAAGTGCTAGTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL9384 Dicrotendipes sp. water mite diet isolate 9384-BHL032417-GBD2127_12308-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATAAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGACGACCCGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCACCAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTACCCCCTTCTCTTACTCTTCTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR283761, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9404 Chironominae sp. water mite diet isolate 9404-BHL032417-GBD25801_17914-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTATAGATATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCTGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTAACTTCTACCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9415 Chironominae sp. water mite diet isolate 9415-BHL032417-GBD10375_19723-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACGACGTGTTACTTTTCTTGGAGATGACCAAATTTACGATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTATGAGCCCCAGATATGGCCTTCCTTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9420 Chironomus sp. water mite diet isolate 9420-BHL032417-GBD14900_14212-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGACTGCTTATTCGAGCAGAATTAGGCCGACCCGGAACTTTCATTGGAGATGACTAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGGGTCTGACTTTTACCCCCCTTTCTTACTCTGCTACTTGCTAGTACGTGCGTAGAAAATGGAGCTGAAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9423 Chironominae sp. water mite diet isolate 9423-BHL032417-GBD21927_12626-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCTAGCAGAACTTGGACGACGTGGTACTTTTATTGGATATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAGTTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTACGTCCCCCTTCATTAACTCATTAACAATCAAGTGCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9425 Chironominae sp. water mite diet isolate 9425-BHL032417-GBD18722_27878-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACAACCTGGTACTTTTACTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAAAAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCAGTTACTTGCAAGTTCTAGTGTATAAAATGGAGCTGAAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9427 Chironominae sp. water mite diet isolate 9427-BHL032417-GBD11701_16410-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCATAACTTGGACCACCTGGTACTTTTATTGGAGAGGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGTGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL944 Cricotopus sp. water mite diet isolate 944-BHL100916-GBD4253_10319-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATAAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAAGAGAAGTTTTTGATCATGACCCCCTTCTCTCACCTTACATCTACCAAGTGCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9457 Chironominae sp. water mite diet isolate 9457-BHL032417-GBD8583_8470-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGTTGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGATAGGAGCCACAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACCTCTTCCCCCTTCATTAACTCTTTAACATTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9468 Dicrotendipes sp. water mite diet isolate 9468-BHL032417-GBD20065_5082-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGGGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAACGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGATTTGGGAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCTCGGATAAATAATATAAGGTTTTGATTACTACCCCCTTCGCTTACTCAGCCTCTTGCTAGAACAATTGTATAAAATCGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL947 Cricotopus sp. water mite diet isolate 947-BHL100916-GBD5844_6140-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTGTATTTTATTTTCGGAGCTTAATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAGCGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGTGGCTCCTGATATAGCTTCCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTAACCTTACTTCTTTCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9473 Culex sp. water mite diet isolate 9473-BHL032417-GBD25672_11191-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATATAGATATTGGCACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTTGGACCTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAA-TTTTTTTATAGTAATACCAATCAGAATTGGAGGATTTGGAAATTGATTAGTTCCTCTAATGTTAGGAGCTCCAGATATGGCCTTTCCGCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTACAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9481 Chironominae sp. water mite diet isolate 9481-BHL032417-GBD24848_24190-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTTTGCTAATTCGAGCAGAACTTGGACGAAGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCACCAGATATGACTTTACCTCGAATAAATAATATAAGTATTTGACTTCGTCCCCCTTCATTAACTCTTTAACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9495 Dicrotendipes tritomus water mite diet isolate 9495-BHL032417-GBD23976_9739-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTCATTTTTGGAGCTTGATCAGGACTAGTTGGGACTTCTCTAAGTATACTTATTCGAGCATAGCTGGGTCGACCTGGAACTTTTATTGGTGACGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTATAGTTATACCAACTTTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGTGGCTCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTCTCTTACTCAACTTCTTGCTAGAACAATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR767066, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9500 Dicrotendipes tritomus water mite diet isolate 9500-BHL032417-GBD25116_9993-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCAGGAATAGTTGGAACTTCTCTAAGTATACTTATTCGAGCAGAACTAGGTCCCCCTGGAACTTTTATTGGTGACGATCAAATTCACAAAGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTGGTTCCTTTAATATTAGGGGCACCAGATATAGCTTTCCCCCCGATAAATAATATAAGTTTTTGATTACTACCCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR173489, identified in GenBank as Dicrotendipes tritomus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9502 Culex sp. water mite diet isolate 9502-BHL032417-GBD14732_11387-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGCAACTGCTCATGCTTTTATTATAA-TTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGATTACTCCCCCCTTCTCTTACTCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9509 Chironominae sp. water mite diet isolate 9509-BHL032417-GBD24831_9359-Lq48 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTATGTTTGCTAATTCGAGCAGAACGTGGACGACGTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTATAGTTATGCCAATTTTAATTGGAAGTTTTGGAAATTAACTTATTCCTTTAATGTTAGTATCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9540 Chironomidae sp. water mite diet isolate 9540-BHL032417-GBD22189_16106-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9541 Chydorus brevilabris water mite diet isolate 9541-BHL032417-GBD15757_21125-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCTAGCAGAATTAGGACAAAGCGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9542 Orthocladiinae sp. water mite diet isolate 9542-BHL032417-GBD4367_8800-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCCTGATCTGGGATAGTTGGAACTTCTTTAAGAATTCTTATTCGTGCAGAATTAGGACATGCTGGTTCCTTAATTGGAGACGACCAAATTTATAATGTAATTGTTACCGCTCACGCTTTTGTAATAATTTTTTTATAGTTATACCTATTTTAATTGGGGGGGTTTGGAAACTGACTAGTTCCCTTAATATTAGGAGCACCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTACTTCCCCCTTCTTTAACTCTTCTTTTATCAAGCTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR678405, identified in GenBank as Orthocladiinae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL9543 Chydorus brevilabris water mite diet isolate 9543-BHL032417-GBD14838_11168-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGGGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGAGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTTCCTCGTCTAAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGTGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9545 Chironomidae sp. water mite diet isolate 9545-BHL032417-GBD12346_15317-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL955 Cricotopus sp. water mite diet isolate 955-BHL100916-GBD4176_17872-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTGCATTAGGTCATGCCGGGTCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTTGAAACTGATTAGTTCCTTTAATGTTAGGGTCTCCTGATATAGCTTTCCCTCGAAAAAACAATATAAGTTTTTGATTATTACCCCCCTTCTCTCACCTTACTTCTTGCAAGTGCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9552 Chydorus brevilabris water mite diet isolate 9552-BHL032417-GBD2040_12619-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTCTTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGTCTGTTAATTCGAGCTGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCGCATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCTTAATTGGGGGGTTTGGAAACTGGCTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9555 Chydoridae sp. water mite diet isolate 9555-BHL032417-GBD18962_2634-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.7% identical to accession ID MG449309, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9557 Chydorus brevilabris water mite diet isolate 9557-BHL032417-GBD8862_11882-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTTTTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGTCTGTTTATTCGAGCAGAATTAGGACAAAGAGGGACCTTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGAGGGTTTGGAAATTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9559 Chydorus sp. water mite diet isolate 9559-BHL032417-GBD6605_22514-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTTTTTGGAATTTGATCTGGAATAGTGGGCACTTCTTTTAGCCTGTTTATTCGAGCAGAATTAGGACAAAGCGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATTATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTATTAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9569 Chydorus sp. water mite diet isolate 9569-BHL032417-GBD14430_17651-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGAACCTGGTATAGCCTTCCCTCGTCTTAATAATGTAAGTGTCTGGCGTCGGCCCCCAGCTTTAACCCTGCTTTTAGTAGGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9571 Chydorus sp. water mite diet isolate 9571-BHL032417-GBD7098_20340-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.2% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9572 Chydorus sp. water mite diet isolate 9572-BHL032417-GBD4131_16541-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATTTTAATTGGGGGGTTTGGGAACTGACTTGTCCCCCTAATATTAGGGGCGCCTGATATAGCCTTCTCTCGGCATAATAATTAAAGTTTCTGGATTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL9577 Chydorus sp. water mite diet isolate 9577-BHL032417-GBD14606_2286-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTGTATTTTCAATTTGGAATTTGAGATGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAAGTAGGACAAATAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGGCAGTATAAAATGGCGCTGGAGCA	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9583 Chydorus brevilabris water mite diet isolate 9583-BHL032417-GBD18731_12634-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGGCCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAACCTTCCCTCGTCTTAAAAATTTAAATTTCTGGCTTCTTCCCCCAACTTTAACCCTTCTTTTAATAGGGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9585 Chydorus brevilabris water mite diet isolate 9585-BHL032417-GBD23705_25350-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTCTTTGGAATTTGAGCTGGAGTAGCGGGCACTGCTCTTTGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTGCCCCCAGCTTTAACCCTTCGTTTAGGAGGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9589 Chydorus brevilabris water mite diet isolate 9589-BHL032417-GBD25805_19689-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TATTCTTTGTTTTATATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGCCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCTTAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATATAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9595 Chydorus sp. water mite diet isolate 9595-BHL032417-GBD29572_14751-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTCTTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATTATAATTGGGGGGGTTTGGAAACTGGCTTGTCCCCCTAATATTGGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGGTTCTGGCTTCTTCCCCCAGCTTTAACCCTACTTGTAGGAGGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL960 Cricotopus sp. water mite diet isolate 960-BHL100916-GBD14969_8237-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATCTTAATTCGAGCTAAATTAGGACATCCCGGATCATTAATTGGAGATGATCAAATTTATAATGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGGTTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAAAAAATAATAAAAATTTTTGATTATTACCCCCCTTCTCTGACCCTACTTCTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9602 Chydorus sp. water mite diet isolate 9602-BHL032417-GBD8854_25330-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTTTTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGGCTTCCCTCGGCTTAAAAAATAGAGGTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9611 Chydorus sp. water mite diet isolate 9611-BHL032417-GBD11013_15943-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCTTAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTTATATTAGGGGCACCTGATATAGCCTTCCCCCCTCCTAATAAATTAAATTTCCGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9616 Chydorus sp. water mite diet isolate 9616-BHL032417-GBD12537_20870-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGATCTGGAATAGTGGGCACTGCTTTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATCTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATTTTAATTGGGGGGTTTGGGAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCCTCCCTCGTCTTAATAAATTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9623 Chydorus brevilabris water mite diet isolate 9623-BHL032417-GBD24480_8423-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCTCTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGATGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAACTTAAGTTTCTGGCTACGTCCCCCAGCGTTAACCCTTCATTAAGTAGGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL9624 Chydorus sp. water mite diet isolate 9624-BHL032417-GBD15472_25366-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTTTTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAAAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCTTAATTGGGGGGTTTGGAAGCTGACTTGTCCCCCTAATATTAGGGACACCTGATGTAACCTTCCCTCGTATTAAAAATTAAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTAGAGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9643 Chydorus sp. water mite diet isolate 9643-BHL032417-GBD20833_22213-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTTTATTTTCTTTTTGGAATTTGAGCTGGAATAGTGGGCACTGCTTTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGTCCATTATTGGAGATGATCAAATTTATAATGTTATTGTTACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATTTTAATTGGGGGGGTTTGGAAACTGACTTGTCCCCCTGATATTAGGGGCACCTGATATAGCCTTCCCTCGACTAAATAATATAAGTTTCTGGCTACTTCCCCCAGCTTTAACCCTTCTTTTAGCAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9649 Chironomidae sp. water mite diet isolate 9649-BHL032417-GBD18230_5604-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTAATTTTGGAGCTTGATAGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATGAGGACACCCAGGCTCATTAATCGCAGACGCTCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGCGCTGGACCAG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9658 Chydorus sp. water mite diet isolate 9658-BHL032417-GBD7038_12200-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTTTTTGGAGTTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTTCCTCGTCATAATAAATAAAGTTTCTGGCATCTTCCCCCAGCTTTAGCCCTTCCTTTAGTAGGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL966 Chironomidae sp. water mite diet isolate 966-BHL100916-GBD23814_20054-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTGTATATTTTATTTTTGGAGTTTGATCGGGGATAGTAGGCACTTCTTTTAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGCAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTAATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTAATATTAGGGGCTCCTGACATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9682 Chydorus sp. water mite diet isolate 9682-BHL032417-GBD22943_11591-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAACAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATTATAATTGGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCCCCTGATATAGCCTTCCCCCGTCAAAATAAATAAAATTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTA-GGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9687 Chydorus brevilabris water mite diet isolate 9687-BHL032417-GBD25461_8420-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTATTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTGCGTGCCCCAGCTTAAAACCGTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAGCAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9689 Chydorus brevilabris water mite diet isolate 9689-BHL032417-GBD29109_11868-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTCTTCGGAATTTGGGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGACTTCGTCCCCCAGCTTTAACCCATCTTTAAGAAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9690 Chydorus brevilabris water mite diet isolate 9690-BHL032417-GBD9570_9422-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAAGGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCCCCTGATATAGCCTTCCCCCGCCTTATTAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTAAACCCTTCTTTTAGTAGAGGGGGCAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9698 Chydorus sp. water mite diet isolate 9698-BHL032417-GBD6637_12383-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGGGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGATTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGAAATACCCTTCCCCCGACTTAAAAATTAAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTTCTTTTAGTA-GGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL9702 Chydorus brevilabris water mite diet isolate 9702-BHL032417-GBD25814_20532-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTTTTAATTCGAGCAGAATTAGGACAACGAGGTCCCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAAATAAAGTTTCTGTCTTCTTCCCCCAGCGTTAACCCTTCTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9703 Chydorus sp. water mite diet isolate 9703-BHL032417-GBD13440_20220-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTCCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAACTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTCATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGAATTGTCCCCCTAATATTAGGGGCACCTGAAATAGCCTTCCCACGTCATAAAAAATTAAATTTCTGGCTTATTCCCCCAGCTTTAACCCTTCTTTTAGTAGGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.4% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9710 Chydorus brevilabris water mite diet isolate 9710-BHL032417-GBD19293_8020-Lq56 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTGTTTGGAATTTGAGCTGGTATAGTGGGCACTGCTCTTAGCCTTTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATCTTTTTTATAGTTATACCCATCATAATTGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTGAATAACTAAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTACATTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9712 Chironominae sp. water mite diet isolate 9712-BHL040517-GBD5755_17749-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAA-TTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9713 Culex pipiens water mite diet isolate 9713-BHL040517-GBD27066_20619-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGGAATGATCAAATTTATAGTGTTATTTTAACTGCTCATGCTTTTATTACAATTTTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9714 Chironomidae sp. water mite diet isolate 9714-BHL040517-GBD11968_17683-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAAAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9715 Chironominae sp. water mite diet isolate 9715-BHL040517-GBD11615_11540-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATATTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTCATTGTAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTT-ATTATAATTTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCGGATATGGCTTTCCCTCGAGTAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9716 Lebertia quinquemaculosa water mite diet isolate 9716-BHL040517-GBD6938_11306-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATACTTCGCTTTTGGGGCTTGATCAGGAATGGTGGGAGCAAGACTAAGAACTTTAATCCGTTTAGAATTAGGACAACCAGGAACTCTCCTAGGAAGAGACCAAATTTATAATACTATCGTAACAGCTCACGCCTTCGTTATAATTTTCTTTATAGTTATGCCAATAATAATTGGAGGATTCGGAAATTGACTAGTCCCATTGATGATTAGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGACTTTTACCCCCCCTCTTTAACTCTTCTACTATCTAGTTCTTTCACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID MG811666, identified in GenBank as Lebertia quinquemaculosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9718 Culex sp. water mite diet isolate 9718-BHL040517-GBD12024_14656-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTACAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCCCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9719 Chironominae sp. water mite diet isolate 9719-BHL040517-GBD4051_10367-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTACGTATGCTCATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTGGAATAAATAATATAAGATTTTGACTACTTCCCCCTTCATTAACTCTTTTACTGTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL972 Chironomidae sp. water mite diet isolate 972-BHL100916-GBD10729_28306-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGTCAACCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTGTTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGAGCTCCTGATATAGCTTTCCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTGTATCAACATCAGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9721 Chironomidae sp. water mite diet isolate 9721-BHL040517-GBD9199_3902-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAAC---TCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9722 Culex sp. water mite diet isolate 9722-BHL040517-GBD24763_13821-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGCTTGGGCTGGGATTGTTGGAACTTCTTTTAGTTTACTTATTCGAGCAGGATTTAGTCAACCATGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTACAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9725 Chironominae sp. water mite diet isolate 9725-BHL040517-GBD8506_22696-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTGGG-GCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGAAATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9726 Chironominae sp. water mite diet isolate 9726-BHL040517-GBD26503_13038-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTTTATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTTAGTATGCTAATTCGAGCAGAATTTGGACTACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACAAGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTATCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9728 Culex sp. water mite diet isolate 9728-BHL040517-GBD25897_8372-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGCTTGAGCTGGAATAGTTGGAACTTCTTTTAGTTTACTAATTCGAGCTGGATTAAGTCAACCAGGTTTATTTATTGGAAATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTACAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACCCTACTACTATCAAGTAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9730 Chironominae sp. water mite diet isolate 9730-BHL040517-GBD3661_8337-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTAGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAAC---CTTACTTTAATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9733 Chironominae sp. water mite diet isolate 9733-BHL040517-GBD16675_8033-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATCTTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTATGTATGCTAATTCGAGTAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACTAAATTTACAATGTAATTGTCACAGCACACGCTTATATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9735 Culex sp. water mite diet isolate 9735-BHL040517-GBD13631_8393-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGCTTTAGTTGGAATTGTTGGAACTTTTTTTAGTTTTCTAATTCGAGCAGAATTAAGTCAACCAGGTATATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTACAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACCTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9740 Culex sp. water mite diet isolate 9740-BHL040517-GBD12279_26246-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGCTTTAGCCGGCATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTTAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTACAATTTTTTTTATAGTAATACCAATCATAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL9741 Culex sp. water mite diet isolate 9741-BHL040517-GBD8461_7044-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTACAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATGTAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9744 Culex sp. water mite diet isolate 9744-BHL040517-GBD23912_15120-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACATTATATTTTATTTT-GGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGCGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTAGTTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.8% identical to accession ID KM593053, identified in GenBank as Culex conspirator. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9747 Culex sp. water mite diet isolate 9747-BHL040517-GBD13662_10112-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGCTTTAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTTATTCGGGCTGGATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTACAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGATTTTGAATACTACCTCCATCATTGACACTACTACTTTCAAGTAGTGTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9748 Chironominae sp. water mite diet isolate 9748-BHL040517-GBD8408_11354-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCCTTCATTAACTCGTTGACTGTCAAGTTTTATTGTAGAAAATGGAGCTGCAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL975 Cricotopus sp. water mite diet isolate 975-BHL100916-GBD18668_18214-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGGATCTTAATTCGAGCTGCATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATCATGACCCCCTTCGCTCACCTAACATCAATCAAGTGCAATAGTTGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9750 Paratanytarsus sp. water mite diet isolate 9750-BHL040517-GBD4983_20994-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTAATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTCTCCTCGAATAAATAATATAAGATTTTGACTTCATCCCCCCTCTTTAACTCTGTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9752 Chironominae sp. water mite diet isolate 9752-BHL040517-GBD8813_20814-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCACTAATCGGAGACGATCAAATTTATAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATACAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR278045, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9754 Culex sp. water mite diet isolate 9754-BHL040517-GBD3580_16074-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGCTTGAGCTGGAATTGTTGGAACTTCTTTAGGTTTACTAATTCGGGCAGGATTAAGTCAACCCGGGGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTACAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTCTTGAATACTACCTCCTTCATTGACCCTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL976 Cricotopus sp. water mite diet isolate 976-BHL100916-GBD28543_16392-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTTGGAGCTTGATCAGGAATAGTAGGGACTTCCTTGAGAATTTTAATTCGAGTTGAATTAGGTCATGCGGGATATTTAATTGGAGATGATCAAATTTATAACGATATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGTAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCTCACCTTACTTCTTTCAAGTTCAATTGTTGAAAATGGACCTGGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9762 Culex sp. water mite diet isolate 9762-BHL040517-GBD5224_16840-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTCT-GGGGCTTGAGCTGGAATAGTTGGAACTTTTTTTAGTTTACTAATTTGAGCAGGATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTACAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.9% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL9763 Culex sp. water mite diet isolate 9763-BHL040517-GBD9649_19850-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGCTTGAGCTGGAACTGTTGGAACTTCTTTAAGTTTACTTATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTTTAATGTTATTGTTACTGCTCATTCTTTTATTACAATTTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTAGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTATCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9773 Chironominae sp. water mite diet isolate 9773-BHL040517-GBD6191_22708-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCGGAACTTGGACGTCCTGGTACTTTTATTGGTGATGACCAAATTTACAATGTAATTGTCACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCATCATTAACTCTATTACTTTCAAGTACTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9776 Chironominae sp. water mite diet isolate 9776-BHL040517-GBD18032_14501-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCTTTTAGTATGTTAATTCGAGCCGAATTAGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTTACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATATTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9777 Chironominae sp. water mite diet isolate 9777-BHL040517-GBD21587_14571-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTAATTTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAAAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATATTTTTTTTATATTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTCTTTGACTTCTTCCCCCTTCATTAACACTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9779 Culex sp. water mite diet isolate 9779-BHL040517-GBD17578_23963-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGCTTTAGCTGGAATAGTTGGGACTTCTTTTAGTTTACTAATTCGGGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATTATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTACAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATTTTAGGAGCTCCAGATATGGCATTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTATCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL978 Cricotopus sp. water mite diet isolate 978-BHL100916-GBD15856_26880-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGGTACTGCCTTGAGAATCTTAATTCGAGCGGAATTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGGGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGATTATTACCCCCTTCTCCCACCTAACATCAATCAAGTTCAATAGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9780 Culex sp. water mite diet isolate 9780-BHL040517-GBD12823_18691-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTGGGGCCTT-AGCTGGAATTGTTGGAACTTCTTTTTGTTTACTAATTTGAGCAGAATTTAGTCAACCAGGGGTATTTATTGGAAATGATTAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTACAATTTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCATTTCCTCGAATAAATAATATAAGATTTTGAATACTACCTCCTTCATTGACACTACTACTATCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9781 Culex sp. water mite diet isolate 9781-BHL040517-GBD16967_2753-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGCTTGAGCGGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAAGTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAAATTATAAGGTTATTGTAACGGCTCATGCTTTTATTACAATTTTTTTTATAGTAACACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACCCTACTACTTTCACGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9784 Culex sp. water mite diet isolate 9784-BHL040517-GBD25559_14191-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGCTTGAGCTGGAATAGTTGGGACTTCTTTAAGTTTTCTTATTCGAGCAGGATTTAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTACAATTTTTTTTATAGTAATACCAATCATAATTGGAGGGTTTGGAAATTGATTAGTTCCTTTAATGTTGGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTCTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9788 Culex sp. water mite diet isolate 9788-BHL040517-GBD14203_15773-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGCTTTAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGGGCAGGATTAAGTCAACCAGGGATATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTACAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCAGATATAGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCCCCTTCATTGACACTACTTCTTTCAAGTAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL979 Cricotopus sp. water mite diet isolate 979-BHL100916-GBD16851_14386-Lunk70 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GAACATTATATTTTATTTTCGGAGCTTGATCAGGAATAGTAGTGACTTCCTTGAGAATCTTAATTCGAGCTTATTTAGGTCATGCCGGATCATTAATTGGAGATGATCAAATTTATAACGTTATTGTTACAGCTCATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGCTCTCCCTCGAATAAATAACATAAGTTTTTGATTATTACCCCCCTTCTCTCACCTGACTGCTTTCAAGTTCAATTGTTGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR279261, identified in GenBank as Cricotopus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9798 Chironominae sp. water mite diet isolate 9798-BHL040517-GBD17792_3544-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACATTATATTTCATTTTTGGAGCTTGATCAGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTTGTACTTTTATTGGAGATGACCAAATTTACCATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCAAGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.6% identical to accession ID MG449049, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9800 Culex sp. water mite diet isolate 9800-BHL040517-GBD27603_15450-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGCTTGAGCTGGGATAGTTGGAACTTCTTTTAGTTTTCTAATTCGGGCAGGATTTAGTCAAACAGGGGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTTACTTCTCATGCTTTTATTACAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCCCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9805 Culex pipiens water mite diet isolate 9805-BHL040517-GBD27856_16812-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGG-CTTGAACTGGAATTGTTGGTACTTCTTTAAGTTTACTAATTCGGGCAGAATTTAGGCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTACAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTGTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.6% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9808 Culex sp. water mite diet isolate 9808-BHL040517-GBD17747_4170-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGACAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGCTTGAGCAGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAAGTAAGTCAACCAGGTTTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTACAATTTTTTTTATAGTAATACCAGTCCTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACCCTACTACTTTCAAGTAGTTTAGTAGAAACTGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9819 Culex pipiens water mite diet isolate 9819-BHL040517-GBD12635_23427-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTACAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTGTCCTCGAATAAATAATATAAGTTTTTGAACACTACCTCCTTCATTGACACGACTACGAACAAGTAGTTTAGTAGAAAATGGAGCAGGAAC	Using NCBI BLASTN in June 2018, this sequence was 96.8% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9821 Culex sp. water mite diet isolate 9821-BHL040517-GBD14049_2582-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGACAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGATTGAGCGGGAATAGTTGGAACTTCTTCAAGTTTACTAAGTCGAGCAGAATTAAGTCAACCAGGCGTATTTATTGGAGATGAGCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTACAATTTTTTTTATAGTAATTCCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACCTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9825 Chironominae sp. water mite diet isolate 9825-BHL040517-GBD7158_7741-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTGGG-GCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTATGCTTATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATCTTAATTGGAGGTTTTGGAAATTGACTTACTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.9% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9827 Culex sp. water mite diet isolate 9827-BHL040517-GBD15915_6178-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGCTTGAGCCGGAATAGGTGGAACTTCCTTAAGGTTACTAAATCGGGCAGAAATAAGGCAACCAGGTTTATTTATTGGAAAAGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTACAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9828 Culex sp. water mite diet isolate 9828-BHL040517-GBD23301_24225-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGCTTGAGCTGGAATAGTTGGAAATTTTTTTAGTTTTCTTATTTGGGCAGGATTAAGGCAACCAGGTGTATTTATTGGAAATGATTAAATTTATAATGCTATTGTAACTGCTCATGCTTTTATTACAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATAGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTATCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL9831 Culex sp. water mite diet isolate 9831-BHL040517-GBD28839_12581-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGCTTGAGCTGGAATAGTTGGCACTTCTTTTAGTTTCCTTATTTGAGCTGAGTTTAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTACAATTTTTTTATAGTAATACCAATAATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGATTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9834 Culex sp. water mite diet isolate 9834-BHL040517-GBD27414_15178-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACATTATATTTTATTTT-GGGGCTTGAGCTGGAATTGTTGGCACTTCTTTCAGTTTTCTAATTCGAGCTGGATTTAGTCAAACAGGTGTATTTATTGGAAATGATCAAATTTTTAATGTTATTGTAACTGCTCATGCTTTTATTACAATTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAACTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGATTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9837 Culex sp. water mite diet isolate 9837-BHL040517-GBD16367_10077-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGCTTGAGCTGGAATAGTTGGAACTTTTTTAAGTTTTCTAATTTGAGCCGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCTAATTTATAATGTTATTGTAACTGCTCCTGCTTTTTTTACAATTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCCCCTTCATTGACACTACTACTATCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9839 Culex sp. water mite diet isolate 9839-BHL040517-GBD24713_22354-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGCTTTAGCTAGAATTGTTGGGACTTCTTTAATTTTACTAATTCGTGCAGAATTTAGTCAACCAGGTATATTTATTGGAAATGATCAAATTTTTAATGTTATTGTAACTGCTCATGCTTTTATTACAATTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9841 Culex sp. water mite diet isolate 9841-BHL040517-GBD11253_20020-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGCACATTATATTTTATTTT-GGGGCTTGAGCTGGAATAGATGGAACTTGTTTATGTTTACTAATTTGGACATGATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTACAATTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9842 Culex pipiens water mite diet isolate 9842-BHL040517-GBD13336_28231-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGCTTGAGCTGGAATAGGTGGTACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGGTCATGCTTTTATTAAAATTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCGTTAATGTTAGGAGCTCCAGATATGGCCTCTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9844 Culex sp. water mite diet isolate 9844-BHL040517-GBD14372_19207-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGCTTTAGCTGGAATTGATGGGAATTCTTTTAGCTTTCTAATTTGGGCAGAATTTAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTTACTGCTCATGCTTTTATTACAATTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9845 Culex sp. water mite diet isolate 9845-BHL040517-GBD20757_16892-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTT-GGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTACAATTTTTTTATAGTAATACCAATTATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCATTCCTCGAATAAATAATATAAGTTTTTGAAGACAACATCCTTGATTGACACGACGACTTACAAGTAGATTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9849 Chironominae sp. water mite diet isolate 9849-BHL040517-GBD15215_17445-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATAAGGCCTTCCCCCCAAAAAATAATAAAAATTTTTGACTTCTCCCCCCCTTCAATAACCCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9851 Chironominae sp. water mite diet isolate 9851-BHL040517-GBD24661_23623-1Lq57 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTTTATATTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATTCGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTAAAATGTAATTGTTACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGATTTTGGAAATTGACTTTTTCCTTTAATATTAGGAGCCCCAGATATGGCATTCCCTCGAATAAATAATATAAGTTTTTGACTACTTCCCCCTTCATTAACTCTATTACTATCAAGCTCTATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.0% identical to accession ID KR296026, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL9852 Oligochaeta sp. water mite diet isolate 9852-BHL040517-GBD9380_25321-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTCTTTCTGGTTATACCAGTATTTATTGGTGGATTTGGAAATTGACTTCTACCTCTAATACTCGGAGCACCAGATATAGCTTTCCCACGACTTAACAATTTAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 85.6% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL9853 Paratanytarsus sp. water mite diet isolate 9853-BHL040517-GBD4974_15114-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCACTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9854 Chironomus sp. water mite diet isolate 9854-BHL040517-GBD20828_13575-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGATCCGGAA-TTTCATTGGAGATGACCAAATTTATAATGTTGTTGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGAACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9855 Dicrotendipes sp. water mite diet isolate 9855-BHL040517-GBD19648_18541-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATGGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9856 Amphichaeta sp. water mite diet isolate 9856-BHL040517-GBD3719_15196-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTGCAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTCCACATGCATTTTTAATAATTTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGTGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCCCATCACTAATTCTATTAGATGCATCGGCTGCAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL9858 Chironomus crassicaudatus water mite diet isolate 9858-BHL040517-GBD14189_22406-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGAACCCTTTATATATTATTTTTGGTGCTTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACTTTTATTGGTGATGACCAAATTTATAATGTAGTAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCCTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9859 Chironominae sp. water mite diet isolate 9859-BHL040517-GBD8654_5678-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTCGATTATTACCTCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR765094, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9860 Culex pipiens water mite diet isolate 9860-BHL040517-GBD6332_25467-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGTTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTTCTCATGCTTTTATTATAA-TTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTCTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACCACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9861 Cryptochironomus sp. water mite diet isolate 9861-BHL040517-GBD27152_22579-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTAATTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTCATGGTTATACCAATTTTAATTGGAGGATTCGGAAATTGATTAGTACCTTTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTACCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR271921, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9862 Chironominae sp. water mite diet isolate 9862-BHL040517-GBD5131_14433-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACATTATGTTTTATTTTTGGAGCTTGATCTGGTATAGTAGGTACTTCTTTAAGTATGCTAATACGAGCAGAACTTGGACGACCTGGTACTTTTATTGGAGATGACCAAATTTACAATGTAATTGTCACAGCACACGCTTTTATTATAATTTTTTTTTATAGTTATGCCAATTTTAATTGGAGGTTTTGGAAATTGACTTATTCCTTTAATGTTAGGAGCCCCAGATATGGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTTCCCCCTTCATTAACTCTTTTACTTTCAAGTTCTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KR274046, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL9863 Amphichaeta sp. water mite diet isolate 9863-BHL040517-GBD3733_15185-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGAATATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTATTATTACCATTTTTTATTGGAGGAGTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGCAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL9864 Chironomidae sp. water mite diet isolate 9864-BHL040517-GBD19833_14485-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATTAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGGAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.8% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9865 Paratanytarsus sp. water mite diet isolate 9865-BHL040517-GBD22666_23423-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTTGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGACTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9866 Amphichaeta raptisae water mite diet isolate 9866-BHL040517-GBD19446_25338-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATCCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTTTATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCCATCACTAATTCTATTAGTAGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.3% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL9867 Chironomus sp. water mite diet isolate 9867-BHL040517-GBD28050_19024-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCCGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCACTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9868 Chironomus riparius water mite diet isolate 9868-BHL040517-GBD18264_6706-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGTGGCTTGTTCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTATCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCATTCATAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9869 Lebertia quinquemaculosa water mite diet isolate 9869-BHL040517-GBD6736_19667-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATACTTCGCTTTTGGGGCTTGATCAGGAATGGTGGGAGCAAGACTAAGAACTTTAATCCGTTTAGAATTAGGACAACCAGGAACTCTCCTAGGAAGAGACCAAATTTATAATACTATCGTAACAGCTCACGCCTTCGTTATAATTTTCTTTATAGTTATGCCAATAATAATTGGAGGATTCGGAAATTGACTAGTCCCATTGATGATTAGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGACTTTTACCCCCCCTCTTTAACTCTTCTACTATCTAGTTCTTTCACAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.5% identical to accession ID MG811666, identified in GenBank as Lebertia quinquemaculosa. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9870 Paratanytarsus sp. water mite diet isolate 9870-BHL040517-GBD15316_24364-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGGACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR757714, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9871 Dicrotendipes sp. water mite diet isolate 9871-BHL040517-GBD10463_24551-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCGGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.8% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9872 Paratanytarsus sp. water mite diet isolate 9872-BHL040517-GBD15739_18315-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTCATTTTCGGTGTCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGCACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTACTTCCCCCCTCTTTAACCCTTTTACTATCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL9873 Chironomus sp. water mite diet isolate 9873-BHL040517-GBD25919_23155-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTGATTGGAGGATTTGGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCATCTTTAACTCCTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.0% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9874 Chironomidae sp. water mite diet isolate 9874-BHL040517-GBD6802_21516-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTATATTTTATTTTTGGCGCCTGATCTGGGATAATCGGGACTTCTCTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGTGACGACCAAATTTATAACGTAATTGTTACAGCCCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTTTAATTGGAGGATTTGGGAATTGATTGGTCCCTCTTATATTAGGAGCCCCAGACATAGCTTTCCCCCGTATAAATAATATAAGTTTTTGGCTTTTTACCCCCGTCATTAACTTTACTTCTTTCTAGTTCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KM994761, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9875 Chironominae sp. water mite diet isolate 9875-BHL040517-GBD12234_14228-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTCGGTGCCTGATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR285570, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9876 Diptera sp. water mite diet isolate 9876-BHL040517-GBD11469_4964-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCACATGCATTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCATTAACCTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.5% identical to accession ID MF381678, identified in GenBank as Anopheles eiseni geometricus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9877 Chironomus sp. water mite diet isolate 9877-BHL040517-GBD7289_12060-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCCTAATACTTGGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9878 Culex sp. water mite diet isolate 9878-BHL040517-GBD2372_18313-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 90.4% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9880 Chironomidae sp. water mite diet isolate 9880-BHL040517-GBD23342_24153-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCA--TCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.4% identical to accession ID KR272544, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9881 Chironomidae sp. water mite diet isolate 9881-BHL040517-GBD2668_17797-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTTATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAAGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCCTTTCCGCGAAAAAAAAAAATAAGAATTTGATTATTACCCCCCTTCATTAACCTTGCTTTTATCAAAATCAATAGTAGAAAATGGAGCTGGAACAG	Using NCBI BLASTN in June 2018, this sequence was 96.3% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9883 Chironomus riparius water mite diet isolate 9883-BHL040517-GBD24011_22209-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGAGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTTTAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGATTTGTCCCCCTAATACTTGGATCACCTGACATAGCCTTTCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCCCTCTCTTACTCTTCCTCTTTCTAGTTCTTTCCTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.7% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9884 Culex sp. water mite diet isolate 9884-BHL040517-GBD20267_12032-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCGTAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGTCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAATAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.8% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL9885 Chironomus sp. water mite diet isolate 9885-BHL040517-GBD25041_8599-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAGTTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGCTTTTGACTTCTCCCCCCATCTTTAACTCCTCTTCTTTCTAATTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9886 Culex sp. water mite diet isolate 9886-BHL040517-GBD25372_6843-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGAATATTGGAACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGGACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATAGGGTCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9887 Oligochaeta sp. water mite diet isolate 9887-BHL040517-GBD19784_7127-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCA--AGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.5% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL9888 Dicrotendipes sp. water mite diet isolate 9888-BHL040517-GBD28852_12529-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTGGGAAATTGATCAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9889 Paratanytarsus sp. water mite diet isolate 9889-BHL040517-GBD21502_20526-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTAATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTCTCCTCGAATAAATAATATAAGATTTTGACTTCTCCCCCCCCATCTTTAACTCCTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9891 Chironomidae sp. water mite diet isolate 9891-BHL040517-GBD13329_7397-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATCAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTGATACCTATTTTAATTGGAGGCTTTGGAAATTGATTAGTACCTTTGATATTAGGGGCTCCTGATATAGCTTTTCCGCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCCTCTTTAAC---TCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID KJ209369, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9893 Paratanytarsus sp. water mite diet isolate 9893-BHL040517-GBD28530_17284-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCACCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACCTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.9% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9894 Dicrotendipes sp. water mite diet isolate 9894-BHL040517-GBD11703_5833-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTACACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTTCAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTTTTACCCCCACCTCTCTTACTCTTCTTCTTCCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9895 Chironominae sp. water mite diet isolate 9895-BHL040517-GBD12896_26935-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCAGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGTTTTTGATTATTACCTCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID KR765094, identified in GenBank as Chironominae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9896 Paratanytarsus sp. water mite diet isolate 9896-BHL040517-GBD18494_24335-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCCCGAATAAATAATATAAGATTTTGACTTTTGCCCCCATCCTTGACTCGTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID KR294834, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL9897 Oligochaeta sp. water mite diet isolate 9897-BHL040517-GBD4317_7339-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial CAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAATTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 86.5% identical to accession ID KF952300, identified in GenBank as Chaetogaster limnaei. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL9902 Paratanytarsus sp. water mite diet isolate 9902-BHL040517-GBD9762_20182-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACTTTATATTTTATTTTTGGAGCTTGATCGGGAATAGTAGGCACTTCTTTAAGAATTTTAATTCGACTAGAATTAGGACACCCAGGCTCATTAATCGGAGACGATTAAATTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCATTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID KM905578, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9903 Chironomus sp. water mite diet isolate 9903-BHL040517-GBD21105_11178-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AAAGATATTGGTTCATTATACTTCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTTAGAATATTAATTCGAGCAGAATTAGGACGTCCTGGAACATTTATTGGTGATGACCAAATTTATAATGTAATAGTTACAGCTCACGCATTTATTATAATTTTCTTTATAGTTATACCAATTTTAATTGGAGGTTTCGGAAATTGACTTGTCCCTTTAATATTAGGAGCTCCAGATATGGCCTTCCCTCGAATAAATAATATAAGTTTTTGACTTCTCCCCCCCATCTTTAACTCTTCTTCTTTCTAGTTCATTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.5% identical to accession ID KP954640, identified in GenBank as Chironomus crassicaudatus. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9904 Paratanytarsus sp. water mite diet isolate 9904-BHL040517-GBD21386_3394-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGATCATTATACTTTATTTTCGGTGCCTGATCCGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTACCCCCTTCATTAAC---CTTACTTTTATCAAGATCAATAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.0% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9906 Culex sp. water mite diet isolate 9906-BHL040517-GBD14889_16194-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGTTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.6% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9908 Chironomus riparius water mite diet isolate 9908-BHL040517-GBD2500_16383-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCAGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACATTTACCCCCCCATCTTTAACTCTACTTCTTTCTAGTCCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9909 Chironomidae sp. water mite diet isolate 9909-BHL040517-GBD8864_12414-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTGTACATTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCATATGCTTTTATTATAATTTTTTTCATAGTTATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTC-TATTAGTTGTATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 88.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9912 Paratanytarsus sp. water mite diet isolate 9912-BHL040517-GBD14720_12230-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTTCATTATACTTCATTTTCGGTGCCTAATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 94.5% identical to accession ID KR292109, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9913 Chironomidae sp. water mite diet isolate 9913-BHL040517-GBD23888_21694-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GTACATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTTATACCAATTTTAATTGGAGGATTTGGTAATTGACTCTTGCCATTAATACTAGGAGCCCCAGATATAGCCTTTCCTCGAATAAATAAAATAAGTTTTTGACTTCTTCCCCCCTCTTTAAATCTTTTACTTTCAAGTAGAATAGTGGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.9% identical to accession ID KR285164, identified in GenBank as Chironomidae sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9916 Paratanytarsus sp. water mite diet isolate 9916-BHL040517-GBD25003_18484-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTCATTATACTCCATTTTTGGTGCCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCTGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCATTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTATTACCTCCATCTCTAACATTATTACTTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.1% identical to accession ID KR277530, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL9917 Chironomus riparius water mite diet isolate 9917-BHL040517-GBD13605_6609-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTAGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTCATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATCCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGTCATAGCTTTTCCTCGAATAAATGATATAAGTTTCTGACTTTTACCCCCCCCTCTCTTACTCTTCTTCTTTCTAATTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9923 Amphichaeta raptisae water mite diet isolate 9923-BHL040517-GBD2231_18889-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAAAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTCTTAATAATACCAGTTTTTATTGGAGGATTTGGAAATTGATTTTTACCTTTAATATTTGGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.6% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL9926 Chironomus sp. water mite diet isolate 9926-BHL040517-GBD11532_25285-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACCCTTTATACATTATTTTTGGGGCTTGATCCGGAATAGTAGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCTGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.5% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9928 Amphichaeta sp. water mite diet isolate 9928-BHL040517-GBD22481_5052-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTCTGACTACTACCACCTTCACTAATCCTATTAGTTTCTTCTGCTGCCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL9929 Lepidoptera sp. water mite diet isolate 9929-BHL040517-GBD20029_11138-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGCACTCTATACTTAATCTTAGGAGTTTGAGCTGGAATAACTGGAACAGGAACTAGAATATTAATTCGGATTGAATTATCTCAACCAGGATCATTCCTAGGAAGAGATCAACTATATAATACTCTAGTAACTGCACATGCATTCCTAATAATTTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.0% identical to accession ID KM576860, identified in GenBank as Glyphodes pyloalis. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9931 Dicrotendipes sp. water mite diet isolate 9931-BHL040517-GBD10654_28290-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCGTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9933 Chironomus riparius water mite diet isolate 9933-BHL040517-GBD23745_12445-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTGGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGGCTTGTCCCCCTAATACTTGGAGCACCTGACATAGTTTTTCCTCGAATAATTAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9934 Amphichaeta sp. water mite diet isolate 9934-BHL040517-GBD19627_19375-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGATCAAGACTATTAATTCGTCTTGAATTAACCCATCCTGGCGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAAATTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTGATACTTGGGGCACCTGATATAGCATTCCCACGAATAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCATCGGCAGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.7% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL9936 Chironomus riparius water mite diet isolate 9936-BHL040517-GBD10381_12942-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTTGAGCAGAATTAGGACAACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTTTTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTGGGAAACTGATTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9937 Paratanytarsus sp. water mite diet isolate 9937-BHL040517-GBD15053_22394-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTAATCAGGAATAGTGGGAACTTCCTTAAGAATATTAATTCGAGTTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTGATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTAGTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGG	Using NCBI BLASTN in June 2018, this sequence was 97.5% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL9939 Chironomus riparius water mite diet isolate 9939-BHL040517-GBD24930_18379-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGTTCATTATACATTATTTTTGGGGCTTGATCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAACATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTCTCTAATTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9940 Paratanytarsus sp. water mite diet isolate 9940-BHL040517-GBD14912_24951-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGTCTGATCAGGAATAGTAGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTGCCCCCATCCTTGACTCTTCTTCTTTCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.2% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9942 Paratanytarsus sp. water mite diet isolate 9942-BHL040517-GBD20200_14296-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACTTTATTTTTGGGGCTTGATCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTATTTGTTACAGCTCATGCTTTTTTTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTACTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 93.1% identical to accession ID KR280756, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9946 Diptera sp. water mite diet isolate 9946-BHL040517-GBD4128_21035-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTGGAATAGTTGGAACTTCTTTAAGTTTACTAATTCGAGCAGAATTAAGTCAACCAGGTGTATTTATTGGAAATGATCAAATTTATAATGTTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 89.5% identical to accession ID JQ958370, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9951 Paratanytarsus sp. water mite diet isolate 9951-BHL040517-GBD13037_23562-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACTTCATTTTCGGTGCCTAATCAGGAATAGTGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTCATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTATTATTAGGAGCCCCAGATATAGCCTCTCCTCGAAAAAATAAAATAAGATTTTGACTTCTTCCCCCCTCCTTAACTCTTTTACTTTCAAGGAGAATAGTGGAAAATGGAACTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 96.4% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9954 Dicrotendipes sp. water mite diet isolate 9954-BHL040517-GBD23101_24671-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACACTATATTTTATTTTTGGAGCTTGATCAGGGATATTAGGAACCTCATTAAGTATATTATTTCGAGCAGAATTAGGACGACCAGGAACTTTTATTGGAGACGACCAAATTTATAATGTAATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCCTTTAATATTAGGAGCCCCCGATATAGCTTTCCCGCGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.4% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9959 Oligochaeta sp. water mite diet isolate 9959-BHL040517-GBD20917_13020-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTAGGAGTATGAGCAGGAATAGTTGGTACAGGAACAAGACTATTAATTCGTATTGAATTAACCCATCCTGGAGCCTTTTTAGGAAGAGACCAACTATATAATACCTTAGTTACTGCACATGCATTTTTAATAATTTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTAACCCTTCTTCTTTCTAGATCAATT---GTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 87.9% identical to accession ID AF534829, identified in GenBank as Amphichaeta raptisae. For oligochaetes, the % identity was used to identify this accession's name according to the following: >=92.0%, species; 90.0-91.9%, only to genus; 80 - 89.9%, only as oligochaeta. Matches <80% not used.
>RL9962 Chironomus riparius water mite diet isolate 9962-BHL040517-GBD23548_14691-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTCTTGGGGCTTGATCCGGAATAGTGGTAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGACCCGGAACTTTCATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTTGAGCGCCTGACATAGCTTTTCCTCGAATAAATAATATAAGGTTCTGACTTTTACCCCCCTCTCTTACTCTTCTACTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAAC	Using NCBI BLASTN in June 2018, this sequence was 97.9% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9967 Chironomus riparius water mite diet isolate 9967-BHL040517-GBD13262_27281-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGCACTTTATACATTATTTTTGGGGCTTGCTCCGGAATAATGGGAACTTCATTAAGAATGCTTATTCGAGCAGAATTAGGACGCCCCGAAACTTTTATTGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTACTTCTTTCTAGTTCTTTCGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9971 Cryptochironomus sp. water mite diet isolate 9971-BHL040517-GBD10624_22265-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial AACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGAACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACTACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTTGGAAATTGATTAGTACCTCTTATACTGGGAGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTGTTGCCCCCATCCTTGACTCTACTTCTATCAAGATCAATTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 91.2% identical to accession ID KJ207490, identified in GenBank as Cryptochironomus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.

>RL9978 Paratanytarsus sp. water mite diet isolate 9978-BHL040517-GBD10419_4497-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TTGGTTCATTATACGTCATTTTCGTTGCCTAATCAGGAATAGGGGGAACTTCCCTAAGAATATTAATTCGAGCTGAACTAGGACATCCCGGAACTTTTATTGGAGATGACCAAATTTATAATGTAATTGTTACAGCTTATGCATTTATTATAATTTTTTTCATAGTTATACCTATTTTAATTGGAGGATTTGGGAACTGATTATTGCCTTTAATATTAGGAGCCCCAGATATAGCTTCTCCTCGAATAAATAATATAAGATTTTGACTTCTTCCCCCCTCTTTAACTCTTTTGCTTTCAAGTAGAATAGTGGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.0% identical to accession ID KR281451, identified in GenBank as Paratanytarsus sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9981 Chydorus brevilabris water mite diet isolate 9981-BHL040517-GBD11360_27090-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TACTCTTTATTTTCTATTTGGAATTTGAGCTGGAATAGTGGGCACTGCTCTTAGCCTGTTAATTCGAGCAGAATTAGGACAAAGAGGGACCCTTATTGGAGATGATCAAATTTACAATGTTATTGTCACTGCACATGCTTTTGTTATAATTTTTTTTATAGTTATACCCATCATAATTGGGGGGGTTTGGAAACTGACTTGTCCCCCTAATATTAGGGGCACCTGATATAGCCTTCCCTCGTCTTAATAATTTAAGTTTCTGGCTTCTTCCCCCAGCTTTAACCCTACTTTTAGTAGGGGGGGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 98.2% identical to accession ID MG450056, identified in GenBank as Chydorus brevilabris. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9986 Dicrotendipes sp. water mite diet isolate 9986-BHL040517-GBD10799_22287-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ACTCTTTACTTTATTTTTGGAGCTTGATCTGGAATAGTAGGGACTTCCTTAAGTATACTTATTCGAGCCGAATTAGGACGACCCTGGACATTTATTTGAGATGATCAAATTTACAATGTAATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTTATGGTTATACCTATTCTAATTGGAGGATTCGGAAATTGATTAGTCCATTTAATATTAGGAGCCCCCGATATAGCTTTCCCACGAATAAATAATATAAGTTTCTGACTATTACCTCCTTCTCTATCCCTGCTTCTTTCTAGATCAATTGTATAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 95.7% identical to accession ID KR767252, identified in GenBank as Dicrotendipes sp. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9987 Culex sp. water mite diet isolate 9987-BHL040517-GBD18350_13717-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial GGTCAACAAATCATAAAGATATTGGTTCATTATATTTTATTTTTGGAGCCTGATCAGGAATAGTTGGAACTTCCTTAAGAATATTAATTCGAGCTGAATTAGGACATCCTGGTACTTTTATTGGAGATGATCAAATTTATAATGTAATTGTTACTGCACATGCTTTCATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATGTTAGGAGCTCCAGATATGGCCTTTCCTCGAATAAATAATATAAGTTTTTGAATACTACCTCCTTCATTGACACTACTACTTTCAAGTAGTTTAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 92.4% identical to accession ID LC090051, identified in GenBank as Culex pipiens. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9991 Lepidoptera sp. water mite diet isolate 9991-BHL040517-GBD15724_6373-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial TCAACAAATCATAAAGATATTGGAACCCTTTACTTTATTTTTGGAGCTTGATCTGGAATAATAGGAACTTCCTTAAGTATACTTATTCGAGCCGAGTTAGGACGACCCGGGACATTTATTGGAGATGATCAAATCTACAATGTAATCGTTACAGCTCATGCTTTTATTATAATTTTTTTTCTTAGTAATACCAGTTTTTATTGGAGGATTTGGAAATTGAATTCTACCTTTAATACTTGGGGCACCTGATATAGCATTCCCACGATTAAATAATATAAGATTTTGACTATTACCCCCATCACTAATTCTATTAGTTGCA--TCGGCTGCAGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 84.4% identical to accession ID AY488857, identified in GenBank as Tegeticula yuccasella. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.
>RL9999 Chironomus riparius water mite diet isolate 9999-BHL040517-GBD16388_6300-2Lq58 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial ATTGGAACTTTATACATTATTTTTTGGGGCTTGAGCCGGAATAGTGGGAACTTCATTAAGAATGCTTATTTGAGCAGAATGAGGACGACCCTGAACTTTCATAGGAGATGACCAAATTTATAATGTTGTAGTTACTGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTTTAATTGGAGGATTCGGAAACTGACTTGTCCCCCTAATACTTGGAGCACCTGACATAGCTTTTCCTCGAATAAATAATATAAGTTTCTGACTTTTACCCCCCTCTCTTACTCTTCTTCTTTCTAGTTCTTTTGTAGAAAATGGAGCTGGAACAGG	Using NCBI BLASTN in June 2018, this sequence was 97.3% identical to accession ID KR657116, identified in GenBank as Chironomus riparius. The % identity was used to identify this accession's name according to the following: >=96.5%, species; 90.0-96.4% only to genus; 80 - 89.9%, family or higher taxon. Matches <80%, not used.